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Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
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	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>4498</u>	AA Sequence (#) <u>10</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>6/21/02</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>6/21/02</u>	Litigation _____	Lexis/Nexis _____
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Online Time: <u>15</u>	Other _____	Other (specify) _____

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:00:24 ; Search time 48.19 Seconds
(without alignments)
88.382 Million cell updates/sec

Title: US-09-674-857-6

Perfect score: 585

Sequence: 1 APELLGGPSVFLPPPKPDT.....CKVSNKALPAPIETISKTK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	568	97.1	330	1 GC1_HUMAN	P01857 homo sapien
2	565	96.6	290	1 GC3_HUMAN	P01860 homo sapien
3	541	92.5	327	1 GC4_HUMAN	P01861 homo sapien
4	540	92.3	326	1 GC2_HUMAN	P01859 homo sapien
5	460	78.6	333	1 GCB_RAT	P20761 rattus norv
6	458	78.3	329	1 GC2_CAVPO	P01862 cavia porce
7	450	76.9	323	1 GC_RABIT	P22436 mus musculu
8	437	74.7	329	1 GC3_MOUSE	P01870 oryctolagus
9	437	74.7	398	1 GC3_MOUSE	P03987 mus musculu
10	422.5	72.2	324	1 GC1_MOUSE	P01868 mus musculu
11	422.5	72.2	393	1 GC1_MOUSE	P01869 mus musculu
12	418	71.5	335	1 GCAB_MOUSE	P01864 mus musculu
13	415	70.9	330	1 GCAA_MOUSE	P01863 mus musculu
14	415	70.9	399	1 GCAM_MOUSE	P01865 mus musculu
15	410	70.1	329	1 GCC_RAT	P20762 rattus norv
16	408	69.7	336	1 GCB_MOUSE	P01866 mus musculu
17	408	69.7	405	1 GCMB_MOUSE	P01867 mus musculu
18	392	67.0	326	1 GC1_RAT	P20759 rattus norv
19	353	60.3	322	1 GCA_RAT	P20760 rattus norv
20	169.5	29.0	428	1 EPC_HUMAN	P01854 homo sapien
21	155	26.5	429	1 EPC_RAT	P01855 rattus norv
22	155	26.5	457	1 MUC_SUNMU	P20768 suncus muri
23	147	25.1	421	1 EPC_MOUSE	P06336 mus musculu
24	144	24.6	454	1 MUC_HUMAN	P01871 homo sapien
25	142	24.3	391	1 MUCB_HUMAN	P04220 homo sapien
26	135	23.1	454	1 MUC_MESAU	P06337 mesocricetu
27	135	23.1	455	1 MUC_MOUSE	P01872 mus musculu
28	135	23.1	476	1 MUC_MOUSE	P01873 mus musculu
29	128.5	22.0	340	1 ALC2_HUMAN	P01877 homo sapien
30	128.5	22.0	353	1 ALC1_GORGO	P20758 gorilla gor
31	128.5	22.0	353	1 ALC1_HUMAN	P01876 homo sapien
32	128	21.9	106	1 KAC_HUMAN	P01834 homo sapien
33	124.5	21.3	299	1 ALC_RABIT	P01879 oryctolagus

ALIGNMENTS

RESULT 1

ID	GC1_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	IGHG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RT	acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RT	acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RX	SEQUENCE (MYELOMA PROTEIN NIE).			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a			
RT	monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The			
RT	chymotryptic peptides of the H-chain, alignment of the tryptic			
RT	peptides and discussion of the complete structure.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary			
RT	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

34	124	21.2	458	1 MUC_RABIT	P03988 oryctolagus
35	124	21.2	479	1 MUCM_RABIT	P04221 oryctolagus
36	123	21.0	450	1 MUC_CANFA	P01874 canis famil
37	120.5	20.6	370	1 HVC1_HETFR	P23084 heterodontu
38	115.5	19.7	393	1 HVC3_HETFR	P23086 heterodontu
39	115.5	19.7	438	1 HVC2_HETFR	P23085 heterodontu
40	110.5	18.9	344	1 ALC_MOUSE	P01878 mus musculu
41	110.5	18.9	438	1 HVCS_HETFR	P23087 heterodontu
42	110.5	18.9	461	1 HVCML_HETFR	P23088 heterodontu
43	109	18.6	103	1 LAC_CHICK	P20763 gallus gall
44	108	18.5	106	1 KAC_MOUSE	P01837 mus musculu
45	104.5	17.9	446	1 MUC_CHICK	P01875 gallus gall

RP REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC).
RX MEDLINE=77021516; PubMed=823945;
RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
RT Structure of the Fc fragment of immunoglobulin G3.";
RN Biochem. Biophys. Res. Commun. 71:907-914(1976).
RL [4]
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX MEDLINE=82247835; PubMed=6808505;
RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA Franklin E.C., Hood L., Buxbaum J.N.;
RT "Gamma Heavy chain disease in man: cDNA sequence supports partial
RT gene deletion model";
RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC -1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
CC INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
CC NORMALLY PRESENT IN THE HINGE REGION.
CC -1- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
CC REP.2.
CC -1- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
CC AND ALL OF THE CHI REGION.
CC -1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
CC OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
CC GAMMA-3 HEAVY CHAINS.
CC -1- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
CC OR ANOTHER GAMMA CHAIN SUBCLASS.
CC -1- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
CC TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
CC IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
CC SEGMENT (12-28).
CC -----
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CC -----
DR EMBL; J00231; AAA52805.1; ALT_SEQ.
DR PIR; A02149; G3HUM1.
DR HSP; P01857; 1FC1.
DR MIM; 147120; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.
FT DOMAIN 12 73
FT HINGE.
FT DOMAIN 74 183
FT CH2.
FT DOMAIN 184 289
FT CH3.
FT REPEAT 29 43
FT REPEAT 44 58
FT REPEAT 59 73
FT MOD_RES 1 1
FT CARBOHYD 6 6
FT N-LINKED (GLCNAC. . .).
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 7 7
FT DISULFID 24 24
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 27 27
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 33 33
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 39 39
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 42 42
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 48 48
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 54 54
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 57 57
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 63 63
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 69 69
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 72 72
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT CARBOHYD 140 140
FT N-LINKED (GLCNAC. . .).

FT	MOD_RES	290	290	REMOVED POST-TRANSLATIONALLY.
FT	VARIANT	126	127	QV -> EB (IN ZUC).
FT				/FTIG-VAR_003890.
FT	VARIANT	134	134	P -> L (IN OMM).
FT				/FTIG-VAR_003891.
FT	VARIANT	139	139	F -> Y (IN OMM).
FT				/FTIG-VAR_003892.
FT	VARIANT	182	182	T -> A (IN OMM).
FT				/FTIG-VAR_003893.
FT	VARIANT	227	227	S -> N (IN OMM).
FT				/FTIG-VAR_003894.
FT	VARIANT	227	227	MISSING (IN ZUC).
FT				/FTIG-VAR_003895.
FT	VARIANT	279	279	F -> Y (IN OMM).
FT				/FTIG-VAR_003896.
FT	SEQUENCE	290 AA; 32331 MW; E69CBC95705B2F46	CRC64;	
SQ				

Query Match 96.6%; Score 565; DB 1; Length 290;
Best Local Similarity 95.5%; Pred. No. 7.1e-51;
Matches 105; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVVHNAKTK 60
|||||
Db 74 APELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVVHNAKTK 133
|||||

QY 61 PREEQNSTFRVSVTLVHQDLNKGKEYCKVSNKALPAPIETISKTK 110
|||||
Db 134 PREQQNSTFRVSVTLVHQDLNKGKEYCKVSNKALPAPIETISKTK 183
|||||

RESULT 3
GC4_HUMAN STANDARD; PRT; 327 AA.
ID AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-4 chain C region.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207360; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
CC -----
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CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; G4HU.
DR HSP; P01842; 7FAB.
DR MIM; 147130; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig_like.

The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.";
 J. Immunol. 125:1048-1054(1980).
 [5] SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 MEDLINE=80001357; PubMed=113060;
 Connell G.E., Parr D.M., Hofmann T.;
 "The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";
 Can. J. Biochem. 57:758-767(1979).
 [6] SEQUENCE OF 238-275 (ZIE).
 MEDLINE=80114419; PubMed=118920;
 Hofmann T., Parr D.M.;
 "A note of the amino acid sequence of residues 381-391 of human immunoglobulin gamma chains.";
 Mol. Immunol. 16:923-925(1979).
 [7] REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 Hofmann T., Parr D.M.;
 Submitted (MAR-1980) to the PIR data bank.
 [8] SEQUENCE OF 1-121 (DOT).
 MEDLINE=95255298; PubMed=7737190;
 Stoppani M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 "Characterization of the two unique human anti-flavin monoclonal immunoglobulins.";
 Eur. J. Biochem. 228:886-893(1995).
 [9] DISULFIDE BONDS.
 MEDLINE=72033500; PubMed=4940472;
 Milstein C., Frangione B.;
 "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 Biochem. J. 121:217-225(1971).
 [10] DISULFIDE BONDS.
 MEDLINE=69064124; PubMed=5782707;
 Frangione B., Milstein C., Pink J.R.L.;
 "Structural studies of immunoglobulin G.";
 Nature 221:145-148(1969).

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 EMBL: J00230; AAB59393.1; -
 PIR: A02148; G2HU.
 HSP: P01857; 1FC1.
 MM: 147110; -
 InterPro: IPR003006; Ig_MHC.
 InterPro: IPR003597; Ig_C1.
 InterPro: IPR003600; Ig_Like.
 Pfam: PF00047; Ig; 3.
 SMART: SM00410; Ig_Like; 1.
 SMART: SM00407; IGCL; 2.
 PROSITE: PS00290; IG_MHC; 2.
 Immunoglobulin domain; Immunoglobulin C region.
 NON_TER 1 98
 DOMAIN 1 98
 HINGE 99 110
 DOMAIN 111 219
 CH2 111 219
 DOMAIN 220 326
 CH3 220 326
 INTERCHAIN (WITH A LIGHT CHAIN). 14 14
 DISULFID 27 83
 DISULFID 102 102
 DISULFID 103 103
 DISULFID 106 106
 DISULFID 109 109
 DISULFID 140 200
 DISULFID 140 200

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FT DISULFID 246 304
FT SITE 156 156
FT MOD_RES 326 326
FT VARIANT 60 60
FT CONFLICT 109 109
SQ SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;

Query Match 92.3%; Score 540; DB 1; Length 326;
Best Local Similarity 94.3%; Pred. NO. 3e-48;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 LGPSVFLPPPKKDTLMISRPETCVVVDVSHEDPEVQFKYVGVYVHNAKTKPRE 64
Db 114 VAGPSVFLPPPKKDTLMISRPETCVVVDVSHEDPEVQFKYVGVYVHNAKTKPRE 173

QY 65 QYNSFRVSVLTVLHQDLNCKEYKCKVSNKALPAPIEKTISKTK 110
Db 174 QYNSFRVSVLTVLHQDLNCKEYKCKVSNKGLPAPIEKTISKTK 219

RESULT 5
GCB_RAT
ID GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 78.6%; Score 460; DB 1; Length 333;
Best Local Similarity 75.2%; Pred. NO. 5e-40;
Matches 82; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

QY 2 PELGGPSVFLPPPKKDTLMISRPETCVVVDVSHEDPEVQFKYVGVYVHNAKTKP 61
Db 118 PELGGPSVFLPPPKKDTLMISRPETCVVVDVSHEDPEVQFKYVGVYVHNAKTKP 177

QY 62 REEQNSTFRVSVLTVLHQDLNCKEYKCKVSNKALPAPIEKTISKTK 110
Db 178 REEQNSTFRVSVLTVLHQDLNCKEYKCKVSNKALPAPIEKTISKTK 226
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RESULT 6
GCB_RAT
ID GCB_RAT STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshtein B.K., Hussain O.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). 3. Amino acid sequence of the region around the half-cystine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2 antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2 antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC 1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSP; P01772; 2F84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
```

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FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 78.38; Score 458; DB 1; Length 329;
Best Local Similarity 78.98; Pred. No. 7.9e-40;
Matches 86; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 2 PELGGPSVFLEPPPKDITLMSITPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNATKTP 61
DB 113 PENLGGPSVFLEPPPKDITLMSITPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNATKTP 172

QY 62 REEQNSTFRVSVLTVLHQQDLNGKCKYKSNKALPAPIEKTISKTK 110
DB 173 RVEQNTTFRVSVLTVLHQQDLNGKCKYKSNKALPAPIEKTISKTK 221

RESULT 7
GC_RABBIT
ID GC_RABBIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8403030; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RL F-1 haplotype.";
RN [2]
RP Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RL immunoglobulin G of different allotype.";
RN [3]
RP Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RL heavy chain and identification of two genomic C gamma genes.";
RN [4]
RP Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RL immunoglobulin G.";
RN [5]
RP Biochem. J. 116:249-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (In) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER.
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC MARKERS AND REF.5 THE E15 MARKER.
CC
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CC
CC EMBL; M16426; AAA31289.1; -.
CC PIR; A02161; GHRB.
CC HSP; P01857; 1FC1.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig_cl.
CC Pfam; PF00047; ig; 3.
CC SMART; SM00407; Igcl; 2.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 76.98; Score 450; DB 1; Length 323;
Best Local Similarity 75.28; Pred. No. 5.2e-39;
Matches 82; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 2 PELGGPSVFLEPPPKDITLMSITPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNATKTP 61
DB 108 PELGGPSVFLEPPPKDITLMSITPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNATKTP 167

QY 62 REEQNSTFRVSVLTVLHQQDLNGKCKYKSNKALPAPIEKTISKTK 110
DB 168 REEQNSTFRVSVLTVLHQQDLNGKCKYKSNKALPAPIEKTISKTK 216

RESULT 8
GC3_MOUSE
ID GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
CC
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DR EMBL; J00451; -, NOT_ANNOTATED_CDS.
DR PIR; B02156; G3MSC.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG-like; 1.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00410; IG-like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 98 113 CH1.
FT DOMAIN 114 223 HINGE.
FT DOMAIN 224 327 CH2.
FT DOMAIN 328 333 CH3.
FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 329 AA; 36222 MW; F45827171A182BAD6 CRC64;

Query Match 74.7%; Score 437; DB 1; Length 329;
Best Local Similarity 73.8%; Pred. No. 1.le-37;
Matches 79; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 4 ILGGSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKWYVDGVEVHNKTPRE 63
Db 116 ILGGSVFIFFPKPKDALMISLTPKVTCCVVVDSEDDPDVHVSFWFDNKEVHTAQPRE 175

QY 64 EQYNSTFRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKTK 110
Db 176 AQYNSTFRVSVLPIQHDWNRGKFKCKVNNKALPAPIERTISKPK 222

RESULT 9
GC3M_MOUSE
ID GC3M_MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=8401483; PubMed=6314258;
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
CC -----
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CC -----
DR EMBL; J00451; AAB59655.1; -.
DR EMBL; V01526; CAA24767.1; ALT_SEQ.
DR PIR; A02155; G3MSM.
DR HSSP; P01857; 1FC1.
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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG-like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 98 113 CH1.
FT DOMAIN 114 223 HINGE.
FT DOMAIN 224 327 CH2.
FT DOMAIN 328 333 CH3.
FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 74.7%; Score 437; DB 1; Length 398;
Best Local Similarity 73.8%; Pred. No. 1.4e-37;
Matches 79; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 4 ILGGSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKWYVDGVEVHNKTPRE 63
Db 116 ILGGSVFIFFPKPKDALMISLTPKVTCCVVVDSEDDPDVHVSFWFDNKEVHTAQPRE 175

QY 64 EQYNSTFRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKTK 110
Db 176 AQYNSTFRVSVLPIQHDWNRGKFKCKVNNKALPAPIERTISKPK 222

RESULT 10
GC1_MOUSE
ID GC1_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salsler W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=78242288; PubMed=98524;
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[illegible]

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EMBL; J00471; AAB59661.1; ALT_INIT.
PIR; A02152; G2MSA.
HSP; P01842; 7EAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003600; Ig-like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; Ig-like; 1.
SMART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
NON_TER 1
DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 144 204
DISULFID 250 308
MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 70.9%; Score 415; DB 1; Length 330;
Best Local Similarity 69.1%; Pred. No. 2.1e-35;
Matches 76; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

1 APELLGSPVFLPPKPKDTLMSRTPEVTCVVVDVSHEDPEVQFKWYDGVVHNAKT 60
114 APNLGSPVFIIPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISFVNNVEVHTAQ 173
61 PREQYNSTFRVSVTLVLDHQLNGKEYKCKVSNKALPAPIETISKTK 110
174 THREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKDLPAPIERTISKPK 223

RESULT 14
GCAM_MOUSE STANDARD; PRT; 399 AA.
AC P01865;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82222190; PubMed=6283537;
RA Yanawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF THE A ALLELE.

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EMBL; J00471; AAB59661.1; ALT_INIT.
PIR; A02154; G2MSAM.
HSP; P01857; IFCL.
MGD; MGI:96443; Igh-1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003600; Ig-like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; Ig-like; 1.
SMART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
NON_TER 1
DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 144 204
DISULFID 250 308
DISULFID 346 363
TRANSMEM 364 399
DOMAIN 180 180 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 180 180
SEQUENCE 399 AA; 44020 MW; 4C38138BEAED3FF0 CRC64;

Query Match 70.9%; Score 415; DB 1; Length 399;
Best Local Similarity 69.1%; Pred. No. 2.6e-35;
Matches 76; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

1 APELLGSPVFLPPKPKDTLMSRTPEVTCVVVDVSHEDPEVQFKWYDGVVHNAKT 60
114 APNLGSPVFIIPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISFVNNVEVHTAQ 173
61 PREQYNSTFRVSVTLVLDHQLNGKEYKCKVSNKALPAPIETISKTK 110
174 THREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKDLPAPIERTISKPK 223

RESULT 15
GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT "Sequencing of a rat immunoglobulin gamma 2c heavy chain constant region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).

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EMBL; X07189; CAA30169.1; -.
PIR; S00847; S00847.

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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:59:31 ; Search time 176.89 Seconds

(without alignments)
107.578 Million cell updates/sec

Title: US-09-674-857-6
Perfect score: 585
Sequence: 1 APELLGGPSVFLPPPKPDKT.....CKVSNKALPAPIEKTISKTK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	568	97.1	701	4 Q96PQ8	Q96pq8 homo sapien
2	474	81.0	337	6 Q95M34	Q95m34 equus cabal
3	422.5	72.2	437	11 Q9R1A4	Q9rla4 mus musculus
4	422.5	72.2	463	11 Q99LQ4	Q99lc4 mus musculus
5	418	71.5	473	11 Q9D8L4	Q9d8l4 mus musculus
6	411	70.3	468	11 Q99L31	Q99l31 mus musculus
7	411	70.3	473	11 Q99L25	Q99l25 mus musculus
8	408	69.7	473	11 Q91Z05	Q91z05 mus musculus
9	144	24.6	375	4 Q9BSZ1	Q9bsz1 homo sapien
10	144	24.6	597	4 Q9QB8	Q9qb8 homo sapien
11	144	24.6	597	4 Q9BU10	Q9bu10 homo sapien
12	144	24.6	597	4 Q9GBB9	Q9gbb9 homo sapien
13	144	24.6	613	4 Q96EY0	Q96ey0 homo sapien
14	144	24.6	614	4 Q96GA6	Q96ga6 homo sapien
15	144	24.6	618	4 Q96AA6	Q96aa6 homo sapien
16	128.5	22.0	384	4 Q9UP60	Q9up60 homo sapien

17	128.5	22.0	416	4 Q9NPP6	Q9npp6 homo sapien
18	128.5	22.0	494	4 Q96K68	Q96k68 homo sapien
19	128.5	22.0	496	4 Q96KX8	Q96kx8 homo sapien
20	128.5	22.0	496	4 Q96DK0	Q96dk0 homo sapien
21	124.5	21.3	500	4 Q9BRV0	Q9brv0 homo sapien
22	122.5	20.9	684	13 Q90544	Q90544 ginglymosto
23	111.5	19.1	486	11 Q91Z07	Q91z07 mus musculus
24	111.5	19.1	487	11 Q99KA4	Q99ka4 mus musculus
25	110.5	18.9	479	11 Q99M22	Q99m22 mus musculus
26	110.5	18.9	484	11 Q99LA6	Q99la6 mus musculus
27	110	18.8	211	11 Q91XLO	Q91xl0 mus musculus
28	109.5	18.7	479	11 Q91WPS	Q91wp5 mus musculus
29	109.5	18.7	481	11 Q91WT3	Q91wt3 mus musculus
30	109.5	18.7	481	11 Q91WT1	Q91wt1 mus musculus
31	109.5	18.7	482	11 Q91X92	Q91x92 mus musculus
32	109.5	18.7	488	11 Q91WRI	Q91wr1 mus musculus
33	108.5	18.5	426	11 Q9DCD9	Q9dcd9 mus musculus
34	108.5	18.5	480	11 Q91XEL	Q91xel mus musculus
35	108	18.5	233	11 Q91WS9	Q91ws9 mus musculus
36	108	18.5	234	11 Q91WP8	Q91wf8 mus musculus
37	108	18.5	235	11 Q91WI2	Q91wi2 mus musculus
38	108	18.5	238	11 Q99M37	Q99m37 mus musculus
39	106	18.1	214	11 Q9R1A5	Q9rla5 mus musculus
40	105.5	18.0	233	4 Q96I69	Q96i69 homo sapien
41	105.5	18.0	236	4 Q96E61	Q96e61 homo sapien
42	102.5	17.5	130	11 Q9D8W4	Q9d8w4 mus musculus
43	102.5	17.5	233	11 Q91V32	Q91v32 m adult mal
44	97.5	16.7	235	11 Q99M11	Q99m11 mus musculus
45	96	16.4	1215	5 Q9V787	Q9v787 drosophila

ALIGNMENTS

RESULT 1

ID	Q96PQ8	PRELIMINARY;	PRT;	701 AA.
AC	Q96PQ8;			
DT	01-DEC-2001 (Tremblrel. 19, Created)			
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE	FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21477448; PubMed=11593034;			
RA	Hu Z., Garen A.;			
RT	"Targeting tissue factor on tumor vascular endothelial cells and tumor			
RT	cells for immunotherapy in mouse models of prostatic cancer.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).			
DR	EMBL; AF272774; AAK58686.1; -.			
SQ	SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;			

Query Match	97.1%;	Score 568;	DB 4;	Length 701;
Best Local Similarity	96.4%;	Pred. No. 1.8e-55;		
Matches 106;	Conservative 2;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1 APELLGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVQFKWYDGVGVHNAKTK 60			
Db	485 APELLGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVFNKYNVDGVGVHNAKTK 544			
QY	61 PREEQYNSTRVSVTLVTLHQDLNGCKEYKCKVSNKALPAPIEKTISKTK 110			
Db	545 PREEQYNSTRVSVTLVTLHQDLNGCKEYKCKVSNKALPAPIEKTISKTK 594			
RESULT 2				
ID	Q95M34	PRELIMINARY;	PRT;	337 AA.

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AC Q95M34;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IMMUNOGLOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
DE (FRAGMENT).
GN IGHCL.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Wagner B.; (DEC-2000) to the EMBL/GenBank/DBJ databases.
RL Submitted
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199;105-119(1998).
DR EMBL; AJ300675; CAC44624.1; -.
FT NON_TER 1
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFDF6 CRC64;

Query Match 81.0%; Score 474; DB 6; Length 337;
Best Local Similarity 76.4%; Pred. No. 3e-45;
Matches 84; Conservative 17; Mismatches 9; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFKWYDGVGVHNAKTK 60
Db 119 APELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFKWYDGVGVHNAKTK 178
QY 61 PREQYNSTFRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKTK 110
Db 179 PKEQFNSTFRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKTK 228

RESULT 3
QY Q9RIA4 PRELIMINARY; PRT; 437 AA.
ID Q9RIA4
AC Q9RIA4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
```

```
Query Match 72.2%; Score 422.5; DB 11; Length 437;
Best Local Similarity 70.6%; Pred. No. 2.6e-39;
Matches 77; Conservative 16; Mismatches 13; Indels 3; Gaps 1;

QY 2 PELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFKWYDGVGVHNAKTKP 61
Db 225 PEV---SSVFIFPPKPKDVLATITLTPKVTCTVVDISKDDPEVQFSWFDVDDVEVHTAQTQP 281

QY 62 REEQYNSTFRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKTK 110
Db 282 REEQFNSTFRSVSELPIMHQDWLNKGYCKVSNKALPAPIEKTISKTK 330

RESULT 4
QY Q99LC4 PRELIMINARY; PRT; 463 AA.
ID Q99LC4
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 72.2%; Score 422.5; DB 11; Length 463;
Best Local Similarity 70.6%; Pred. No. 2.8e-39;
Matches 77; Conservative 16; Mismatches 13; Indels 3; Gaps 1;

QY 2 PELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFKWYDGVGVHNAKTKP 61
Db 251 PEV---SSVFIFPPKPKDVLATITLTPKVTCTVVDISKDDPEVQFSWFDVDDVEVHTAQTQP 307

QY 62 REEQYNSTFRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKTK 110
Db 308 REEQFNSTFRSVSELPIMHQDWLNKGYCKVSNKALPAPIEKTISKTK 356

RESULT 5
QY Q9D8L4 PRELIMINARY; PRT; 473 AA.
ID Q9D8L4
AC Q9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1810060009RIK PROTEIN.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

PT immunoglobulin molecules derived from B cell lymphoma cells

XX Example 10; Page 123-124; 177pp; English.

XX This protein comprises an immunoglobulin (Ig) C-gamma-3 region.
 CC The invention provides a method for the production of tumour-
 CC specific Ig derived from a B-cell lymphoma patient. In the novel
 CC method, expression plasmids containing the patient's VH region(s)
 CC joined to either a C-gamma-3 (see AAT97188) or C-gamma-4 (see AAT97189)
 CC sequence and expression plasmids containing the patient's VL
 CC region(s) joined to either a C-kappa (see AAT97190) or C-lambda-2
 CC (see AAT97191) sequence are cotransfected along with a selectable and
 CC amplifiable marker into a cell line (e.g. BW5147.G.1.4), and
 CC transfected cells are then subjected to selection and amplification.
 CC The method permits the production of a multivalent vaccine which
 CC reflects the degree of somatic variation found within the patient's
 CC tumour. These novel multivalent vaccines provide superior vaccines
 CC for the treatment of B-cell lymphoma.

XX Sequence 377 AA;

Query Match 100.0%; Score 585; DB 18; Length 377;
 Best Local Similarity 100.0%; Pred. No. 6.1e-50;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APELLGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKYKVDGVEVHNATK 60
 Db 161 apellggsvflfpkpkdtlmisrtpevtcvvvdshedpevqfkwydvgevhnaatk 220

Qy 61 PREQYNSTRFVSVTLVTLHODWLNKGEYKCKVSNKALPAPIETISKT 110
 Db 221 preeqynstrfsvsvtlvhlqdwlngkeykckvsnkalpapietisktk 270

RESULT 2
 ID AAY31671 standard; Protein; 494 AA.

XX AAY31671;

XX 09-NOV-1999 (first entry)

XX Human IgG3 chain C.

XX IgG3; C-gamma-3; antibody; fusion protein; circulating half-life;
 XX human; drug delivery.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 1..117 /note= "the identity of these residues is not
 XX specified"

XX W09943713-A1.

XX 02-SEP-1999.

XX 24-FEB-1999; 99WO-US03966.

XX 25-FEB-1998; 98US-0075887.

XX (LEXI-) LEXIGEN PHARM CORP.

XX Gillies SD, Lan Y, Lo K, Wesolowski J;

XX WPI; 1999-527594/44.

XX New antibody-based fusion proteins, used for the delivery of e.g. a
 PT cy, ligand-binding protein or protein toxin to target cells in
 PT vi

PS Disclosure; Page 33-34; 41pp; English.

XX The present sequence represents the constant region of human IgG
 CC isotype 3 (IgG3, C-gamma-3). C-gamma-3 and C-gamma-1 (see AAY31669)
 CC bind Fc receptors with high affinity, whereas C-gamma-4 (see
 CC AAY31672) has 10-fold lower binding affinity and C-gamma-2 (see
 CC AAT31670) does not bind to Fc receptor gamma-1. The invention
 CC provides methods for the genetic construction and expressing of
 CC antibody-based fusion proteins with enhanced circulating half-lives.
 CC The fusion proteins lack the ability to bind to immunoglobulin Fc
 CC receptors, either as a consequence of the antibody isotype used
 CC for protein construction, i.e. a C-gamma-2 constant region (Fc)
 CC or a C-gamma-4 Fc receptor, or through directed mutagenesis of
 CC antibody isotypes that normally bind Fc receptors, i.e. C-gamma-1
 CC or C-gamma-3. Introduction of a mutation or a deletion at one or
 CC more amino acid of C-gamma-3 selected from Leu281, Leu282,
 CC Gly283, Gly284, Asn344, and pro378, produces an Ig heavy chain
 CC having reduced binding affinity for an Fc receptor. The methods
 CC can be used for increasing the circulating half-life of a non-Ig
 CC protein such as a cytokine, e.g. tumour necrosis factor (TNF), an
 CC interleukin or a lymphokine such as a lymphotoxin or a colony
 CC stimulating factor, a ligand-binding protein, e.g. CD4, CTLA-4,
 CC TNF receptor or an interleukin receptor, or a protein toxin
 CC (claimed). The fusion proteins are used to deliver selectively the
 CC second non-Ig protein to a target cell in vivo so that the second
 CC non-Ig protein can exert a localised biological effect.

XX Sequence 494 AA;

Query Match 100.0%; Score 585; DB 20; Length 494;
 Best Local Similarity 100.0%; Pred. No. 8.4e-50;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APELLGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKYKVDGVEVHNATK 60
 Db 278 apellggsvflfpkpkdtlmisrtpevtcvvvdshedpevqfkwydvgevhnaatk 337

Qy 61 PREQYNSTRFVSVTLVTLHODWLNKGEYKCKVSNKALPAPIETISKT 110
 Db 338 preeqynstrfsvsvtlvhlqdwlngkeykckvsnkalpapietisktk 387

RESULT 3
 ID AAB07477 standard; protein; 218 AA.

XX AAB07477;

XX 20-OCT-2000 (first entry)

XX Amino acid sequence of native IgG Fc region humIgG3.

XX IgG antibody; light chain; Fc region; effector function; cancer;
 XX allergy; asthma; LFA-1-mediated disorder; tumour; cancer.

XX Homo sapiens.

XX WO200042072-A2.

XX 20-JUL-2000.

XX 14-JAN-2000; 2000WO-US00973.

XX 15-JAN-1999; 99US-0116023.

XX (GETH) GENENTECH INC.

XX Presta LG;

XX WPI; 2000-476035/41.

XX New Fc region-containing polypeptides that have altered effector

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run On: June 21, 2002, 08:36:07 ; Search time 224.82 seconds
(without alignments)
54.346 Million cell updates/sec

Title: US-09-674-857-6
Perfect score: 585
Sequence: 1 APELLGGPSVFLFPKPKDT.....CKVSNKALPAPIEKTISKTK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
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11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
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21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	585	100.0	377	AAW37345	Immunoglobulin C-g
2	585	100.0	494	AAAY31671	Human IgG3 chain C
3	581	99.3	218	AAAB07477	Amino acid sequenc
4	581	99.3	218	AAAB67204	Human IgG3. Homo
5	581	99.3	218	AAAB76424	Human IgG3. Fc regi
6	570	97.4	110	AAAR41713	Undefined ORF3 enc
7	568	97.1	110	AAAR27680	Human immunoglobul
8	568	97.1	110	AAAR41684	Undefined ORF2 enc
9	568	97.1	116	AAAY42621	Human IgG1 Fcgamma
10	568	97.1	212	AAAR87023	Immunoglobulin G1
11	568	97.1	212	AAAR97264	Human immunoglobul

12	568	97.1	212	17	AAW02305	Human IgG1 Fc regi
13	568	97.1	212	19	AAW47354	Human immunoglobul
14	568	97.1	212	20	AAAY23637	IgG1 Fc protein us
15	568	97.1	212	20	AAW92411	Human IgG1 Fc prot
16	568	97.1	212	21	AAAY9937	Human IgG1 Fc regi
17	568	97.1	212	21	AAAY97182	Human immunoglobul
18	568	97.1	212	21	AAAY97250	Human immunoglobul
19	568	97.1	212	21	AAAB03809	FC region of human
20	568	97.1	212	22	AAAB62062	Human immunoglobul
21	568	97.1	212	22	AAAY72750	Native IgG Fc regi
22	568	97.1	218	21	AAAB07474	Native IgG Fc regi
23	568	97.1	218	21	AAAB07475	Human IgG Fc 1 all
24	568	97.1	218	22	AAAB67201	Human IgG Fc 1 all
25	568	97.1	218	22	AAAB67202	Human IgG Fc 1 all
26	568	97.1	218	22	AAAB76421	Human IgG1 non-A F
27	568	97.1	218	22	AAAB76422	Human IgG1 A allot
28	568	97.1	224	8	AAAP70173	Sequence of human
29	568	97.1	224	9	AAAP82508	Immunoglobulin G F
30	568	97.1	228	21	AAAB16955	Human IgG1 Fc prot
31	568	97.1	228	21	AAAY98529	Human IgG1 Fc chai
32	568	97.1	228	22	AAAB98953	Human IgG1 Fc regi
33	568	97.1	232	18	AAW26232	Human IgG1 hinge/F
34	568	97.1	232	21	AAAB28690	Human IgGammal hi
35	568	97.1	232	21	AAAY95579	Human immunoglobul
36	568	97.1	232	21	AAAY70251	Human immunoglobul
37	568	97.1	232	22	AAE02642	Human immunoglobul
38	568	97.1	232	22	AAAY72915	Human partial IgG1
39	568	97.1	232	22	AAAB80897	Human IgGammal hi
40	568	97.1	232	22	AAAB49155	Human immunogloblin
41	568	97.1	233	20	AAAY06617	Human Fc (IgG1).
42	568	97.1	235	20	AAAY01372	Amino acid sequenc
43	568	97.1	235	22	AAAM50246	Human IgG1 Fc regi
44	568	97.1	243	21	AAAB17957	FC-MMP inhibitor f
45	568	97.1	247	21	AAAB16958	FC-TMP protein seq

ALIGNMENTS

RESULT 1
AAW37345
ID AAW37345 standard; Protein; 377 AA.
XX
XX AAW37345;
XX
XX
DT 11-MAY-1998 (first entry)
XX
XX Immunoglobulin C-gamma-3 region.
DE
DE
KW Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;
KW gene amplification; immunotherapy; therapy; immunoglobulin;
KW C-gamma-3; constant region.
XX
XX Homo sapiens.
OS
XX
XX WO9741244-A1.
XX
XX 06-NOV-1997.
PD
XX
XX 25-APR-1997; 97WO-US07039.
PF
XX
XX 06-DEC-1996; 96US-0761277.
PR
XX
XX 01-MAY-1996; 96US-0644664.
PR
XX
XX (GENI-) GENTOPE CORP.
XX
XX Denney DW;
XX
XX WPI: 1997-549743/50.
DR
XX
XX N-PSDB; AAT97188.
DR
XX
XX Multivalent vaccine to treat B cell lymphoma or leukaemia -
PT
PT comprises at least 2 different recombinant variable regions of

RL Submitted (NOV-2001) to the EMBL/GenBank/DDJ databases.
 DR EMBL; BC017356; AAH17356.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 618 AA; 67758 MW; 96DBDAC7C696E0A6 CRC64;

Query Match 24.6%; Score 144; DB 4; Length 618;
 Best Local Similarity 29.7%; Pred. No. 9.9e-08;
 Matches 30; Conservative 24; Mismatches 45; Indels 2; Gaps 2;

QY 10 VFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNST 69

Db 368 VFAIPPS-FASIFLTKSTKLTLCLVTLDTTYD-SVLISWTRQNGEAVKTHTNISESHPNAT 425

QY 70 FRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTIKTK 110

Db 426 FSAVGEASICEDDDWNSGERFTCTVTHDLPSPKQITSRPK 466

Search completed: June 21, 2002, 08:59:32
 Job time: 1631 sec

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=PRIMARY B-CELLS FROM TONSILS;
RC Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC011857; AAH11857.1; -.
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 24.6%; Score 144; DB 4; Length 613;
Best Local Similarity 29.7%; Pred. No. 9.8e-08;
Matches 30; Conservative 24; Mismatches 45; Indels 2; Gaps

QY 10 VLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNATKPKPEQYNST 69
   || || :: ::::: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB 363 VFAIPPS-FASIFLTKSTKLCLVTLDTLTYD-SVTISWTRQNGEAVKTHTNISESHPNAT 420

QY 70 FRVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKTK 110
   | | :: ||: ||: :: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB 421 FSAVGEASICEDDWNSEGFCTCTVHTHDLSPKLQTI SRPK 461

RESULT 14
Q96GA6 PRELIMINARY; PRT; 614 AA.
ID Q96GA6
AC Q96GA6; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=PRIMARY B-CELLS FROM TONSILS;
RC Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC009851; AAH09851.1; -.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 24.6%; Score 144; DB 4; Length 614;
Best Local Similarity 29.7%; Pred. No. 9.8e-08;
Matches 30; Conservative 24; Mismatches 45; Indels 2; Gaps

QY 10 VLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNATKPKPEQYNST 69
   || || :: ::::: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB 364 VFAIPPS-FASIFLTKSTKLCLVTLDTLTYD-SVTISWTRQNGEAVKTHTNISESHPNAT 420

QY 70 FRVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKTK 110
   | | :: ||: ||: :: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB 422 FSAVGEASICEDDWNSEGFCTCTVHTHDLSPKLQTI SRPK 462

RESULT 15
Q96AA6 PRELIMINARY; PRT; 618 AA.
ID Q96AA6
AC Q96AA6; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 67.8 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=LYMPH, AND LYMPHOMA;
RC Strausberg R.;

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SEQUENCE FROM N.A.

RC STRAIN=C57BL/60; TISSUE=PANCREAS;

RX MEDLINE=2108560; PubMed=11217851;

RA Kawai J., Shingagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,

RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fiehlmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fietcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki I.;

RT Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL; AK007918; BAB25349.1; -.

DR HSSP; P01842; 7FAB.

DR MGD; MGI:96443; Igh-1.

DR InterPro; IPR003589; Ig.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003600; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; ig; 4.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; Igc1; 3.

DR SMART; SM00406; IGV; 1.

DR SMART; SM00410; IG-like; 1.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

SQ SEQUENCE 473 AA; 51699 MW; 9DED57A54475FBB CRC64;

Query Match	71.5%	Score 418;	DB 11;	Length 473;
Best Local Similarity	68.2%;	Pred. NO. 9.2e-39;		
Matches 75; Conservative	17;	Mismatches 18;	Indels 0;	Gaps 0;

QY	1	APELLGGPSVFLPPPKDKFLMTSRPEVTCVVVDVSHEDDEPQVKFYVGVGVVHNAKTK	60
Db	257	APDLLGGPSVFLPPPKDKFLMTSLSPMTTCVVVDVSEDDPQVISEFVNNVEVHTAQIQ	316
QY	61	PREEQYNSTRFVSVLTVLHQDLNKGKEYCKCKSNKALPAPIEKTTSKTK	110
Db	317	THREDYNSTRLVVSALPIQHQDWMMSGEKPKCKVNNREALSPIEKTSKPR	366

RESULT 6
Q99L31
ID Q99L31
PRELIMINARY;
PRT; 468 AA

DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -;
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig cl.

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DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00409; Ig_2.
DR SMART: SM00407; Igcl; 3.
DR SMART: SM00406; IgV; 1.
DR SMART: SM00410; Ig_like; 1.
DR PROSITE: PS00290; Ig_MHC; UNKNOWN 1.
DR SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 70.3% Score 411; DB 11; Length 468;
Best Local Similarity 69.1%; Pred. No. 5.6e-38;
Matches 76; Conservative 14; Mismatches 20; Indels 0; Gaps

QY 1 APELLGSPSVFLFPFKPKDTLMISRTPEVTCVVYVDVSHEDPEVQFKWYVDGVVHNAKTG 60
  || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 252 APNLLGSPSVFIFFPKIKDVLMISSLSPWTCVVYVDVEDDPDQVQISFVNNEVLTAQIQ 311
  || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 PREEQYNSTFRVSVLVLVHODWLVNGEYKCKVSNKALPAPIERTTSKTK 110
  _ ||||| ||||| _ ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 312 THREDYNSTLVRSALPIQIHDWMSGRFEKCKVNNKALPAPIERTTSKPK 361
  _ ||||| ||||| _ ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Query Match 70.3%; Score 411; DB 11; Length 468;
Best Local Similarity 69.1%; Pred. No. 5.6e-38;
Matches 76; Conservative 14; Mismatches 20; Indels

RESULT	7		
ID	Q99L25	PRELIMINARY;	PRT; 473 AA.
AC	Q99L25;		
DT	01-JUN-2001	(TremBRel; 17, Created)	
DD	01-JUN-2001	(TremBRel; 17, Last sequence update)	
DT	01-DEC-2001	(TremBRel; 19, Last annotation update)	
DE	SIMILAR TO RIKEN CDNA 181006O009 GENE.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae		
CC	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		

RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

```

EMSL; BC003888; AAH03888.1; -.
HSSP; P01842; 7FAB.
DR DR InterPro; IPR003599; Ig.
DR DR InterPro; IPR003597; Ig_c1.
DR DR InterPro; IPR003600; Ig_like.
DR DR InterPro; IPR003006; Ig_MHC.
DR DR InterPro; IPR003596; Ig_v.
DR DR Pfam; PF00047; Ig_4.
DR DR SMART; SM00409; Ig; 2.
DR DR SMART; SM00407; Ig_c1; 3.
DR DR SMART; SM00406; Igv; 1.
DR DR SMART; SM00410; Ig_like; 1.
DR DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
DR DR SEQUENCE 473 AA; 52449 MW; BE3889B7986DA155 CRC64;
SQ

```

Query Match	70.3%	Score 411;	DB 11;	Length 473;
Best Local Similarity	69.1%	Pred. No. 5.7e-38;		
Matches 76;	Conservative 14;	Mismatches 20;	Indels 0;	

Qy	1	APELLGGPSVFLFPKKPKDTLMISRPEVTVVVDVSHEDPVPQKFWYDVGVEVENAKTK	60
I			
Dd	257	APNLLGSPVFIFPPKI KDWLSIPMTVCVVVDSEDDPDQVSFVNNEVLTAQTQ	316
Qy	61	PREEQNSTRFVSVLTJLHQDLNGKEYCKVKSNKALPAPIEKIISKTK	110
I			
Dd	317	THREDYNSTRLVYSALPIQHQQWMSGEFKCKVNKNALPAPIETISIKPK	366

RESULT 8
Q91Z05
ID Q91Z05 PRELIMINARY; PRT; 473 AA.

PT function due to one or more amino acid modifications in the Fc region,
 useful in the treatment of cancer and allergic conditions such as
 asthma -

PS Disclosure; Fig 22A; 132pp; English.

XX AAB07474-78 represent native IgG Fc regions. The proteins are used to
 CC produce Fc region-containing polypeptides that have altered effector
 CC function as a consequence of one or more amino acid modifications in
 CC the Fc region. The variant polypeptides are useful for treating
 CC cancer, allergic conditions such as asthma (with an anti-IgE antibody),
 CC and LFA-1-mediated disorders. Where the polypeptide binds the HER2
 CC receptor, the disorder preferably is HER2-expressing cancer, e.g. a
 CC benign or malignant tumour characterized by overexpression of the
 CC HER2 receptor. Such cancers include breast cancer, squamous cell
 CC cancer, small-cell lung cancer, non-small cell lung cancer,
 CC gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical
 CC cancer, ovarian cancer, bladder cancer, hepatoma, colon cancer,
 CC colorectal cancer, endometrial carcinoma, salivary gland carcinoma,
 CC kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid
 CC cancer, hepatic carcinoma and various types of head and neck cancer.

XX Sequence 218 AA;

Query Match 99.3%; Score 581; DB 21; Length 218;
 Best Local Similarity 99.1%; Pred. No. 8e-50;
 Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGSPVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVQFKWYVDCGEVHNATK 60
 |||||
 Db 2 apellgspvflppkpkdmlsrtpetvcvvdvshedpevqfkwyvdcgevhnatk 61

QY 61 PREEQYNSTRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKTK 110
 |||||
 Db 62 preeqfnstfrvsvltvlhqdwlngkeyckvsnkalpapiektisktk 111

RESULT 4

AAB67204
 ID AAB67204 standard; protein; 218 AA.

XX AAB67204;

XX 10-APR-2001 (first entry)

XX Human IgG3.

XX Fusion protein; immunoglobulin; multidimerization domain; ligand.

XX Homo sapiens.

XX WO200102440-A1.

XX 11-JAN-2001.

XX 30-JUN-2000; 2000WO-US18185.

XX 02-JUL-1999; 99US-0142088.

XX (GETH) GENENTECH INC.

XX Dennis MS; Lazarus RA;

XX WPI; 2001-123106/13.

XX Novel fusion polypeptides comprising a peptide ligand domain which
 PT functions to target hybrid molecule to target cell, and immunoglobulin
 PT constant region multidimerization domain -

PS Disclosure; Fig 2; 69pp; English.

XX The present invention relates to a fusion protein, comprising a

CC peptide ligand and an immunoglobulin (Ig) constant region
 CC multimerization domain (Ib). The hybrid molecules comprising
 CC the peptide ligands and their functional derivatives can be used
 CC in the same applications as, a peptide ligand can be used. For
 CC example the peptide ligand can bind ErbB2. The peptide ligand
 CC may bind to and inhibit the activity associated with a particular
 CC target molecule.

XX Sequence 218 AA;

Query Match 99.3%; Score 581; DB 22; Length 218;
 Best Local Similarity 99.1%; Pred. No. 8e-50;
 Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGSPVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVQFKWYVDCGEVHNATK 60
 |||||
 Db 2 apellgspvflppkpkdmlsrtpetvcvvdvshedpevqfkwyvdcgevhnatk 61

QY 61 PREEQYNSTRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKTK 110
 |||||
 Db 62 preeqfnstfrvsvltvlhqdwlngkeyckvsnkalpapiektisktk 111

RESULT 5

AAB76424
 ID AAB76424 standard; Protein; 218 AA.

XX AAB76424;

XX 10-APR-2001 (first entry)

XX Human IgG3 Fc region amino acid sequence.

XX Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia;

KW metabolic disorder; nutritional deficiency; Alzheimer's disease;

KW Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea;

KW Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.

XX Homo sapiens.

XX WO200101748-A2.

XX 11-JAN-2001.

XX 30-JUN-2000; 2000WO-US18283.

XX 02-JUL-1999; 99US-0142232.

XX (GETH) GENENTECH INC.

XX Dennis MS;

XX WPI; 2001-123048/13.

XX Non-naturally occurring peptide ligands which compete for binding human
 PT erbB2 gene products, useful for treating e.g. Alzheimer's disease,
 PT multiple sclerosis and diabetic neuropathy -

XX Disclosure; Figure 2A; 116pp; English.

XX This invention relates to non-naturally occurring peptide ligands which
 CC bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides
 CC represented in AAB76350 - AAB76420 and AAB76432 - AAB76509 are examples
 CC of the ErbB2 binding ligands of the invention. Sequences

CC AAB76421 - AAB76431 represent antibody Fc amino acid sequences used in
 CC the isolation of the peptides of the invention. The peptides compete for
 CC binding ErbB2 with naturally occurring ligands, and may be used to treat
 CC disorders characterized by over expression of HER2/erbB2 such as cancers,
 CC diseases of the nervous system, musculature and epithelia, e.g. nervous
 CC system damage resulting from trauma, surgery, strokes, ischaemia,
 CC infection, metabolic disorders, nutritional deficiency or toxic agents.
 CC In particular the synthetic peptide ligands may be used to treat

CC Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis,
 CC Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease
 CC and neuropathy associated with diabetes.

XX Sequence 218 AA;

Query Match 99.3%; Score 581; DB 22; Length 218;
 Best Local Similarity 99.1%; Pred. No. 8e-50; Mismatches 0; Indels 0; Gaps 0;
 Matches 109; Conservative 1;

QY 1 APELLGSPSVFLPPPKDKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNATK 60
 Db 2 apellgspsvflfppkpkdtlmisrtpevtcvtvvdvshedpevqfkwyvdgvevhnatk 61
 QY 61 PREOYNSTFRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKTK 110
 Db 62 preeqfnstfrvsvltvlhqdwlngkeyckvsnkalpapiektisktk 111

RESULT 6
 AAR27680
 ID AAR41713 standard; Protein; 110 AA.

XX AAR41713;
 DT 20-OCT-1993 (first entry)
 DE Undefined ORF3 encoded by plasmid pAH4807.

XX Polymerase chain reaction; primer; PCR; amplify; murine; pAH4525;
 KW heavy; light; chain; variable; constant; region; anti-human; pAH4807;
 KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
 KW endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;
 KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
 KW Parkinsons disease; Alzheimers disease; SP2/0 cell.

XX Synthetic.
 XX WO9310819-A.
 PN 10-JUN-1993.
 XX 24-NOV-1992; 92WO-US10206.
 PF 26-NOV-1991; 91US-0800458.
 PR (ALKE-) ALKERMES INC.
 XX Friden PM;
 PI WPI; 1993-196742/24.
 XX N-PSDB; AAQ43847.

XX Antibody conjugates specific for transferrin receptor - used
 PT for diagnosis and treatment of cancer, AIDS and neurological
 PT disorders
 XX Disclosure; Fig 18M; 151pp; English.

XX The sequences given in AAR41710-14 are encoded by the expression vector
 CC pAH4807. This vector represents the cloning of the human gamma
 CC isotype, gamma-3, with the variable region of the murine monoclonal
 CC antibody 128.1. This plasmid encodes a chimeric monoclonal antibody
 CC in which the heavy chain (VH) is derived from a murine source and the
 CC sequences encoding CH1, CH2 and CH3 are derived from a human source.
 CC This vector, in combination with the chimeric light chain vector,
 CC pAG4611 (see also AAQ43845), was transfected into SP2/0 cells and clones
 CC were isolated. 128.1 is an anti-human transferrin receptor antibody
 CC which binds to the transferrin receptor on brain capillary endothelial
 CC cells. This antibody may be used in a conjugate in which it is linked
 CC to a neuropharmaceutical or diagnostic agent. The conjugate may be
 CC used to treat or prevent neurological disorders eg. brain tumours,

CC AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may
 CC also be used for diagnostic methods.

XX Sequence 110 AA;

Query Match 97.4%; Score 570; DB 14; Length 110;
 Best Local Similarity 98.2%; Pred. No. 4.4e-49;
 Matches 108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGSPSVFLPPPKDKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNATK 60
 Db 1 apellgspsvflfppkpkdtlmisrtpevtcvtvvdvshedpevqfkwyvdgvevhnatk 60
 QY 61 PREOYNSTFRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKTK 110
 Db 61 lreeqynstfrvsvltvlhqdwlngkeyckvsnkalpapiektiskak 110

RESULT 7
 AAR27680
 ID AAR27680 standard; Protein; 110 AA.

XX AAR27680;
 DT 10-MAR-1993 (first entry)
 DE Human immunoglobulin IgG1 CH2 region.

XX Isoallotype; IgG1 G1m(1,2,17); anti-allotype response;
 KW humanised Ab.
 XX Homo sapiens.
 OS WO9216562-A.
 PN 01-OCT-1992.

XX 12-MAR-1992; 92WO-GB00445.
 XX 12-MAR-1991; 91GB-0005245.
 XX (LYNX-) LYNXVALE LTD.
 XX Clark MR;
 XX WPI; 1992-349162/42.

XX Humanised antibodies having modified allotypic determinant -
 PT useful for matching allotypes in therapy with decreased
 PT likelihood of causing undesirable immune responses
 XX Disclosure; Fig 4C; 57pp; English.
 XX In humans, IgG1 may exist as either of two allotypes at site 1, 2
 CC or 17. The inventor's propose eliminating these allotypes by
 CC amino acid changes to agree with the sequences of IgG2, IgG3 and
 CC IgG4. None of the allotype sites (1, 2 and 17) are located within
 CC the CH2 domain. New "isoallotypes" should be suitable for therapeutic
 CC use in all patients. See AAR27678-R27681.

XX Sequence 110 AA;

Query Match 97.1%; Score 568; DB 13; Length 110;
 Best Local Similarity 96.4%; Pred. No. 7e-49; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGSPSVFLPPPKDKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNATK 60
 Db 1 apellgspsvflfppkpkdtlmisrtpevtcvtvvdvshedpevqfkwyvdgvevhnatk 60
 QY 61 PREOYNSTFRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKTK 110

ID AAR87023 standard; protein; 212 AA.

AC AAR87023;

DT 11-JUN-1996 (first entry)

XX Immunoglobulin G1 Fc region.

DE BZLF2; Epstein-Barr virus; EBV; C-type lectin; beta chain; MHC; antigen;
KW major histocompatibility complex; immunoglobulin; cytotoxic T cell;
KW autoimmune disease; myasthenia gravis; multiple sclerosis; allergy;
KW systemic lupus erythematosus; organ transplant rejection; asthma; IL-7;
KW tissue transplant rejection; therapy; cancer; viral disease; mouse;
KW interleukin-7.

XX Homo sapiens.

OS WO930015-A2.

PN 09-NOV-1995.

XX 28-APR-1995; 95WO-US05348.

XX 28-APR-1994; 94US-0235397.

XX (IMMV) IMMUNEX CORP.

PA (UMOR) UNIV MISSOURI.

PA (USSH) US NAT INST OF HEALTH.

XX Alderson M, Armitage RJ, Cohen JR, Comeau MR, Farrah TM;

PI Hutt-fletcher LM, Spriggs MK;

XX WPI; 1995-393086/50.

XX Epstein-Barr virus BZLF2 fusion proteins - used for treating e.g.
PT auto-immune disease, transplant rejection, allergy, asthma, cancer
PT or viral infection.

PS Example 1; Page 38-39; 51pp; English.

XX This sequence represents the human immunoglobulin G1 Fc region, and was
CC used in creating a BZLF2-immunoglobulin Fc fusion protein (BZLF2/Fc).
CC BZLF2 is a Epstein-Barr virus (EBV) protein. To create BZLF2/Fc, this
CC sequence, the leader sequence of mouse interleukin-7 (IL-7) (see
CC AAR87021), a Flag octapeptide (see AAR87022) and a flexible linker (see
CC AAR87024) are joined to the extracellular domain (residues 34 to 223) of
CC the BZLF2 sequence (see AAR87020). The BZLF2/Fc fusion protein
CC containing this sequence is referred to in claim 4. BZLF2 proteins are
CC members of the C-type lectin family. The C-type lectin domain is found
CC in type II membrane proteins. The BZLF2 protein is capable of binding
CC the beta chain of a major histocompatibility complex (MHC) class II
CC antigen. Fusion proteins with an oligomerising zipper domain (OZD),
CC instead of an immunoglobulin Fc region, can also be created. BZLF2
CC proteins inhibit antigen-specific antibody formation, proliferation of
CC blood mononuclear cells and cytotoxic T cell responses. They also
CC exhibit superantigen-like activity. The proteins can be used for
CC treating or preventing autoimmune diseases such as myasthenia gravis,
CC multiple sclerosis and systemic lupus erythematosus. Also, for treating
CC organ or tissue transplant rejection and for treating or preventing
CC allergy or asthma. They can be used for treating cancer and viral
CC disease, especially EBV infection.

XX Sequence 212 AA;

Query Match 97.1%; Score 568; DB 16; Length 212;

Best Local Similarity 96.4%; Pred. No. 1.5e-48;

Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYDGVGVHNAKTK 60

Db 14 apellgspvflfpkpkdtlmisrtpetvcvvdvshedpevkfnwydgvghnaktk 73

QY 61 PREEQYNSTFRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKTK 110

Db 74 preeqynstfrvsvltvlhqdwlngkeyckvsnkalpapiektiskak 123

RESULT 11

AAR97264

ID AAR97264 standard; protein; 212 AA.

XX AAR97264;

DT 14-FEB-1997 (first entry)

XX Human immunoglobulin G1 Fc region.

DE HVS14; major histocompatibility complex; MHC; Class II; allergy;
KW binding protein; inhibition; antigen presentation; superantigen;
KW treatment; cancer; viral disease; immunoglobulin; IgG1; Fc region;
KW fusion protein.

XX Homo sapiens.

XX WO9617939-A1.

XX 13-JUN-1996.

XX 07-DEC-1995; 95WO-US15948.

XX 06-JUN-1995; 95US-0485549.

XX 07-DEC-1994; 94US-0351901.

XX (IMMV) IMMUNEX CORP.

XX Alderson M, Armitage R, Spriggs M, Yao Z;

XX WPI; 1996-287183/29.

XX Isolated Herpes virus Saimiri 14 proteins - useful for treating
PT autoimmune disorders, transplant rejection, allergy, asthma, cancer
PT or viral disease

XX Claim 4; Page 32; 45pp; English.

XX The present sequence is a human immunoglobulin G1 Fc region, which
CC can form a claimed fusion protein with the Herpesvirus Saimiri
CC (HVS) major histocompatibility complex (MHC) Class II binding
CC protein, HVS14. The fusion protein can be used to treat cancer or
CC viral disease, as HVS14 inhibits antigen presentation, or acts as
CC a superantigen.

XX Sequence 212 AA;

Query Match 97.1%; Score 568; DB 17; Length 212;

Best Local Similarity 96.4%; Pred. No. 1.5e-48;

Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYDGVGVHNAKTK 60

Db 14 apellgspvflfpkpkdtlmisrtpetvcvvdvshedpevkfnwydgvghnaktk 73

QY 61 PREEQYNSTFRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKTK 110

Db 74 preeqynstfrvsvltvlhqdwlngkeyckvsnkalpapiektiskak 123

RESULT 12

AAW02305

ID AAW02305 standard; Protein; 212 AA.

XX AAW02305;

XX 05-DEC-1996 (first entry)

```
XX Human IgG1 Fc region.
DE
XX
XX IgG1; Interleukin-17 receptor; IL-17R.
KW
XX
XX Homo sapiens.
OS
XX
XX WO9629408-A1.
PN
XX
XX 26-SEP-1996.
PD
XX
XX 21-MAR-1996; 96WO-US04018.
PF
XX
XX 07-AUG-1995; 95US-0538765.
PR
XX 23-MAR-1995; 95US-0410535.
XX
XX (IMMV ) IMMUNEX CORP.
PA
XX
XX Fanslow WC, Spriggs MK, Yao Z;
PI
XX WPI; 1996-443184/44.
XX
XX DNA encoding interleukin-17 receptor - useful for regulating immune
PT and inflammatory responses, or to suppress graft rejection
XX
XX Example 1; Page 33; 52pp; English.
XX
XX The human IgG1 Fc region (AAW02305) can be used as a fusion partner
CC for interleukin-17 receptor (IL-17R) proteins (see also AAW04184-85),
CC allowing purification of recombinant IL-17R using protein A or
CC protein G affinity chromatography. Fusions between Fc and HVS13
CC (see also AAW02387), a viral homologue of IL-17, and between Fc
CC and murine CTLA8 (AAW02386) were used to identify cells that
CC express the murine IL-17R. Selected murine thymoma EL4 cells
CC were used as a source of murine IL-17R cDNA (AAAT33800).
XX
XX Sequence 212 AA;
SQ

Query Match 97.1%; Score 568; DB 17; Length 212;
Best Local Similarity 96.4%; Pred. No. 1.5e-48;
Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFKWYDGVGVHNAKTK 60
DB 14 apellggpsvflppkpkdtlmisrtpetvcvvdvshedpevkfnwydgvgevhnaatk 73

QY 61 PREEQNSTFRVSVLTVLHQDLNGKEYKCKVSNKALPAPIETKTSKTK 110
DB 74 preeqnstyrvsvltvlhqdlngkeykckvsnkalpapietktskak 123

RESULT 13
AAW47354
ID AAW47354 standard; protein; 212 AA.
XX
XX AAW47354;
AC
XX
XX 01-JUN-1998 (first entry)
DT
XX
XX Human immunoglobulin G1 Fc fragment.
DE
XX
XX EBV; B2LF2; beta-chain; major histocompatibility complex; MHC;
KW class II; antigen; prevention; treatment; autoimmune disease;
KW transplant rejection; allergy; asthma; super-antigen; IgG1;
KW Epstein-Barr virus; human; immunoglobulin G1; Fc fragment.
XX
XX Homo sapiens.
OS
XX
XX US5726286-A.
PN
XX
XX 10-MAR-1998.
PD
XX
```

```
PF 28-APR-1995; 95US-0430633.
XX
XX 28-APR-1995; 95US-0430633.
PR
XX 28-APR-1994; 94US-0235397.
XX
XX (IMMV ) IMMUNEX CORP.
PA
XX
XX Alderson M, Armitage RJ, Cohen JI, Comeau MR, Farrah TM;
PI Hutt-Fletcher LM, Spriggs MK;
XX
XX WPI; 1998-192827/17.
DR
XX
XX Epstein-Barr virus protein - binds to major histocompatibility
PT complex class II beta chain, useful for treating, e.g. auto-immune
PT diseases or transplant rejection
XX
XX Example 1; Columns 31-32; 25pp; English.
PS
XX
XX The present sequence was used in the preparation of a synthetic
CC construct containing the Epstein-Barr virus (EBV) BZLF2 protein,
CC which is capable of binding a beta-chain of a major
CC histocompatibility complex (MHC) class II antigen.
CC The protein can be used to inhibit antigen-specific antibody
CC formation, peripheral blood mononuclear cell proliferation and
CC cytotoxic T-cell responses, e.g. in the prevention or treatment of
CC autoimmune diseases, transplant rejection, allergies or asthma,
CC and as a super-antigen.
XX
XX Sequence 212 AA;
SQ

Query Match 97.1%; Score 568; DB 19; Length 212;
Best Local Similarity 96.4%; Pred. No. 1.5e-48;
Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFKWYDGVGVHNAKTK 60
DB 14 apellggpsvflppkpkdtlmisrtpetvcvvdvshedpevkfnwydgvgevhnaatk 73

QY 61 PREEQNSTFRVSVLTVLHQDLNGKEYKCKVSNKALPAPIETKTSKTK 110
DB 74 preeqnstyrvsvltvlhqdlngkeykckvsnkalpapietktskak 123

RESULT 14
AAI23637
ID AAY23637 standard; protein; 212 AA.
XX
XX AAY23637;
AC
XX
XX 06-SEP-1999 (first entry)
DT
XX
XX IgG1 Fc protein used to make BZLF2 fusion proteins.
DE
XX
XX BZLF2 protein; beta chain; blood mononuclear mononuclear cell;
KW Class II major histocompatibility complex antigen; proliferation;
KW cytotoxic T cell response; antigen specific response; asthma;
KW autoimmune disease; transplant rejection.
XX
XX Homo sapiens.
OS
XX
XX US5925734-A.
PN
XX
XX 20-JUL-1999.
PD
XX
XX 24-SEP-1997; 97US-0936854.
PF
XX
XX 28-APR-1995; 95US-0430633.
PR
XX 28-APR-1994; 94US-0235397.
XX
XX 24-SEP-1997; 97US-0936854.
XX
XX (IMMV ) IMMUNEX CORP.
PA
XX
```

PI Alderson M, Armitage RJ, Cohen JL, Comeau MR, Farrah TM;
 XX Hutt-Fletcher LM, Spriggs MK;
 DR WPI; 1999-418295/35.
 XX

PT Epstein-Barr virus BZLF2 proteins
 XX

PS Claim 2; Column 31-32; 25pp; English.
 XX

CC The present sequence represents a protein used to create fusion proteins
 CC with the Epstein-Barr virus BZLF2 proteins of the invention. The BZLF2
 CC protein is capable of binding to a beta chain of a Class II major
 CC histocompatibility complex antigen to inhibit an antigen-specific
 CC response. BZLF2 is useful for inhibiting antigen-specific antibody
 CC formation, the proliferation of blood mononuclear mononuclear cells,
 CC and cytotoxic T cell responses. BZLF2 is also useful for inhibiting
 CC undesirable antigen specific responses, e.g. in the treatment or
 CC prevention of asthma; for preventing or treating autoimmune disease;
 CC and for preventing tissue or organ transplant rejection.
 XX

SQ Sequence 212 AA;

Query Match 97.1%; Score 568; DB 20; Length 212;
 Best Local Similarity 96.4%; Pred. No. 1.5e-48;
 Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 APELLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNATK 60
 |||||
 Db 14 apellgspsvflppkpkdtlmisrtpevtcvcvvdvshedpevkfnwydgvvhnatk 73

OY 61 PREEQYNSTFRVSVTLVLHQDWLNGKEYCKVSNKALPAPIEKTISKTK 110
 |||||
 Db 74 preeqynstyrsvsvtlvlhqdwlngkeyckvsnkalpapiektiskak 123

RESULT 15

AAW92411
 ID AAW92411 standard; Protein; 212 AA.
 XX

AC AAW92411;
 XX

DT 21-APR-1999 (first entry)
 XX

DE Human IgG1 Fc protein fragment.
 XX

KW IL-17R; human; interleukin-17 receptor; immunoregulator; inhibitor;
 KW T cell proliferation; T cell activation; organ; graft; rejection;
 KW autoimmune disease; allergy; asthma; treatment; inflammatory disease;
 KW B cell proliferation; immunoglobulin secretion; immunogen; IgG1; Fc.
 XX

OS Homo sapiens.
 XX

XX US5869286-A.
 PN

XX 09-FEB-1999.
 PD

XX 21-MAR-1996; 96US-0620694.
 PF

XX 21-MAR-1996; 96US-0620694.
 PR

XX 23-MAR-1995; 95US-0410535.
 PR

XX 07-AUG-1995; 95US-0538765.
 XX

XX (IMMV) IMMUNEX CORP.
 PA

XX Fanslow WC, Spriggs MK, Yao Z;
 PI

XX WPI; 1999-152766/13.
 DR

XX Isolated interleukin-17 receptor DNA - used to develop products for
 PT treating e.g. organ or graft rejection, autoimmune disease, allergy,
 PT asthma or inflammatory disease
 PT

XX

PS Example 1; Column 31-32; 25pp; English.
 XX

CC This sequence represents a human IgG1 Fc fragment which is used in the
 CC construction of a fusion protein with human interleukin-17 receptor
 CC (IL-17R). IL-17R polypeptides have immunoregulatory activity. They can be
 CC used for inhibiting T cell proliferation, or for inhibiting T cell
 CC activation. In particular they can be used for preventing or treating
 CC organ or graft rejection, autoimmune disease, allergy or asthma. They can
 CC also be used for the prevention or treatment of inflammatory disease in
 CC which activated T cells play a role or for inhibiting B cell
 CC proliferation or immunoglobulin secretion. The IL-17 polypeptides can
 CC also be used as immunogens, reagents in in vitro assays, or as binding
 CC agents for affinity purification procedures.
 XX

SQ Sequence 212 AA;

Query Match 97.1%; Score 568; DB 20; Length 212;
 Best Local Similarity 96.4%; Pred. No. 1.5e-48;
 Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 APELLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNATK 60
 |||||
 Db 14 apellgspsvflppkpkdtlmisrtpevtcvcvvdvshedpevkfnwydgvvhnatk 73

OY 61 PREEQYNSTFRVSVTLVLHQDWLNGKEYCKVSNKALPAPIEKTISKTK 110
 |||||
 Db 74 preeqynstyrsvsvtlvlhqdwlngkeyckvsnkalpapiektiskak 123

Search completed: June 21, 2002, 08:36:08
 Job time: 322 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:37:54 ; Search time 102.05 Seconds

(without alignments)
103.575 Million cell updates/sec

Title: US-09-674-857-7
Perfect score: 583
Sequence: 1 APEFLGGPSVFLPPPKDPT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	583	100.0	327	1 G4HU	Ig gamma-4 chain C
2	551	94.5	234	2 PT0207	Ig gamma chain C r
3	551	94.5	255	4 S31866	Ig gamma-1 chain C
4	551	94.5	330	1 GHRU	Ig gamma-1 chain C
5	551	94.5	374	2 S69339	Ig heavy chain V r
6	541	92.8	377	2 A60764	Ig gamma-3 chain C
7	541	92.8	377	2 A23511	Ig gamma-3 chain C
8	528	90.6	289	1 G3HUWI	Ig gamma-3 heavy c
9	528	90.6	326	1 G2HU	Ig gamma-2 chain C
10	470	80.6	328	2 I47160	Ig gamma 2b chain
11	470	80.6	328	2 I47159	Ig gamma 2a chain
12	465	79.8	277	2 I47162	Ig gamma 4 chain c
13	444	76.2	328	2 I47161	Ig gamma 3 chain c
14	444	76.2	328	2 I47158	Ig gamma 1 chain c
15	443	76.0	323	1 GHRB	Ig gamma chain C r
16	443	76.0	333	2 PS0018	Ig gamma-2b chain
17	437	75.0	329	1 G2GP	Ig gamma-2 chain C
18	436	74.8	308	2 C30554	Ig heavy chain C r
19	436	74.8	472	2 S31459	Ig gamma-1 chain r
20	434	74.4	470	2 S22080	Ig heavy chain pre
21	416	71.4	329	1 G3MSC	Ig gamma-3 chain C
22	416	71.4	398	1 G3MSM	Ig gamma-3 chain C
23	409	70.2	327	2 S06611	Ig gamma-2 chain C
24	407	69.8	329	2 S00847	Ig gamma-2c chain
25	405	69.5	324	1 G1MS	Ig gamma-1 chain C
26	405	69.5	393	1 G1MSM	Ig gamma-1 chain C
27	405	69.5	444	2 PC4436	monoclonal antibod
28	403	69.1	335	1 G2MSAB	Ig gamma-2a chain
29	399	68.4	330	1 G2MSA	Ig gamma-2a chain

30	399	68.4	399	1 G2MSAM	Ig gamma-2a chain
31	399	68.4	469	2 S37483	Ig gamma-2a chain
32	398	68.3	405	1 G2MSBM	Ig gamma-2b chain
33	398	68.3	474	1 G2MS11	Ig gamma-2b chain
34	389	66.7	326	2 PS0017	Ig gamma-1 chain C
35	389	66.7	446	2 S40295	Ig gamma-2a chain
36	384	65.9	475	2 S01321	Ig gamma-2b chain
37	343	58.8	322	2 PS0019	Ig gamma-2a chain
38	311	53.3	112	2 B30503	Ig gamma-2a chain
39	278	47.7	88	2 A30503	Ig gamma-2b chain
40	258	44.3	180	2 I46732	Ig gamma heavy cha
41	167.5	28.7	426	2 I36948	Ig epsilon-chain -
42	166.5	28.6	428	1 EHHU	Ig epsilon chain C
43	165	28.3	152	2 S14236	Ig gamma-1 chain C
44	154	26.4	549	2 S04845	Ig heavy chain pre
45	151	25.9	429	1 EHRT	Ig epsilon chain C

ALIGNMENTS

RESULT 1
G4HU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104
A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constan
A:Reference number: A90249; MUID:70207360
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30;81-326 <PIN>
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 583; DB 1; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.1e-50;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLPPPKDPTLMISRTPTCVVVDVDSQEDPEVQFNWYDGVGVHNAKTK 60
|||||

Db 111 APEFLGGPSVFLPPPKDPTLMISRTPTCVVVDVDSQEDPEVQFNWYDGVGVHNAKTK 170
|||||

QY 61 PREEQNSYRVVSVLTVLHQDLNGCKYKCKVSNKGLPSSIEKTISKAK 110
|||||

Db 171 PREEQNSYRVVSVLTVLHQDLNGCKYKCKVSNKGLPSSIEKTISKAK 220
|||||

RESULT 2

PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (Chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 94.5%; Score 551; DB 2; Length 234;
Best Local Similarity 93.6%; Pred. No. 1.1e-47;
Matches 103; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCWVDVSQEDPEVFQFNWYDGVGVHNAKTK 60

Db 25 APELLGGPSVFLFPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 84

QV 61 PREEOFNSTYRVVSVITVIHODWINGCKVKVSNKCIDSSSTVMTICVAV 110

b6
85 DREFOVNCSTVDINCSVI WAT HODOT NCOTDUNOVCNCTZT
| | : | | | | | | | | : | | | |
| | | | | | | | | | | | | |

RESULT 3

S11866
 Ig gamma-1 chain C region - synthetic
 C:Species: synthetic
 A:Note: Homo sapiens (man) gene engineered and expressed in *Escherichia coli*
 C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
 C:Accession: S11866
 R:Rif^rputa, D.
 Submitted to the EMBL Data Library, February 1993
 A:Description: Screening method for protein-protein interactions of cloned genes

Accession: G33066
Molecule type: mRNA
A:Residues: 1-255 <FIL>
A:Cross-references: EMBL:X70421; NID:g33068; PID:CAA49866.1; PID:g33069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 94.5%; Score 551; DB 4; Length 255;
Best Local Similarity 93.6%; Pred. No. 1.3e-47;
Matches 103; Conservative 3; Mismatches 4; Indels 0; Gaps 0.

QY 1 APEFLGGPSVLEFPKPKKDTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAKTK 60

```
db 39 APEI LGGPSVFLFPBPKKQIMTSPTDEVTCAVAVNVCHEHNNVFENLVAIVDITFCHYITRIRSRDQV
```

[illegible]

```
07 FREEQFNSIIRKWSVEIVLHQDWLNGKEYCKRVSNRGLPSSIERISKAK IIO
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
08
```

RESULT A

4
 RESULT
 GHUU
 Ig gamma-1 chain C region - human
 C-Species Homo sapiens (man)
 C-Sequence#
 C-Accession: A93433
 C-Date: 31-Jan-1981
 C-Update: 18-Aug-1982
 C-Text_change 16-Jul-1999
 C-Release: A93433; S38631; S38817; B90563; A30564; B91668; A91723; A02146
 C-Release: J.N.; Ellison, J.N.; Berson, B.J.; Hood, L.E.
 C-Release: Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: EMBL:Z17370
A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A:Reference number: S33887; MUID:83001943
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:Cross-references: EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, G.M.;
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A:Reference number: A90563; MUID:71064024
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-135 <CUN>
A:Note: this sequence has the G1m(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A:Reference number: A90564; MUID:71064025
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2
A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni
igen Primaerstruktur.
A:Reference number: A91668; MUID:77070269
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 2
A:Note: this sequence has the G1m(17) and G1m(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <
A:Note: this sequence has the G1m(3) and G1m(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul
A:Reference number: A90565; MUID:71064027
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunog
enamide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1

A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:CROSS-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A>Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A>Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, an
A:Reference number: A92809; MUID:81007873
A:Contents: myeloma protein TII
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19,'O','Z','59','A','61-193,'D','195-325 <WAN>
A>Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A>Title: The amino acid sequence of the three heavy chain constant region domains of
A:Reference number: A90752; MUID:80001357
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24,'E','26-57','EV',60-85;132-171,'ZZZ','175','B','177-193,'D','195-196,'Q','1
A>Note: This sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A>Title: A note on the amino acid sequence of residues 381-391 of human immunoglobuli
A:Reference number: A93132; MUID:80114419
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A>Note: the revised sequence differs from that shown in having 60-Ala and in the amid
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A>Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A>Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:CROSS-references: GDB:I19338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/disulfide bonds: #status experimental
F:102,103,106-109/disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

	Query Match	Score	DB 1:	Length	326;
Best Local Similarity	92.5%;	Pred. No.	3.4e-45;		
Matches	98;	Conservative	4;	Mismatches	4;
				Indels	0;
				Gaps	0;

QY 5 LGGPSVFELPPPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYGVGVHNATKPRE 64
| | | | |
Db 114 VAGPSVFELPPPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYGVGVHNATKPRE 173
| | | | |
OY 65 QFNSTYRVSVLTVLFDQLNGKEYCKRVSNKGFLPSSIEKTISKAK 110

[illegible]

I47162

Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A;Reference number: I47158; MUID:95015845
A;Accession: I47162
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C;Genetics:
A;Gene: IgG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IM>

Query Match 79.8%; Score 465; DB 2; Length 277;
Best Local Similarity 80.8%; Pred. No. 5.5e-39;
Matches 84; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 7 GPSVFLPPPKPDILMSRTPEVCVVVDVSQEDPEVOFNWYDGVGHNAKTKEPQQF 56
||| :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
Db 65 GPSAFIFPPKPDITMSRTPEVKTCVVVDVSQENPEVQFSWYVDGVHVTATRPKEQF 124
||||| :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 67 NSTYRVSVLVTLHQDWLNGREYCKVSNKGLPSSIEKTISKAK 110
||||| :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 125 NSTYRVSVLPIQHDWLNGREFKCKVNKKDLPAPITRIISKAK 168
||||| :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 13

I47161

Ig gamma 3 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47161
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A;Reference number: I47158; MUID:95015845
A;Accession: I47161
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128
C;Genetics:
A;Gene: IgG3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IM>

Query Match 75.2%; Score 444; DB 2; Length 328;
Best Local Similarity 77.1%; Pred. No. 8.5e-37;
Matches 81; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 5 LGGPSVLFFPKPDITLMISRTPEVTCVVVDVSQEDPEVOFNWYDGVGHNAKTKEPREE 64
||| :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
Db 114 VAGPSVFIFPPKPDITLMISQTPEVTCVVVDVSQEHAEVQFSWYVDGVHVTATRPKEE 173
||||| :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 65 QFNSTYRVSVSLTVLHQDWLNGKEYCKVSNKGLPSSIEKTISKAK 109
||||| :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 174 QFNSTYRVSVSLPTQHQLNGKSEKCKVNNVDLPAPITRTISKAK 218
||||| :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 14

I47158

Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158

R:Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845

A:Accession: I47158

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-328 <RAC>

A:Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122

C:Genetics:

A:Gene: IgG1

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:133-202/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 76.2%; Score 444; DB 2; Length 328;

Matches 81; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 5 LGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREE 64

Db 114 VAGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREE 173

QY 65 QFNSTRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTISKAK 109

Db 174 QFNSTRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTISKAK 218

RESULT 15

GHRB

Ig gamma chain C region - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 16-Jul-1999

C:Accession: A91749; A90290; A93928; A90245; A94416; A02161

R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.

Immunogenetics 18, 387-397, 1983

A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot

A:Reference number: A91749; MUID:84030930

A:Accession: A91749

A:Molecule type: mRNA

A:Residues: 1-323 <BER>

A:Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr

R:Pratt, D.M.; Mole, L.E.

Biochem. J. 151, 337-349, 1975

A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob

A:Reference number: A90290; MUID:76135469

A:Accession: A90290

A:Molecule type: protein

A:Residues: 1-47, 'E', '49-71, 'pv', '72-128 <PRA>

R:Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982

A:Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain

A:Reference number: A93928; MUID:83299917

A:Accession: A93928

A:Molecule type: mRNA

A:Residues: 88-103, 'M', '105-143, 'E', '145-184, 'A', '186, 'E', '188-266 <MAR>

A:Cross-references: GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:g165112

A:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marke

R:Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.

Biochem. J. 116, 249-259, 1970

A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin

A:Reference number: A90245; MUID:70110015

A:Accession: A90245

A:Molecule type: protein

A:Residues: 132-143, 'E', '145-161 <FRU>

R:Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.

in Gamma Globulins, Nobel Symp. 3, Killander/ J., ed., pp.109-127, Almqvist and Wiksell,

A:Reference number: A94416

A:Accession: A94416

A:Molecule type: protein

A:Residues: 129-131;155-172, 'D', '174-184, 'A', '186, 'E', '188-200, 'D', '202-217, 'E', '219-232, 'Q',

A:Note: this has the e15 allotypic marker, 185-Ala

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-92/Domain: immunoglobulin homology <IMI>

F:130-199/Domain: immunoglobulin homology <IM2>

F:236-303/Domain: immunoglobulin homology <IM3>

F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 76.0%; Score 443; DB 1; Length 323;

Matches 81; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 2 PEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKP 61

Db 108 PELLGGPSVFIFFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFTWYINNEQVTRTPPL 167

QY 62 REQFNSTRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTISKAK 110

Db 168 REQFNSTRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTISKAR 216

Search completed: June 21, 2002, 08:37:54

Job time: 428 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:32:13 ; Search time 77.71 Seconds
(without alignments)
34.261 Million cell updates/sec

Title: US-09-674-857-2
Perfect score: 580
Sequence: 1 APPVAGSVFLFPKPKDTEL.....CKVSNKGLPSSIEKTSKTK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2.6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2.6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2.6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2.6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2.6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2.6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	98.6	109	3	US-08-444-644-30
2	572	98.6	109	4	US-08-232-246A-30
3	572	98.6	432	3	US-08-477-460B-2
4	572	98.6	432	3	US-08-379-516-2
5	572	98.6	432	4	US-09-329-916-2
6	572	98.6	432	4	US-08-485-372A-2
7	572	98.6	432	4	US-09-409-006A-2
8	572	98.6	432	5	PCT-US93-07422-2
9	572	98.6	530	3	US-08-477-460B-4
10	572	98.6	530	3	US-08-379-516-4
11	572	98.6	530	4	US-09-329-916-4
12	572	98.6	530	4	US-08-485-372A-4
13	572	98.6	530	4	US-09-409-006A-4
14	572	98.6	530	5	PCT-US93-07422-4
15	569	98.1	450	2	US-08-788-800-12
16	569	98.1	459	2	US-07-934-373C-23
17	569	98.1	469	3	US-08-437-642B-23
18	569	98.1	552	5	PCT-US93-07832-23
19	562	96.9	326	2	US-08-656-586-9
20	536	92.4	109	2	US-08-070-116A-4
21	536	92.4	110	3	US-08-444-644-44
22	536	92.4	110	4	US-08-232-246A-44
23	536	92.4	327	2	US-08-761-277A-47
24	536	92.4	382	1	US-08-470-299-7
25	536	92.4	443	5	PCT-US96-13152-4
26	536	92.4	467	1	US-08-704-744-81
27	536	92.4	467	2	US-07-916-098A-45

28	536	92.4	467	4	US-08-523-894-8	Sequence 8, Appli
29	535	92.2	382	1	US-08-470-299-10	Sequence 10, Appl
30	535	92.2	467	4	US-08-523-894-10	Sequence 10, Appl
31	535	92.2	467	4	US-08-523-894-12	Sequence 12, Appl
32	532.5	91.8	326	3	US-08-808-720-3	Sequence 1, Appli
33	532.5	91.8	328	3	US-08-808-720-1	Sequence 1, Appli
34	532.5	91.8	331	3	US-08-808-720-5	Sequence 5, Appli
35	532.5	91.8	331	3	US-08-808-720-7	Sequence 7, Appli
36	529	91.2	377	2	US-08-761-277A-45	Sequence 45, Appl
37	529	91.2	468	4	US-09-485-737B-67	Sequence 67, Appl
38	529	91.2	711	4	US-09-485-737B-90	Sequence 90, Appl
39	524	90.3	116	2	US-08-232-539D-55	Sequence 55, Appl
40	524	90.3	212	1	US-08-430-633-4	Sequence 4, Appli
41	524	90.3	212	2	US-08-620-694A-4	Sequence 4, Appli
42	524	90.3	212	2	US-08-936-854-4	Sequence 4, Appli
43	524	90.3	212	3	US-09-022-253-4	Sequence 4, Appli
44	524	90.3	212	3	US-09-022-696-4	Sequence 4, Appli
45	524	90.3	212	3	US-09-022-253-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-444-644-30
; Sequence 30, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear


```

; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-09-329-916-2

Query Match 98.6%; Score 572; DB 4; Length 432;
Best Local Similarity 98.2%; Pred. No. 3.7e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0

Qy 1 APPVAGSVFLFPKPKDITLMISTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKP 60
Db 217 APPVAGSVFLFPKPKDITLMISTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKP 276

Qy 61 REEFNFTFRVSVLTIVVHODWLNKREYCKVSNKGLPSSIEKTIISKTK 109
Db 277 REEFNFTFRVSVLTIVVHODWLNKREYCKVSNKGLPAPIEKTIISKTK 325

RESULT 6
US-08-485-372A-2
; Sequence 2, Application US/08485372A
; Patent No. 6187748
; GENERAL INFORMATION:
; APPLICANT: Beaudry, Gary A.
; APPLICANT: Magdon, Paul J.
; TITLE OF INVENTION: CD4-GAMMA2 CD4-GAMMA2 CD4-IgG2 CHIMERAS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,372A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,227
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37690-II-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien

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; CELL TYPE: lymphocyte
US-08-485-372A-2

Query Match 98.6%; Score 572; DB 4; Length 432;
Best Local Similarity 98.2%; Pred. NO. 3.7e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy	61	REEQFNSTRVSVLTVVHQDWLNGKEYCKVSNKGLPSSIEKTSKTK	109
Dd	277	REEQFNSTRVSVLTVVHQDWLNGKEYCKVSNKGLPAIKTSKTK	325

RESULT 7
US-09-409-006A-2
; Sequence 2, Application US/09409006A
; Patent No. 6342586
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA

Query Match 98.6%; Score 572; DB 4; Length 432;
Best Local Similarity 98.2%; Pred. No. 3.7e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

[illegible]

QY 61 REEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPSSIEKTIKTK 109
 |||
 Db 277 REEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAIEKTIKTK 325

RESULT 8
PCT-US93-07422-2
; Sequence 2, Application PC/TUS9307422
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.

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Query Match          98.6%; Score 572; DB 5; Length 432;
Best Local Similarity 98.2%; Pred. No. 3.7e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db	217	APPVAGPSVFLFPBPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYDGVGEVHNAKTKP	276

QY	61	REEQNSTFRVSVLTVVHQDLNCKEYCKKVSNGKLPSSTIKTK	109
Db	277	REEQNSTFRVSVLTVVHQDLNCKEYCKKVSNGKLPAPIKTISKTK	325

RESULT 9
US-08-477-460B-4
; Sequence 4, Application US/08477460B
; Patent No. 6034223
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-379-516-4

Query Match          98.6%; Score 572; DB 3; Length 530;
Best Local Similarity 98.2%; Pred. No. 4.8e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSVLFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVVHNAKTKP 60
Db 315 APPVAGSVLFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVVHNAKTKP 374

QY 61 REQQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIKTK 109
Db 375 REQQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTIKTK 423

RESULT 11
US-09-329-916-4
; Sequence 4, Application US/09329916
; Patent No. 6177549
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/329,916
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,460
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-09-329-916-4

Query Match          98.6%; Score 572; DB 4; Length 530;

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; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA: US/09/409,006A
; FILING DATE: 29-SEP-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT-JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
; US-09-409-006A-4

Query Match          98.6%; Score 572; DB 4; Length 530;
Best Local Similarity 98.2%; Pred. No. 4.8e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 APPVAGSVLFPKPKDITLMISRTPEVTCCVVVDVSHEDPEVOFNWYDVGVHNAKTKP 60
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Db      315 APPVAGSVLFPKPKDITLMISRTPEVTCCVVVDVSHEDPEVOFNWYDVGVHNAKTKP 374
        |||||||

QY      61 REEQNFSTFRVSVLTVVHQDLWGKEYCKVKSNKGLPSSIEKTISKTK 109
        |||||||
Db      375 REEQNFSTFRVSVLTVVHQDLWGKEYCKVKSNKGLPAPIEKTISKTK 423
        |||||||

RESULT 14
PCT-US93-07422-4
; Sequence 4, Application PC/TUS9307422
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham

```


STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 19930806
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
PCT-US93-07422-4

Query Match 98.6%; Score 572; DB 5; Length 530;
Best Local Similarity 98.2%; Pred. No. 4.8e-59;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
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Db 315 APPVAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 374
|||||
QY 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTSKTK 109
|||||
Db 375 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTSKTK 423
|||||

RESULT 15

US-08-788-800-12
Sequence 12, Application US/08788800
Patent No. 5914112
GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
APPLICANT: Thomas, G. Roger
TITLE OF INVENTION: Gross, Cordell E.
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,800
FILING DATE: 22-Jan-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0987r1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-788-800-12

Query Match 98.1%; Score 569; DB 2; Length 450;
Best Local Similarity 97.2%; Pred. No. 8.8e-59;
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
|||||
Db 235 APPVAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGMEVHNAKTKP 294
|||||
QY 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTSKTK 109
|||||
Db 295 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTSKTK 343
|||||

Search completed: June 21, 2002, 08:32:14
Job time: 88 sec.

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:32:14 ; Search time 77.71 Seconds
(without alignments)
34.575 Million cell updates/sec

Title: US-09-674-857-3
Perfect score: 587
Sequence: 1 APPVAGGSPVFLPPPKPDT.....CKVSKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep: *
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5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep: *
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	562	95.7	468	4	US-09-485-737B-67 Sequence 67, Appl
2	562	95.7	711	4	US-09-485-737B-90 Sequence 90, Appl
3	557	94.9	110	3	US-08-444-644-21 Sequence 21, Appl
4	557	94.9	110	4	US-08-232-246A-21 Sequence 21, Appl
5	557	94.9	116	2	US-08-232-539D-55 Sequence 55, Appl
6	557	94.9	212	1	US-08-430-633-4 Sequence 4, Appl
7	557	94.9	212	2	US-08-620-694A-4 Sequence 4, Appl
8	557	94.9	212	3	US-08-936-854-4 Sequence 4, Appl
9	557	94.9	212	3	US-09-022-255-4 Sequence 4, Appl
10	557	94.9	212	3	US-09-022-696-4 Sequence 4, Appl
11	557	94.9	212	3	US-09-022-253-4 Sequence 4, Appl
12	557	94.9	212	3	US-09-022-260-4 Sequence 4, Appl
13	557	94.9	212	4	US-09-022-259-4 Sequence 4, Appl
14	557	94.9	212	4	US-09-022-257-4 Sequence 4, Appl
15	557	94.9	232	2	US-08-595-043A-50 Sequence 50, Appl
16	557	94.9	235	4	US-09-131-247-6 Sequence 6, Appl
17	557	94.9	254	2	US-08-284-391B-33 Sequence 33, Appl
18	557	94.9	254	4	US-09-218-950-33 Sequence 33, Appl
19	557	94.9	316	4	US-09-178-869-4 Sequence 4, Appl
20	557	94.9	331	4	US-09-178-869-2 Sequence 2, Appl
21	557	94.9	347	1	US-07-940-861-43 Sequence 43, Appl
22	557	94.9	347	1	US-08-459-512-43 Sequence 43, Appl
23	557	94.9	347	2	US-08-459-657-43 Sequence 43, Appl
24	557	94.9	347	2	US-08-460-132-43 Sequence 43, Appl
25	557	94.9	347	4	US-08-466-465-8 Sequence 8, Appl
26	557	94.9	347	5	PCT-US92-02050-43 Sequence 43, Appl
27	557	94.9	360	4	US-09-180-100-11 Sequence 11, Appl

28	557	94.9	371	1	US-08-236-311-7	Sequence 7, Appl
29	557	94.9	371	3	US-08-457-918-7	Sequence 7, Appl
30	557	94.9	376	4	US-09-180-100-22	Sequence 22, Appl
31	557	94.9	387	1	US-08-470-299-4	Sequence 4, Appl
32	557	94.9	388	4	US-09-131-247-16	Sequence 16, Appl
33	557	94.9	389	4	US-09-131-247-14	Sequence 14, Appl
34	557	94.9	396	2	US-08-784-512-3	Sequence 3, Appl
35	557	94.9	396	4	US-09-176-228-3	Sequence 3, Appl
36	557	94.9	424	4	US-09-333-593A-8	Sequence 8, Appl
37	557	94.9	424	5	PCT-US95-03866-12	Sequence 12, Appl
38	557	94.9	424	5	PCT-US95-03866-11	Sequence 11, Appl
39	557	94.9	437	5	PCT-US96-10043-11	Sequence 11, Appl
40	557	94.9	442	5	PCT-US96-10043-9	Sequence 9, Appl
41	557	94.9	446	3	US-08-397-411-7	Sequence 7, Appl
42	557	94.9	449	1	US-08-458-516-13	Sequence 13, Appl
43	557	94.9	449	3	US-08-897-236-23	Sequence 23, Appl
44	557	94.9	449	4	US-09-679-397-2	Sequence 2, Appl
45	557	94.9	451	2	US-08-887-352B-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-485-737B-67
; Sequence 67, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patent version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-67

Query Match 95.7%; Score 562; DB 4; Length 468;
Best Local Similarity 95.5%; Pred. No. 1.4e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 APPVAGGSPVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNKYDGVVHNATK 60
Db 251 APELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNKYDGVVHNATK 310
QY 61 PREEQYNSTRYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTISKAK 110
Db 311 PREEQYNSTRYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTISKAK 360

RESULT 2
US-09-485-737B-90
; Sequence 90, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,

```
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

Query Match          95.7%; Score 562; DB 4; Length 711;
Best Local Similarity 95.5%; Pred. No. 2.5e-58;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTK 60
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Db 251 APPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTK 310
   || : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 PREEQNSTYRVVSVLTVHLQDWLNKGKEYCKVSNKGLPSSIEKTIKSAK 110
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 311 PREEQNSTYRVVSVLTVHLQDWLNKGKEYCKVSNKALPASIEKTIKSAK 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
US-08-444-644-21
; Sequence 21, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
```

```
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
US-08-444-644-21

Query Match          94.9%; Score 557; DB 3; Length 110;
Best Local Similarity 94.5%; Pred. No. 8e-59;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTK 60
   || : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 APPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTK 60
   || : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 PREEQNSTYRVVSVLTVHLQDWLNKGKEYCKVSNKGLPSSIEKTIKSAK 110
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 PREEQNSTYRVVSVLTVHLQDWLNKGKEYCKVSNKALPAIEKTIKSAK 110
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
US-08-232-246A-21
; Sequence 21, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
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LEN3TH: 110 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLESCULE TYPE: protein
 FRAGMENT TYPE: Internal
 US-08-232-246A-21

Query Match 94.9%; Score 557; DB 4; Length 110;
 Best Local Similarity 94.5%; Pred. No. 8e-59;
 Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 || : |||||
 Db 1 APELLGGPSVFLFPPPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 || : |||||
 QY 61 PREEQNSTYRVVSVLTVLHQDLNCKEYKCKVSNKGLPSSIEKTIKAK 110
 || : |||||
 Db 61 PREEQNSTYRVVSVLTVLHQDLNCKEYKCKVSNKGLPSSIEKTIKAK 110
 || : |||||

RESULT 5

US-08-232-539D-55
 ; Sequence 55, Application US/08232539D
 ; Patent No. 5965709
 ; GENERAL INFORMATION:
 ; APPLICANT: Presta, Leonard G.
 ; APPLICANT: Jardieu, Paula M.
 ; TITLE OF INVENTION: Ige Antagonists
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/232,539D
 ; FILING DATE: 21-Apr-1994
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/178583
 ; FILING DATE: 07-JAN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/744768
 ; FILING DATE: 14-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Svoboda, Craig G.
 ; REGISTRATION NUMBER: 39,044
 ; REFERENCE/DOCKET NUMBER: P0718P3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1489
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 55:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 116 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-08-232-539D-55

Query Match 94.9%; Score 557; DB 2; Length 116;
 Best Local Similarity 94.5%; Pred. No. 8.6e-59;
 Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 || : |||||

Db 6 APELLGGPSVFLFPPPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 65
 QY 61 PREEQNSTYRVVSVLTVLHQDLNCKEYKCKVSNKGLPSSIEKTIKAK 110
 || : |||||
 Db 66 PREEQNSTYRVVSVLTVLHQDLNCKEYKCKVSNKGLPSSIEKTIKAK 115
 || : |||||

RESULT 6

US-08-430-633-4
 ; Sequence 4, Application US/08430633
 ; Patent No. 5726286
 ; GENERAL INFORMATION:
 ; APPLICANT: ALDERSON, MARK
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: COHEN, JEFFREY
 ; APPLICANT: COMEAU, MICHAEL
 ; APPLICANT: FARRAH, THERESA
 ; APPLICANT: SPRIGGS, MELANIE
 ; TITLE OF INVENTION: Isolated Epstein-Barr Virus BzLF2 proteins
 ; TITLE OF INVENTION: That Bind MHC Class II Beta Chains
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA
 ; ZIP: 98101

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Apple Operating System 7.1
 ; SOFTWARE: Microsoft Word for Apple, Version 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/430,633
 ; FILING DATE: 28-APR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/235,397
 ; FILING DATE: 04/28/94
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia A.
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 2612
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206)587-0430
 ; TELEFAX: (206)233-0644
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 212 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLESCULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: Human
 ; IMMEDIATE SOURCE:
 ; CLONE: IgG1 FC
 ; US-08-430-633-4

Query Match 94.9%; Score 557; DB 1; Length 212;
 Best Local Similarity 94.5%; Pred. No. 1.9e-58;
 Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 || : |||||
 Db 14 APELLGGPSVFLFPPPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
 || : |||||
 QY 61 PREEQNSTYRVVSVLTVLHQDLNCKEYKCKVSNKGLPSSIEKTIKAK 110
 || : |||||
 Db 74 PREEQNSTYRVVSVLTVLHQDLNCKEYKCKVSNKGLPSSIEKTIKAK 123
 || : |||||

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RESULT 7
US-08-620-694A-4
; Sequence 4, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: IgG1 Fc
;
US-08-620-694A-4

Query Match 94.9%; Score 557; DB 2; Length 212;
Best Local Similarity 94.5%; Pred. No. 1.9e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDMLSRPTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : |||||
Db 14 APELLGGPSVFLFPKPKDMLSRPTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
|| : |||||

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
|||||
Db 74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAK 123
|||||

RESULT 8
US-08-936-854-4
; Sequence 4, Application US/08936854
; Patent No. 5925734
; GENERAL INFORMATION:

```

```

; APPLICANT: ALDERSON, MARK
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: COHEN, JEFFREY
; APPLICANT: COMEAU, MICHAEL
; APPLICANT: FARRAH, THERESA
; APPLICANT: SPRIGGS, MELANIE
; TITLE OF INVENTION: Isolated Epstein-Barr Virus B2LF2 Proteins
; THAT BIND MHC CLASS II BETA CHAINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,633
; FILING DATE: 28-APR-1995
; APPLICATION NUMBER: 08/235,397
; FILING DATE: 04/28/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2612
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: IgG1 Fc
;
US-08-936-854-4

Query Match 94.9%; Score 557; DB 2; Length 212;
Best Local Similarity 94.5%; Pred. No. 1.9e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDMLSRPTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : |||||
Db 14 APELLGGPSVFLFPKPKDMLSRPTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
|| : |||||

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
|||||
Db 74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAK 123
|||||

RESULT 9
US-09-022-255-4
; Sequence 4, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Human
IMMEDIATE SOURCE:
CLONE: IgG1 Fc
US-09-022-255-4

Query Match 94.9%; Score 557; DB 3; Length 212;
Best Local Similarity 94.5%; Pred. No. 1.9e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : |||||
DB 14 APPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
QY 61 PREEQYNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 110
|| : |||||
DB 74 PREEQYNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 123

RESULT 10
US-09-022-696-4
Sequence 4, Application US/09022696
Patent No. 6072037
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA

```

```

COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Human
IMMEDIATE SOURCE:
CLONE: IgG1 Fc
US-09-022-696-4

Query Match 94.9%; Score 557; DB 3; Length 212;
Best Local Similarity 94.5%; Pred. No. 1.9e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : |||||
DB 14 APPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
QY 61 PREEQYNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 110
|| : |||||
DB 74 PREEQYNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 123

RESULT 11
US-09-022-253-4
Sequence 4, Application US/09022253
Patent No. 6096305
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh

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; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,253
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694
; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. 6096305 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: IgG1 Fc
;
US-09-022-253-4
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Query Match 94.9%; Score 557; DB 3; Length 212;
Best Local Similarity 94.5%; Pred. No. 1.9e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : |||||
Db 14 APPELLGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
|| : |||||

QY 61 PREEQNSTYRYVSVLTVLHQDLNKGKEYCKVSKNGLPSSIEKTISKAK 110
|| : |||||
Db 74 PREEQNSTYRYVSVLTVLHQDLNKGKEYCKVSKNGLPAPIEKTISKAK 123
|| : |||||
```

```
RESULT 12
US-09-022-260-4
; Sequence 4, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/022,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: IgG1 Fc
;
US-09-022-260-4

Query Match 94.9%; Score 557; DB 3; Length 212;
Best Local Similarity 94.5%; Pred. No. 1.9e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : |||||
Db 14 APPELLGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
|| : |||||

QY 61 PREEQNSTYRYVSVLTVLHQDLNKGKEYCKVSKNGLPSSIEKTISKAK 110
|| : |||||
Db 74 PREEQNSTYRYVSVLTVLHQDLNKGKEYCKVSKNGLPAPIEKTISKAK 123
|| : |||||

RESULT 13
US-09-022-259-4
; Sequence 4, Application US/09022259
; Patent No. 6191104
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
```


;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/410,535
;; FILING DATE: 23 MARCH 1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,695
;; REFERENCE/DOCKET NUMBER: 2617-B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 212 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; ORIGINAL SOURCE:
;; ORGANISM: Human
;; IMMEDIATE SOURCE:
;; CLONE: IgG1 Fc
US-09-022-259-4

Query Match 94.9%; Score 557; DB 4; Length 212;
Best Local Similarity 94.5%; Pred. No. 1.9e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 14 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
QY 61 PREQYNSTYRVVSVLTVLHQDLNKGKEYCKVSKNGLPSSIEKTIKSKAK 110
DB 74 PREQYNSTYRVVSVLTVLHQDLNKGKEYCKVSKNGLPAPIEKTISKAK 123

RESULT 14
US-09-022-257-4
; Sequence 4, Application US/09022257
; Patent No. 6197525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995

;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,695
;; REFERENCE/DOCKET NUMBER: 2617-B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 212 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; ORIGINAL SOURCE:
;; ORGANISM: Human
;; IMMEDIATE SOURCE:
;; CLONE: IgG1 Fc
US-09-022-257-4
Query Match 94.9%; Score 557; DB 4; Length 212;
Best Local Similarity 94.5%; Pred. No. 1.9e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 14 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
QY 61 PREQYNSTYRVVSVLTVLHQDLNKGKEYCKVSKNGLPSSIEKTIKSKAK 110
DB 74 PREQYNSTYRVVSVLTVLHQDLNKGKEYCKVSKNGLPAPIEKTISKAK 123

RESULT 15
US-08-595-043A-50
; Sequence 50, Application US/08595043A
; Patent No. 5935824
; GENERAL INFORMATION:
; APPLICANT: SGARLATO, GREGORY D.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,043A
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: SGAR-00371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-595-043A-50

Query Match 94.9%; Score 557; DB 2; Length 232;
 Best Local Similarity 94.5%; Pred. No. 2.2e-58;
 Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY	1	APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK	60
Db	16	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK	75
QY	61	PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK	110
Db	76	PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTTISKAK	125

Search completed: June 21, 2002, 08:32:14
 Job time: 88 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:36:09 ; Search time 224.82 Seconds
(without alignments)
54.346 Million cell upd

Title: US-09-674-857-10
 Perfect score: 588
 Sequence: 1 APPVAGGSPVFLEPPPKPKDT.....CKVSNKALPAPIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum	DB	seq	length:	0
Maximum	DB	seq	length:	20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_032802:*

1:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
2:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
3:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
4:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
5:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
6:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
7:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
8:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*
9:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*
10:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:*
11:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*
12:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*
13:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*
14:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*
15:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:*
16:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*
17:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:*
18:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
19:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
20:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
21:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
22:	/SIDS1/cgcdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	572	97.3	110	13	AAR27680	Human immunoglobul
2	572	97.3	110	14	AAR41684	Undefined ORF2 enc
3	572	97.3	116	20	AAV42621	Human IgG1 Fc gamma
4	572	97.3	212	15	AAR87023	Immunoglobulin G1
5	572	97.3	212	17	AAR37264	Human immunoglobul
6	572	97.3	212	17	AAW02305	Human IgG1 Fc regi
7	572	97.3	212	19	AAW47354	Human immunoglobul
8	572	97.3	212	20	AAV23637	IgG1 Fc protein us
9	572	97.3	212	20	AAW92411	Human IgG1 Fc prot
10	572	97.3	212	21	AAV99937	Human IgG1 Fc regi
11	572	97.3	212	21	AAV97182	Human immunoglobul

12	572	97.3	212	21	AAV97250	Human immunoglobulin Fc region of human
13	572	97.3	212	21	AAB03809	Fc region of human
14	572	97.3	212	22	AAB62062	Fc region of human
15	572	97.3	212	22	AAV72750	Human immunoglobulin
16	572	97.3	218	21	AAB07474	Native IgG Fc regi
17	572	97.3	218	21	AAB07475	Native IgG Fc regi
18	572	97.3	218	22	AAB67701	Human IgG Fc 1 all
19	572	97.3	218	22	AAB67202	Human IgG Fc 1 all
20	572	97.3	218	22	AAB76421	Human IgG1 non-A F
21	572	97.3	218	22	AAB76422	Human IgG1 A allot
22	572	97.3	224	8	AAP70173	Sequence of human
23	572	97.3	224	9	AAP82508	Immunoglobulin G F
24	572	97.3	228	21	AAB16955	Human IgG1 Fc prot
25	572	97.3	228	21	AAV96529	Human IgG1 Fc chai
26	572	97.3	228	22	AAB98953	Human IgG1 Fc regi
27	572	97.3	232	18	AAW26232	Human IgG1 hinge/F
28	572	97.3	232	21	AAW28690	Human IgGgamma1 hi
29	572	97.3	232	21	AAV95579	Human immunoglobul
30	572	97.3	232	21	AAV70251	Human immunoglobul
31	572	97.3	232	22	AAE02642	Human immunoglobul
32	572	97.3	232	22	AAV72915	Human partial IgG1
33	572	97.3	232	22	AAB80897	Human IgGgamma1 hi
34	572	97.3	232	22	AAW49155	Human immunogloblin
35	572	97.3	233	20	AAV06617	Human Fc (IgG1) .
36	572	97.3	235	20	AAV01372	Amino acid sequenc
37	572	97.3	235	22	AAW50246	Human IgG1 Fc regi
38	572	97.3	243	21	AAB17957	Fc-MMP inhibitor f
39	572	97.3	247	21	AAB16958	Fc-TMP protein seq
40	572	97.3	247	21	AAB16961	TMP-Fc protein seq
41	572	97.3	248	21	AAB17951	Fc-TNF-alpha inhib
42	572	97.3	248	21	AAB17952	TNF-alpha inhibitor
43	572	97.3	248	21	AAB17953	Fc-IL-1 antagonist
44	572	97.3	248	21	AAB17954	IL-1 antagonist-Fc
45	572	97.3	250	21	AAB17958	MMP inhibitor-Fc f

ALIGNMENTS

RESULT	1	
AAR27680	AAR27680	
ID	AAR27680 standard; Protein; 110 AA.	
XX		
XX	AAR27680;	
XX		
XX		
DT	10-MAR-1993 (first entry)	
XX		
DE	Human immunoglobulin IgG1 CH2 region.	
XX		
KW	Isoallotype; IgG1 G1m(1,2,17); anti-allotype response;	
KW	humanised Ab.	
XX		
XX		
OS	Homo sapiens.	
XX		
PN	W09216562-A.	
XX		
PD	01-OCT-1992.	
XX		
PF	12-MAR-1992; 92WO-GB000445.	
XX		
PR	12-MAR-1991; 91GB-0005245.	

Humanised antibodies having modified allotypic determinant useful for matching allotypes in therapy with decreased likelihood of causing undesirable immune responses

Disclosure: Fig 4c; 57pp; English.

XX In humans, IgG1 may exist as either of two allotypes at site 1, 2
 CC or 17. The inventor's propose eliminating these allotypes by
 CC amino acid changes to agree with the sequences of IgG2, IgG3 and
 CC IgG4. None of the allotype sites (1, 2 and 17) are located within
 CC the CH2 domain. New "isoallotypes" should be suitable for therapeutic
 CC use in all patients. See AAR27678-R27681.
 XX
 SQ Sequence 110 AA;

Query Match 97.3%; Score 572; DB 13; Length 110;
 Best Local Similarity 97.3%; Pred. No. 4.9e-50;
 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 II : |||||
 Db 1 apellgppsvflfppkpkdtlmisrtpetvcvvdvshedpevkfnwvdgvevhnaktk 60
 || : |||||

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETISKAK 110
 || : |||||
 Db 61 preeqynstyrsvsvltvlhqdwlngkeyckvsnkalpapiektiskak 110
 || : |||||

RESULT 2
 AAR41684
 ID AAR41684 standard; Protein; 110 AA.
 XX
 AC AAR41684;
 XX
 DT 20-OCT-1993 (first entry)
 XX
 DE Undefined ORF2 encoded by pAH4602.
 XX
 XX Polymerase chain reaction; primer; PCR; amplify; murine; heavy;
 KW light; chain; variable; constant; region; anti-human; transferrin;
 KW receptor; antibody; brain; capillary; endothelial cell; conjugate;
 KW neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke;
 KW epilepsy; Parkinsons disease; Alzheimers disease.
 XX
 OS Synthetic.
 XX
 PN WO9310819-A.
 XX
 PD 10-JUN-1993.
 XX
 PF 24-NOV-1992; 92WO-US10206.
 XX
 PR 26-NOV-1991; 91US-0800458.
 XX
 PA (ALKE-) ALKERMES INC.
 XX
 PI Friden PM;
 XX
 DR WPI; 1993-196742/24.
 XX
 DR N-PSDB; AAQ43844.
 XX
 PT Antibody conjugates specific for transferrin receptor - used
 PT for diagnosis and treatment of cancer, AIDS and neurological
 PT disorders
 XX
 PS Disclosure; Fig 11K; 151pp; English.
 XX
 XX The sequences given in AAR1682-85 are encoded by the expression vector,
 CC pAH4602. This vector contains open reading frames encoding the heavy
 CC chain variable region (VH) of the antibody 128.1, an ampicillin
 CC resistance gene and a histidine (histidinol) selection marker.
 CC Transcription of the VH gene is from the VH promoter of the murine
 CC 27.44 gene. The vector also includes a heavy chain immunoglobulin
 CC enhancer and the human gamma constant region (CH). The VH region of
 CC 128.1 was isolated by polymerase chain reaction and cloned into plasmid
 CC pAH4274. This was achieved by digesting the plasmid and the product
 CC with EcoRV and NheI. The VH gene was inserted in-frame with the human

CC gamma1 CH region CH at the 3' end of the VH-J region by means of a NheI
 CC site. 128.1 is an anti-human transferrin receptor antibody which binds
 CC to the transferrin receptor on brain capillary endothelial cells. This
 CC antibody may be used in a conjugate in which it is linked to a neuro-
 CC pharmacological or diagnostic agent. The conjugate may be used to treat
 CC or prevent neurological disorders eg. brain tumours, AIDS, stroke,
 CC epilepsy, Parkinsons and Alzheimers disease. It may also be used for
 CC diagnostic methods.
 XX
 SQ Sequence 110 AA;

Query Match 97.3%; Score 572; DB 14; Length 110;
 Best Local Similarity 97.3%; Pred. No. 4.9e-50;
 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 II : |||||
 Db 1 apellgppsvflfppkpkdtlmisrtpetvcvvdvshedpevkfnwvdgvevhnaktk 60
 || : |||||

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETISKAK 110
 || : |||||
 Db 61 preeqynstyrsvsvltvlhqdwlngkeyckvsnkalpapiektiskak 110
 || : |||||

RESULT 3
 AAY42621
 ID AAY42621 standard; protein; 116 AA.
 XX
 AC AAY42621;
 XX
 DT 10-JAN-2000 (first entry)
 XX
 DE Human IgG1 Fc gamma2 region.
 XX
 KW Immunoglobulin E; IgE; antagonist; Fc epsilon RI receptor; human; bds;
 KW receptor-binding; binding determinant sequence; anti-IgE antibody;
 KW allergic disease.
 XX
 OS Homo sapiens.
 XX
 PN US5965709-A.
 XX
 PD 12-OCT-1999.
 XX
 PF 21-APR-1994; 94US-0232539.
 XX
 PR 14-AUG-1991; 91US-0744768.
 XX
 PR 07-JAN-1994; 94US-0178583.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta IG;
 XX
 DR WPI; 1999-579941/49.
 XX
 PT Immunoglobulin E variants as peptide antagonists useful for raising and
 PT screening anti-immunoglobulin E (IgE) antibodies, in the isolation and
 PT purification of Fc epsilon RI receptor and in the treatment of allergic
 PT diseases -
 XX
 PS Example 2; Column 61-62; 37pp; English.
 XX
 XX The invention provides immunoglobulin E (IgE) antagonists comprising one
 CC or more of the Fc epsilon RI receptor-binding determinant sites of human
 CC IgE. The antagonists include IgE variants comprising an immunoglobulin
 CC template and binding determinant sequences (bds) CDBds, EFBds and the
 CC sequence shown in AAY42581. The CDBds (CD loop binding determinant
 CC sequence) are selected from the sequences shown in AAY42567-Y42577 and
 CC the EFBds (EF loop binding determinant sequence) are selected from
 CC sequences shown in AAY42578-Y42580. The variants are useful in raising
 CC and screening anti-IgE antibodies, in the isolation and purification of
 CC Fc epsilon RI receptor and in the treatment and prophylaxis of allergic

CC diseases.

XX Sequence 116 AA;

 Query Match 97.3%; Score 572; DB 20; Length 116;

 Best Local Similarity 97.3%; Pred. No. 5.2e-50;

 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

 || : |||||

Db 6 apellgppsvflfpkpdktdlmisrtpetvctvvdshedpevkfnwydvgevhnaakt 65

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110

 |||||

Db 66 preeqynstyrsvsvltvlhqdwlngkeykckvsnkalpapiektiskak 115

RESULT 4

AAR87023

ID AAR87023 standard; protein; 212 AA.

XX

AC AAR87023;

XX

DT 11-JUN-1996 (first entry)

XX

DE Immunoglobulin G1 Fc region.

XX

KW BZLF2; Epstein-Barr virus; EBV; C-type lectin; beta chain; MHC; antigen;

XX

KW major histocompatibility complex; immunoglobulin; cytotoxic T cell;

XX

KW autoimmune disease; myasthenia gravis; multiple sclerosis; allergy;

XX

KW systemic lupus erythematosus; organ transplant rejection; asthma; IL-7;

XX

KW tissue transplant rejection; therapy; cancer; viral disease; mouse;

XX

XX

XX

OS Homo sapiens.

XX

WO9530015-A2.

XX

PD 09-NOV-1995.

XX

PF 28-APR-1995; 95WO-US05348.

XX

PR 28-APR-1994; 94US-0235397.

XX

PA (IMMV) IMMUNEX CORP.

XX

PA (UMOR) UNIV MISSOURI.

XX

PA (USSH) US NAT INST OF HEALTH.

XX

PI Alderson M, Armitage RJ, Cohen JL, Comeau MR, Farrah TM;

XX

PI Hutt-fletcher LM, Spriggs MK;

XX

XX WPI; 1995-393086/50.

XX

XX

XX Epstein-Barr virus BZLF2 fusion proteins - used for treating e.g.

XX

XX auto-immune disease, transplant rejection, allergy, asthma, cancer

XX

XX or viral infection.

XX

XX Example 1; Page 38-39; 51pp; English.

XX

XX This sequence represents the human immunoglobulin G1 Fc region, and was

XX

XX used in creating a BZLF2-immunoglobulin Fc fusion protein (BZLF2/Fc).

XX

XX BZLF2 is a Epstein-Barr virus (EBV) protein. To create BZLF2/Fc, this

XX

XX sequence, the leader sequence of mouse interleukin-7 (IL-7) (see

XX

XX AAR87021), a flag octapeptide (see AAR87022) and a flexible linker (see

XX

XX AAR87024) are joined to the extracellular domain (residues 34 to 223) of

XX

XX the BZLF2 sequence (see AAR87020). The BZLF2/Fc fusion protein

XX

XX containing this sequence is referred to in claim 4. BZLF2 proteins are

XX

XX members of the C-type lectin family. The C-type lectin domain is found

XX

XX in type II membrane proteins. The BZLF2 protein is capable of binding

XX

XX the beta chain of a major histocompatibility complex (MHC) class II

XX

XX antigen. Fusion proteins with an oligomerising zipper domain (OZD),

XX

XX instead of an immunoglobulin Fc region, can also be created. BZLF2

CC proteins inhibit antigen-specific antibody formation, proliferation of

CC blood mononuclear cells and cytotoxic T cell responses. They also

CC exhibit superantigen-like activity. The proteins can be used for

CC treating or preventing autoimmune diseases such as myasthenia gravis,

CC multiple sclerosis and systemic lupus erythematosus. Also, for treating

CC organ or tissue transplant rejection and for treating or preventing

CC allergy or asthma. They can be used for treating cancer and viral

CC disease, especially EBV infection.

XX

XX Sequence 212 AA;

 Query Match 97.3%; Score 572; DB 16; Length 212;

 Best Local Similarity 97.3%; Pred. No. 1.1e-49;

 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

 || : |||||

Db 14 apellgppsvflfpkpdktdlmisrtpetvctvvdshedpevkfnwydvgevhnaakt 73

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110

 |||||

Db 74 preeqynstyrsvsvltvlhqdwlngkeykckvsnkalpapiektiskak 123

RESULT 5

AAR97264

ID AAR97264 standard; protein; 212 AA.

XX

AC AAR97264;

XX

DT 14-FEB-1997 (first entry)

XX

DE Human immunoglobulin G1 Fc region.

XX

KW HVS14; major histocompatibility complex; MHC; Class II; allergy;

XX

KW binding protein; inhibition; antigen presentation; superantigen;

XX

KW treatment; cancer; viral disease; immunoglobulin; IgG1; Fc region;

XX

XX fusion protein.

XX

OS Homo sapiens.

XX

PN WO9617939-A1.

XX

PD 13-JUN-1996.

XX

PF 07-DEC-1995; 95WO-US15948.

XX

PR 06-JUN-1995; 95US-0485549.

XX

PR 07-DEC-1994; 94US-0351901.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Alderson M, Armitage R, Spriggs M, Yao Z;

XX

DR WPI; 1996-287183/29.

XX

XX Isolated Herpes virus Saimiri 14 proteins - useful for treating

XX

XX autoimmune disorders, transplant rejection, allergy, asthma, cancer

XX

XX or viral disease

XX

XX Claim 4; Page 32; 45pp; English.

XX

XX The present sequence is a human immunoglobulin G1 Fc region, which

XX

XX can form a claimed fusion protein with the Herpesvirus saimiri

XX

XX (HVS) major histocompatibility complex (MHC) Class II binding

XX

XX protein, HVS14. The fusion protein can be used to treat cancer or

XX

XX viral disease, as HVS14 inhibits antigen presentation, or acts as

XX

XX a superantigen.

XX

XX Sequence 212 AA;

```
Query Match          97.3%; Score 572; DB 17; Length 212;
Best Local Similarity 97.3%; Pred. No. 1.le-49;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   || : |||||
Db 14 apellggpsvflfpkpkdtlmisrtpetvcvvdvshdpvkfnwydgvevhnaktk 73

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
   |||||
Db 74 preeqynstyrsvsvltvlhqdwlngkeykckvsnkalpapiektiskak 123

RESULT 6
AAW02305
ID AAW02305 standard; Protein; 212 AA.
AC AAW02305;
DT 05-DEC-1996 (first entry)
DE Human IgG1 Fc region.
XX IgG1; interleukin-17 receptor; IL-17R.
KW Homo sapiens.
OS Homo sapiens.
PN WO9629408-A1.
XX 26-SEP-1996.
XX 21-MAR-1996; 96WO-US04018.
XX 07-AUG-1995; 95US-0538765.
XX 23-MAR-1995; 95US-0410535.
XX (IMMV ) IMMUNEX CORP.
PI Fanslow WC, Spriggs MK, Yao Z;
XX WPI; 1996-443184/44.
XX DNA encoding interleukin-17 receptor - useful for regulating immune
PT and inflammatory responses, or to suppress graft rejection
XX Example 1; Page 33; 52pp; English.
XX The human IgG1 Fc region (AAW02305) can be used as a fusion partner
CC for interleukin-17 receptor (IL-17R) proteins (see also AAW04184-85),
CC allowing purification of recombinant IL-17R using protein A or
CC protein G affinity chromatography. Fusions between Fc and HVS13
CC (see also AAW02387), a viral homologue of IL-17, and between Fc
CC and murine CTLA8 (AAW02386) were used to identify cells that
CC express the murine IL-17R. Selected murine thymoma EL4 cells
CC were used as a source of murine IL-17R cDNA (AAT33800).
XX Sequence 212 AA;

Query Match          97.3%; Score 572; DB 17; Length 212;
Best Local Similarity 97.3%; Pred. No. 1.le-49;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   || : |||||
Db 14 apellggpsvflfpkpkdtlmisrtpetvcvvdvshdpvkfnwydgvevhnaktk 73

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
   |||||
Db 74 preeqynstyrsvsvltvlhqdwlngkeykckvsnkalpapiektiskak 123

RESULT 7
AAW47354
ID AAW47354 standard; protein; 212 AA.
AC AAW47354;
DT 01-JUN-1998 (first entry)
DE Human Immunoglobulin G1 Fc fragment.
XX EBV; BZLF2; beta-chain; major histocompatibility complex; MHC;
KW class II; antigen; prevention; treatment; autoimmune disease;
KW transplant rejection; allergy; asthma; super-antigen; IgG1;
KW Epstein-Barr virus; human; immunoglobulin G1; Fc fragment.
XX Homo sapiens.
OS Homo sapiens.
PN US5726286-A.
XX 10-MAR-1998.
XX 28-APR-1995; 95US-0430633.
XX 28-APR-1995; 95US-0430633.
XX 28-APR-1994; 94US-0235397.
XX (IMMV ) IMMUNEX CORP.
PA Alderson M, Armitage RJ, Cohen JI, Comeau MR, Farrah TM;
PI Hutt-Fletcher LM, Spriggs MK;
XX WPI; 1998-192827/17.
XX Epstein-Barr virus protein - binds to major histocompatibility
PT complex class II beta chain, useful for treating, e.g. auto-immune
PT diseases or transplant rejection
XX Example 1; Columns 31-32; 25pp; English.
XX The present sequence was used in the preparation of a synthetic
CC construct containing the Epstein-Barr virus (EBV) BZLF2 protein,
CC which is capable of binding a beta-chain of a major
CC histocompatibility complex (MHC) class II antigen.
CC The protein can be used to inhibit antigen-specific antibody
CC formation, peripheral blood mononuclear cell proliferation and
CC cytotoxic T-cell responses, e.g. in the prevention or treatment of
CC autoimmune diseases, transplant rejection, allergies or asthma,
CC and as a super-antigen.
XX Sequence 212 AA;

Query Match          97.3%; Score 572; DB 19; Length 212;
Best Local Similarity 97.3%; Pred. No. 1.le-49;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   || : |||||
Db 14 apellggpsvflfpkpkdtlmisrtpetvcvvdvshdpvkfnwydgvevhnaktk 73

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
   |||||
Db 74 preeqynstyrsvsvltvlhqdwlngkeykckvsnkalpapiektiskak 123

RESULT 8
AAV23637
ID AAV23637 standard; protein; 212 AA.
AC AAV23637;
XX 06-SEP-1999 (first entry)
XX IgG1 Fc protein used to make BZLF2 fusion proteins.
DE
```

```
XX B2LF2 protein; beta chain; blood mononuclear mononuclear cell;
KW Class II major histocompatibility complex antigen; proliferation;
KW cytotoxic T cell response; antigen specific response; asthma;
KW autoimmune disease; transplant rejection.
XX
OS Homo sapiens.
XX
XX US5925734-A.
XX
XX 20-JUL-1999.
XX
XX 24-SEP-1997; 97US-0936854.
XX
XX 28-APR-1995; 95US-0430633.
XX
XX 28-APR-1994; 94US-0235397.
XX
XX 24-SEP-1997; 97US-0936854.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Alderson M, Armitage RJ, Cohen JI, Comeau MR, Farrah TM;
PI Hutt-Fletcher LM, Spriggs MK;
XX
XX WPI; 1999-418295/35.
XX
XX Epstein-Barr virus B2LF2 proteins
XX
XX Claim 2; Column 31-32; 25pp; English.
XX
XX The present sequence represents a protein used to create fusion proteins
CC with the Epstein-Barr virus B2LF2 proteins of the invention. The B2LF2
CC protein is capable of binding to a beta chain of a Class II major
CC histocompatibility complex antigen to inhibit an antigen-specific
CC response. B2LF2 is useful for inhibiting antigen-specific antibody
CC formation, the proliferation of blood mononuclear mononuclear cells,
CC and cytotoxic T cell responses. B2LF2 is also useful for inhibiting
CC undesirable antigen specific responses, e.g. in the treatment or
CC prevention of asthma; for preventing or treating autoimmune disease;
CC and for preventing tissue or organ transplant rejection.
XX
XX Sequence 212 AA;

Query Match 97.3%; Score 572; DB 20; Length 212;
Best Local Similarity 97.3%; Pred. No. 1.1e-49;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 14 apellggpsvflfpkpkdtlmisrtpevtcvvvdvshedpevkfnwvydgvvhnaktk 73

QY 61 PREEQNSTYRVVSVTLVHLDHQLNGKEYKCKVSNKALPAPIEKTISKAK 110
Db 74 preeqnstyrvvsvtlvhldhqlngkeykckvsnkalpapiektiskak 123

RESULT 9
AAW92411
ID AAW92411 standard; Protein; 212 AA.
XX
XX AAW92411;
XX
XX 21-APR-1999 (first entry)
XX
XX Human IgG1 Fc protein fragment.
XX
XX IL-17R; human; interleukin-17 receptor; immunoregulator; inhibitor;
KW T cell proliferation; T cell activation; organ; graft; rejection;
KW autoimmune disease; allergy; asthma; treatment; inflammatory disease;
KW B cell proliferation; immunoglobulin secretion; immunogen; IgG1; Fc.
XX
XX Homo sapiens.
XX

US5869286-A.
XX
XX 09-FEB-1999.
XX
XX 21-MAR-1996; 96US-0620694.
XX
XX 21-MAR-1996; 96US-0620694.
XX
XX 23-MAR-1995; 95US-0410535.
XX
XX 07-AUG-1995; 95US-0538765.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Fanslow WC, Spriggs MK, Yao Z;
XX
XX WPI; 1999-152766/13.
XX
XX Isolated interleukin-17 receptor DNA - used to develop products for
PT treating e.g. organ or graft rejection, autoimmune disease, allergy,
PT asthma or inflammatory disease
XX
XX Example 1; Column 31-32; 25pp; English.
XX
XX This sequence represents a human IgG1 Fc fragment which is used in the
CC construction of a fusion protein with human interleukin-17 receptor
CC (IL-17R). IL-17R polypeptides have immunoregulatory activity. They can be
CC used for inhibiting T cell proliferation, or for inhibiting T cell
CC activation. In particular they can be used for preventing or treating
CC organ or graft rejection, autoimmune disease, allergy or asthma. They can
CC also be used for the prevention or treatment of inflammatory disease in
CC which activated T cells play a role or for inhibiting B cell
CC proliferation or immunoglobulin secretion. The IL-17 polypeptides can
CC also be used as immunogens, reagents in in vitro assays, or as binding
CC agents for affinity purification procedures.
XX
XX Sequence 212 AA;

Query Match 97.3%; Score 572; DB 20; Length 212;
Best Local Similarity 97.3%; Pred. No. 1.1e-49;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 14 apellggpsvflfpkpkdtlmisrtpevtcvvvdvshedpevkfnwvydgvvhnaktk 73

QY 61 PREEQNSTYRVVSVTLVHLDHQLNGKEYKCKVSNKALPAPIEKTISKAK 110
Db 74 preeqnstyrvvsvtlvhldhqlngkeykckvsnkalpapiektiskak 123

RESULT 10
AAY99937
ID AAY99937 standard; Protein; 212 AA.
XX
XX AAY99937;
XX
XX 10-JAN-2001 (first entry)
XX
XX Human IgG1 Fc region.
XX
XX IL-17R; CTLA-8; interleukin 17; Herpesvirus saimiri; HVS 13;
KW human; antibody; immune suppression.
XX
XX Homo sapiens.
XX
XX US6072037-A.
XX
XX 06-JUN-2000.
XX
XX 12-FEB-1998; 98US-0022696.
XX
XX 21-MAR-1996; 96US-0620694.
XX
XX 23-MAR-1995; 95US-0410535.
```

PR 07-AUG-1995; 95US-0538765.

PA (IMMV) IMMUNEX CORP.

PI Fanslow WC, Spriggs MK, Yao Z;

PX WPI; 2000-411206/35.

XX Antibodies immunoreactive with interleukin-17 receptor protein useful
PT in interfering with receptor binding to CTLA-8, as components of
PT diagnostic or research assays or in affinity purification of the
PT receptor -

PS Disclosure; Column 31-32; 25pp; English.

XX The present invention relates to a novel receptor that binds Interleukin
CC 17 (IL-17, also known as CTLA-8) and a Herpesvirus saimiri homolog,
CC HVS13. The receptor is a type I transmembrane protein which is referred
CC to as IL-17R. Murine thymoma EL4 cells were found to express a
CC receptor for IL-17. An EL4 mammalian expression library was screened
CC and a cDNA encoding the receptor was identified (see AAA61238). The cDNA
CC was used to isolate DNA encoding human IL-17R by cross species
CC hybridisation. The human IL-17R cDNA and protein are described in
CC AAA61240 and AAY99941. The present sequence is a human IgG1 Fc region
CC that may be used with IL-17R to make a fusion protein. Soluble forms of
CC the receptor may be used to regulate immune responses, for example to
CC suppress rejection of organ grafts. Antibodies to IL-17R consisting of
CC amino acids 1-322 of murine IL-17R or 1-320 of human IL-17R may be
CC useful as components of diagnostic or research assays. Such antibodies
CC may also be used in affinity purification of the receptor.

XX Sequence 212 AA;

XX Query Match 97.3%; Score 572; DB 21; Length 212;
XX Best Local Similarity 97.3%; Pred. No. 1.1e-49;
XX Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGSPSVLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTK 60

DB 14 apellggpsvflfpkpkdtlmisrtpetvctvvvdvshedpevkfnwydgvghnaktk 73

QY 61 PREEOYNSTYRVVSVLTVLDHDLNGCKYCKVSNKALPAPIEKTISKAK 110

DB 74 preeqynstyrvvsvltvlhqdwlngckykckvsnkalpapipektiskak 123

RESULT 11

AAY97182

ID AAY97182 standard; Protein; 212 AA.

XX AC AAY97182;

XX DT 04-DEC-2000 (first entry)

XX DE Human immunoglobulin G1 Fc region.

XX IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
KW HVS13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KW anti-asthmatic; immunoglobulin G1; Fc region.

OS Homo sapiens.

XX US6096305-A.

XX PD 01-AUG-2000.

XX PF 11-FEB-1998; 98US-0022253.

XX PR 21-MAR-1996; 96US-0620694.

XX PR 23-MAR-1995; 95US-0410535.

XX PR 07-AUG-1995; 95US-0538765.

XX

PA (IMMV) IMMUNEX CORP.

PI Fanslow WC, Spriggs MK, Yao Z;

PX WPI; 2000-523862/47.

XX Suppressing rejection of a grafted syngeneic or allogeneic organ or
PT tissue in a graft recipient for organ transplantation involves
PT transfusing the organ or tissue with DNA encoding soluble
PT interleukin-17R receptor

PS Example 1; Column 31-32; 27pp; English.

XX A novel interleukin-17 receptor (IL-17R) was identified by screening a
CC cDNA library from T cell thymoma EL4 cells, which were identified as
CC binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
CC region and soluble IL-17 (CTLA-8) protein or a homologous
CC Herpesvirus saimiri (HSV) protein, designated HVS13. Suppressing
CC rejection of a grafted syngeneic or allogeneic organ or tissue in a graft
CC recipient involves transfusing the organ or tissue to be transplanted
CC with DNA encoding soluble IL-17R, so that expression of IL-17R by the
CC engrafted organ or tissue results in suppression of rejection. Soluble
CC IL-17R fragments comprise residues 1-322 of the murine IL-17R, residues
CC 1-320 of the human IL-17R, and fragments of the extracellular domain
CC that bind IL-17. The method is useful for regulating an immunoresponse,
CC for suppressing rejection of grafted organs or tissues in the recipient
CC and for treating or preventing diseases like allergy, asthma and
CC autoimmune diseases.

XX Sequence 212 AA;

XX Query Match 97.3%; Score 572; DB 21; Length 212;
XX Best Local Similarity 97.3%; Pred. No. 1.1e-49;
XX Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGSPSVLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTK 60

DB 14 apellggpsvflfpkpkdtlmisrtpetvctvvvdvshedpevkfnwydgvghnaktk 73

QY 61 PREEOYNSTYRVVSVLTVLDHDLNGCKYCKVSNKALPAPIEKTISKAK 110

DB 74 preeqynstyrvvsvltvlhqdwlngckykckvsnkalpapipektiskak 123

RESULT 12

AAY97250

ID AAY97250 standard; Protein; 212 AA.

XX AC AAY97250;

XX DT 04-DEC-2000 (first entry)

XX DE Human immunoglobulin G1 Fc region.

XX IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
KW HVS13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KW anti-asthmatic; immunoglobulin G1; Fc region.

OS Homo sapiens.

XX US6100235-A.

XX PD 08-AUG-2000.

XX PF 11-FEB-1998; 98US-0022260.

XX PR 21-MAR-1996; 96US-0620694.

XX PR 23-MAR-1995; 95US-0410535.

XX PR 07-AUG-1995; 95US-0538765.

XX PA (IMMV) IMMUNEX CORP.

PI Fanslow WC, Spriggs MK, Yao Z;
 XX WPI; 2000-548298/50.
 XX
 XX Regulating, treating or preventing immune or inflammatory response in a
 PT mammal, especially organ or graft rejection, allergy or asthma,
 PT comprises administering interleukin-17 receptors
 XX
 XX Example 1; Column 31-32; 26pp; English.
 XX
 XX A novel interleukin-17 receptor (IL-17R) was identified by screening a
 CC cDNA library from T cell thymoma EL4 cells, which were identified as
 CC binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
 CC region and soluble IL-17 (CTLA-8) protein or a homologous
 CC Herpesvirus saimiri (HSV) protein, designated HSV13. Regulating an
 CC immune or inflammatory response in a mammal comprises administering
 CC soluble IL-17R. Soluble IL-17R fragments comprise residues 1-322 of the
 CC murine IL-17R, residues 1-320 of the human IL-17R, and fragments of the
 CC extracellular domain that bind IL-17. The method is useful for regulating
 CC an immunoresponse, for treating or preventing diseases like allergy,
 CC asthma and autoimmune diseases, and for suppressing rejection of grafted
 CC organs or tissues in the recipient.
 XX
 XX Sequence 212 AA;
 SQ
 Query Match 97.3%; Score 572; DB 21; Length 212;
 Best Local Similarity 97.3%; Pred. No. 1.1e-49;
 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db 14 apellggpsvfifppkpkdtlmisrtpevtcvvvdvshedpevkfnwvdgvevhnaktk 73
 QY 61 PREEQNSTYRNVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAK 110
 Db 74 preeqnstyrnvsvltvlhqdlngkeyckvsnkalpapiektiskak 123
 QY 61 PREEQNSTYRNVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAK 110
 Db 74 preeqnstyrnvsvltvlhqdlngkeyckvsnkalpapiektiskak 123
 RESULT 13
 AAB03809
 ID AAB03809 standard; Protein; 212 AA.
 XX
 XX AAB03809;
 XX
 DT 13-OCT-2000 (first entry)
 XX
 DE Fc region of human immunoglobulin G1.
 XX
 KW Interleukin-17 receptor; IL-17R; CTLA8; antiinflammatory; antiallergic;
 KW immunosuppressive; organ rejection; graft rejection; autoimmune disease;
 KW allergy; asthma; IgG1; immunoglobulin G1; human.
 XX
 OS Homo sapiens.
 XX
 XX US6072033-A.
 XX
 PD 06-JUN-2000.
 XX
 XX 11-FEB-1998; 98US-0022255.
 XX
 XX 21-MAR-1996; 96US-0620694.
 PR 23-MAR-1995; 95US-0410535.
 PR 07-AUG-1995; 95US-0538765.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 XX Fanslow WC, Spriggs MK, Yao Z;
 XX WPI; 2000-411205/35.
 XX
 XX Interleukin-17 receptor protein useful for regulating immune functions
 PT and for preventing or treating organ or graft rejection, autoimmune

PT disease, allergy or asthma in human -
 XX
 PS Example 1; Column 31-32; 26pp; English.
 XX
 XX This invention relates to an isolated and purified interleukin-17
 CC receptor (IL-17R). A soluble IL-17 protein (CTLA8) and a herpesvirus
 CC siamiri (HVS13) open reading frame (homologous to CTLA8) were expressed
 CC as fusion proteins comprising an immunoglobulin Fc region, and used to
 CC screen for the expression of the IL-17R. The screening identified the
 CC novel receptor of the invention. IL-17R is a type I transmembrane
 CC protein that exhibits antiinflammatory, immunosuppressive, antiasthmatic
 CC and antiallergic activities, and is an inhibitor of T cell proliferation
 CC and activation. IL-17R can be used to regulate immune functions, and is
 CC useful for preventing or treating organ or graft rejection, autoimmune
 CC disease, allergy or asthma. The present sequence represents the Fc region
 CC of human immunoglobulin G1 (IgG1). This fragment of IgG1 forms part of
 CC the IL-17 fusion protein used to identify IL-17R.
 XX
 XX Sequence 212 AA;
 SQ
 Query Match 97.3%; Score 572; DB 21; Length 212;
 Best Local Similarity 97.3%; Pred. No. 1.1e-49;
 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db 14 apellggpsvfifppkpkdtlmisrtpevtcvvvdvshedpevkfnwvdgvevhnaktk 73
 QY 61 PREEQNSTYRNVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAK 110
 Db 74 preeqnstyrnvsvltvlhqdlngkeyckvsnkalpapiektiskak 123
 RESULT 14
 AAB62062
 ID AAB62062 standard; Protein; 212 AA.
 XX
 XX AAB62062;
 XX
 DT 29-MAY-2001 (first entry)
 XX
 DE Fc region of human immunoglobulin IgG1.
 XX
 KW CTLA-8; interleukin-17; IL-17; IL-17 receptor; IL-17R; human; IgG1;
 KW immunosuppressive; antiallergic; antiasthmatic; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 XX US6197525-B1.
 XX
 PD 06-MAR-2001.
 XX
 XX 11-FEB-1998; 98US-0022257.
 XX
 XX 21-MAR-1996; 96US-0620694.
 PR 23-MAR-1995; 95US-0410535.
 PR 07-AUG-1995; 95US-0538765.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 XX Yao Z, Spriggs MK, Fanslow WC;
 XX WPI; 2001-234480/24.
 XX
 XX New assay kits for detecting interleukin-17 (IL-17), IL-17 receptors
 PT and (antagonists or mimetics of) the interaction between IL-17 and
 PT IL-17 receptor, useful for treating autoimmune diseases -
 XX
 XX Example 1; Columns 31-32; 26pp; English.
 XX
 XX The invention is directed towards assays for detection of interleukin-17
 CC (IL-17), IL-17 receptor (IL-17R), and (antagonists or mimetics of) the

CC interaction between IL-17 and IL-17R. The assay kit comprises an IL-17R
 CC protein and a detecting reagent. The method is useful for inhibiting
 CC binding of IL-17 to cells expressing IL-17R. IL-17 receptors are also
 CC useful for preventing or treating organ or graft rejection, autoimmune
 CC diseases, allergy, asthma and inflammatory diseases in which activated
 CC T-cells play an important role. The present sequence represents Fc
 CC region of human immunoglobulin IgG1, used for constructing a murine
 CC CTLA-8/Fc fusion protein.
 XX
 SQ Sequence 212 AA;

Query Match 97.3%; Score 572; DB 22; Length 212;
 Best Local Similarity 97.3%; Pred. No. 1.1e-49;
 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 || : |||||
 Db 14 apellggsavflfpkpkdtlmisrtpevtcvcvvdvshedpevkfnwydgvvhnaktk 73
 || : |||||
 QY 61 PREEQYNSTYRVVSVLTVHLQDWLNKGKEYCKVSNKALPAPIETISKAK 110
 || : |||||
 Db 74 preeqynstyrvvsvltvhlqdwlngkeyckvsnkalpapietiskak 123

RESULT 15

AA72750
 ID AAY72750 standard; Protein; 212 AA.
 XX
 AC AAY72750;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Human immunoglobulin IgG1 Fc region.
 XX
 KW Human; Interleukin-17 receptor; IL-17R; immunosuppressive; antiallergic;
 KW antiasthmatic; antiinflammatory; graft rejection; autoimmune disease;
 KW inflammatory disease; allergy; CTLA-8; immunogen; immunoglobulin G; IgG1;
 KW asthma.
 XX
 OS Homo sapiens.
 XX
 PN US6191104-B1.
 XX
 PD 20-FEB-2001.
 XX
 PF 11-FEB-1998; 98US-0022259.
 XX
 PR 21-MAR-1996; 96US-0620694.
 PR 23-MAR-1995; 95US-0410535.
 PR 07-AUG-1995; 95US-0538765.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Spriggs MK, Fanslow WC;
 XX
 DR WPI; 2001-217901/22.
 XX

PT Suppressing rejection of grafted organ or tissue in graft recipient,
 PT involves administering to recipient a composition comprising
 PT interleukin 17 receptor protein -
 XX

PS Example 1; Column 31-32; 26pp; English.
 XX

CC The present sequence is the Fc region of human immunoglobulin IgG1
 CC which is used for constructing fusion protein with Interleukin-17
 CC receptor (IL-17R).
 CC The invention relates to Interleukin-17 receptors (IL-17R),
 CC Interleukin-17 and their corresponding nucleic acid molecules. IL-17R is
 CC a Type I transmembrane protein which is used for regulating the immune
 CC response. The invention is useful for suppressing rejection of a grafted
 CC organ or tissue in a graft recipient. Soluble IL-17 (CTLA-8) receptors
 CC are useful for preventing or treating organ or graft rejection,
 CC

CC autoimmune disease, allergy, asthma, and inflammatory disease in which
 CC activated T-cells play a role. Soluble IL-17 fusion proteins are used to
 CC screen cells for the expression of IL-17 receptor. Derivatives of IL-17R
 CC are also used as immunogens, reagents in in vitro assays, or as binding
 CC agents for affinity purification procedures.
 XX
 SQ Sequence 212 AA;

Query Match 97.3%; Score 572; DB 22; Length 212;
 Best Local Similarity 97.3%; Pred. No. 1.1e-49;
 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 || : |||||
 Db 14 apellggsavflfpkpkdtlmisrtpevtcvcvvdvshedpevkfnwydgvvhnaktk 73
 || : |||||
 QY 61 PREEQYNSTYRVVSVLTVHLQDWLNKGKEYCKVSNKALPAPIETISKAK 110
 || : |||||
 Db 74 preeqynstyrvvsvltvhlqdwlngkeyckvsnkalpapietiskak 123

Search completed: June 21, 2002, 08:36:10
 Job time: 324 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:59:33 ; Search time 176.89 Seconds
(without alignments)
107.578 Million cell updates/sec

Title: US-09-674-857-10
Perfect score: 588
Sequence: 1 APPVAGGSPVFLPPPKPKDT.....CKVSNKALPAPIKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: sp.archaea:*
 - 2: sp.bacteria:*
 - 3: sp.fungi:*
 - 5: sp.invertebrate:*
 - 6: sp.mammal:*
 - 7: sp.mhc:*
 - 8: sp.organelle:*
 - 9: sp.phage:*
 - 10: sp.plant:*
 - 11: sp.rodent:*
 - 12: sp.virus:*
 - 13: sp.invertebrate:*
 - 14: sp.unclassified:*
 - 15: sp.virus:*
 - 16: sp.bacteriaph:*
 - 17: sp.archaea:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	97.3	701	4 Q96PQ8	Q96pq8 homo sapien
2	469	79.8	337	6 Q95M34	Q95m34 equus caball
3	411	69.9	437	11 Q9R1A4	Q9R1a4 mus musculus
4	411	69.9	463	11 Q99LC4	Q99lc4 mus musculus
5	403	68.5	473	11 Q9P8L4	Q9p8l4 mus musculus
6	401	68.2	473	11 Q91Z05	Q91z05 mus musculus
7	397	67.5	468	11 Q99L31	Q99l31 mus musculus
8	397	67.5	473	11 Q99L25	Q99l25 mus musculus
9	142	24.1	375	4 Q9BSZ1	Q9bsz1 homo sapien
10	142	24.1	597	4 Q9B0B8	Q9b0b8 homo sapien
11	142	24.1	597	4 Q9BU10	Q9bu10 homo sapien
12	142	24.1	597	4 Q96BB9	Q96bb9 homo sapien
13	142	24.1	613	4 Q96EY0	Q96ey0 homo sapien
14	142	24.1	614	4 Q96GA6	Q96ga6 homo sapien
15	142	24.1	618	4 Q96AA6	Q96aa6 homo sapien
16	130.5	22.2	684	13 Q90544	Q90544 ginglymosto

17	123.5	21.0	384	4 Q9UE60	Q9up60 homo sapien
18	123.5	21.0	416	4 Q9NPP6	Q9npp6 homo sapien
19	123.5	21.0	494	4 Q96K68	Q96k68 homo sapien
20	123.5	21.0	496	4 Q96KX8	Q96kx8 homo sapien
21	123.5	21.0	496	4 Q96DK0	Q96dk0 homo sapien
22	119.5	20.3	500	4 Q9BRV0	Q9brv0 homo sapien
23	113.5	19.3	486	11 Q91Z07	Q91z07 mus musculus
24	113.5	19.3	487	11 Q99KA4	Q99ka4 mus musculus
25	112.5	19.1	130	11 Q9DBW4	Q9dbw4 mus musculus
26	112.5	19.1	233	11 Q91V32	Q91v32 m adult mal
27	112.5	19.1	479	11 Q99M22	Q99m22 mus musculus
28	112.5	19.1	484	11 Q99LA6	Q99la6 mus musculus
29	112	19.0	235	11 Q91WL2	Q91wl2 mus musculus
30	111.5	19.0	479	11 Q91WP5	Q91wp5 mus musculus
31	111.5	19.0	481	11 Q91WT3	Q91wt3 mus musculus
32	111.5	19.0	481	11 Q91WT1	Q91wt1 mus musculus
33	111.5	19.0	482	11 Q91X92	Q91x92 mus musculus
34	111.5	19.0	488	11 Q91WR1	Q91wr1 mus musculus
35	110.5	18.8	426	11 Q9DCD9	Q9dcd9 mus musculus
36	110.5	18.8	480	11 Q91XE1	Q91xe1 mus musculus
37	110	18.7	211	11 Q91XL0	Q91xl0 mus musculus
38	110	18.7	233	11 Q91WS9	Q91ws9 mus musculus
39	110	18.7	234	11 Q91WF8	Q91wf8 mus musculus
40	110	18.7	238	11 Q99M37	Q99m37 mus musculus
41	108	18.4	214	11 Q99LA5	Q99la5 mus musculus
42	107.5	18.3	235	11 Q99M11	Q99m11 mus musculus
43	103.5	17.6	233	4 Q96169	Q96169 homo sapien
44	103.5	17.6	236	4 Q96E61	Q96e61 homo sapien
45	101	17.2	1215	5 Q9V787	Q9v787 drosophila

ALIGNMENTS

RESULT 1

Q96PQ8	PRELIMINARY;	PRT;	701 AA.
ID	Q96PQ8	PRELIMINARY;	PRT;
AC	Q96PQ8		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21477448; PubMed=11593034;		
RA	Hu Z., Garen A.;		
RT	"Targeting tissue factor on tumor vascular endothelial cells and tumor		
RT	cells for immunotherapy in mouse models of prostatic cancer.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).		
DR	EMBL; AF272774; AAK58686.1; -.		
SQ	SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;		

Query Match	97.3%;	Score 572;	DB 4;	Length 701;
Best Local Similarity	97.3%;	Pred. No. 1.8e-54;		
Matches 107;	Conservative	1;	Mismatches	2;
Indels	0;	Gaps	0;	
QY	1 APPVAGGSPVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60			
Db	485 APELLGGPSVFLFPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 544			
QY	61 PREOYNSTRVSVLVNVLHODWLNKGEYCKVSNKALPAPIETISKAK 110			
Db	545 PREOYNSTRVSVLVNVLHODWLNKGEYCKVSNKALPAPIETISKAK 594			
RESULT 2				
Q95M34	PRELIMINARY;	PRT;	337 AA.	
ID	Q95M34	PRELIMINARY;	PRT;	

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AC Q95M34;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IMMUNOGLOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
DE (FRAGMENT).
GN IGHC1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Wagner B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199;105-119(1998).
DR EMBL; AJ300675; CAC44624.1; -.
FT NON_TER 1
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 79.8%; Score 469; DB 6; Length 337;
Best Local Similarity 75.5%; Pred. No. 1.6e-43;
Matches 83; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

Qy 1 APPVAGGSVLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATK 60
Db 119 APELLGGPSVFIFFPPNPKDTLMITRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATK 178

Qy 61 PREQYNSTYRVSVLTQLHODWLNKGYCKVSNKALPAPIETISKAK 110
Db 179 PKEQFNSTYRVSVLTQLHODWLNKGYCKVSNKALPAPIETISKAK 228

RESULT 3
Q9RIA4
ID Q9RIA4; PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv)";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
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Query Match 69.9%; Score 411; DB 11; Length 437;
Best Local Similarity 70.6%; Pred. No. 5.5e-37;
Matches 72; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

Qy 9 SVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREQYNS 68
Db 229 SVFIFFPPPKPDLVLTLPKVTCTVVVDISKDDPEVQFSWFDVDDVEVHTAQTQPREQFNS 288

Qy 69 TYRVVSVLTQLHODWLNKGYCKVSNKALPAPIETISKAK 110
Db 289 TFRSVSELPIMHQDWLNKGYCKVSNKALPAPIETISKAK 330

RESULT 4
Q99LC4
ID Q99LC4; PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 69.9%; Score 411; DB 11; Length 463;
Best Local Similarity 70.6%; Pred. No. 5.9e-37;
Matches 72; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

Qy 9 SVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREQYNS 68
Db 255 SVFIFFPPPKPDLVLTLPKVTCTVVVDISKDDPEVQFSWFDVDDVEVHTAQTQPREQFNS 314

Qy 69 TYRVVSVLTQLHODWLNKGYCKVSNKALPAPIETISKAK 110
Db 315 TFRSVSELPIMHQDWLNKGYCKVSNKALPAPIETISKAK 356

RESULT 5
Q9DBL4
ID Q9DBL4; PRELIMINARY; PRT; 473 AA.
AC Q9DBL4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1810060009RIK PROTEIN.
OS IGH-1 OR 181006000RIK.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085860; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Adakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Glissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igc1; 3.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 68.5%; Score 403; DB 11; Length 473;
Best Local Similarity 65.5%; Pred. No. 4.6e-36;
Matches 72; Conservative 19; Mismatches 19; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 257 APDLGGPSVFIPPPKIDVLMISLSPMTVCVVVDVSEDDPDVQISFVNNVEVHTAQTQ 316
QY 61 PREEQYNSTYRVVSVLTVLDHQLNGKEVKKCKVSNKALPAPIETISKAK 110
Db 317 THREDYNSTLRVVSALPIQHDQWMSGKEFKCKVNNKALPAPIETISKPR 366

RESULT 6
Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE HYPOTHETICAL 51.9 KDA PROTEIN.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
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QY 1 APPVAGPSVFLPPPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 257 APNLEGGPSVFIPPPKIDVLMISLTPKVTVCVVVDVSEDDPDVQISFVNNVEVHTAQTQ 316
QY 61 PREEQYNSTYRVVSVLTVLDHQLNGKEVKKCKVSNKALPAPIETISKAK 110
Db 317 THREDYNSTLRVVSALPIQHDQWMSGKEFKCKVNNKALPAPIETISKIK 366

RESULT 7
Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igc1; 3.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 67.5%; Score 397; DB 11; Length 468;
Best Local Similarity 66.4%; Pred. No. 2.1e-35;
Matches 73; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 252 APNLLGGPSVFIPPPKIDVLMISLSPMTVCVVVDVSEDDPDVQISFVNNVEVHTAQTQ 311
QY 61 PREEQYNSTYRVVSVLTVLDHQLNGKEVKKCKVSNKALPAPIETISKAK 110
Db 312 THREDYNSTLRVVSALPIQHDQWMSGKEFKCKVNNKALPAPIETISKPK 361

RESULT 8
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
```

RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; Ig_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 67.5%; Score 397; DB 11; Length 473;
Best Local Similarity 66.4%; Pred. No. 2.1e-35;
Matches 73; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 1 APPVAGSPVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 257 APNLLGGPSVFIPPKIKDVLMSLSPMTVCVVVDVSEDDPDVQISWFEVNNVEVLTAQIQ 316
QY 61 PREEQYNSTRVSVLTVLHODWLNKGYCKVSNKALPAPIETISKAK 110
DB 317 THREDYNSLTRVVSALPIQHDWNSGKFKCKVNNKALPAPIETISKPK 366

RESULT 9
Q9BSZ1 ID Q9BSZ1 PRELIMINARY; PRT; 375 AA.
AC Q9BSZ1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 41.3 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH, LYMPHOMA;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004476; AAH04476.1; -.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00410; Ig_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 375 AA; 41314 MW; BIA0A0998F473619 CRC64;

Query Match 24.1%; Score 142; DB 4; Length 375;
Best Local Similarity 28.7%; Pred. No. 1.9e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 10 VFLFPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69
DB 146 VFAIPPS-FASIFLTSTKTLCLVTLDTTYD-SVTISWTRQNGEAVKTHNISHPNAT 203
QY 70 YRVVSVLTVLHODWLNKGYCKVSNKALPAPIETISKAK 110
DB 204 FSAVGEASICEDDWSGERFTCTVTHTDLPSPKQITSRPK 244

RESULT 10
Q9BQB8 ID Q9BQB8 PRELIMINARY; PRT; 597 AA.
AC Q9BQB8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=RHABDOMYOSARCOMA;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN SEQUENCE FROM N.A.
RP TISSUE=LYMPHOMA;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -.
DR EMBL; BC001872; AAH01872.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igcl; 4.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; Ig_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 24.1%; Score 142; DB 4; Length 597;
Best Local Similarity 28.7%; Pred. No. 3.4e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 10 VFLFPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69
DB 368 VFAIPPS-FASIFLTSTKTLCLVTLDTTYD-SVTISWTRQNGEAVKTHNISHPNAT 425
QY 70 YRVVSVLTVLHODWLNKGYCKVSNKALPAPIETISKAK 110
DB 426 FSAVGEASICEDDWSGERFTCTVTHTDLPSPKQITSRPK 466

RESULT 11
Q9BU10 ID Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 65.3 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH, LYMPHOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003599; Ig.


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DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 5.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGc1; 4.
DR SMART: SM00406; Igv; 1.
DR SMART: SM00410; IGc1; 1.
DR SMART: SM00410; IGc1; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DFA8FB7E055851 CRC64;

Query Match          24.1%; Score 142; DB 4; Length 597;
Best Local Similarity 28.7%; Pred. No. 3.4e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 10 VFLEPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69
Db 368 VFAIPPS-FASIFLTSTKLTCLVTLDTTYD-SVTISWTRQNGEAVKTHNTNISESHPNAT 425

QY 70 YRVVSVLTVLHQDLNGKCYKCKVSNKALPAPIEKTISKAK 110
Db 426 FSAVGEASICEDDWSGERFTCTVTHDLPSPKQIISRPK 466

RESULT 12
Q96BB9 ID Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 65.0 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1; -.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;

Query Match          24.1%; Score 142; DB 4; Length 597;
Best Local Similarity 28.7%; Pred. No. 3.4e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 10 VFLEPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69
Db 368 VFAIPPS-FASIFLTSTKLTCLVTLDTTYD-SVTISWTRQNGEAVKTHNTNISESHPNAT 425

QY 70 YRVVSVLTVLHQDLNGKCYKCKVSNKALPAPIEKTISKAK 110
Db 426 FSAVGEASICEDDWSGERFTCTVTHDLPSPKQIISRPK 466

RESULT 13
Q96EY0 ID Q96EY0 PRELIMINARY; PRT; 613 AA.
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:20337).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPH, AND LYMPHOMA;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011857; AAH11857.1; -.
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011857; AAH11857.1; -.
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match          24.1%; Score 142; DB 4; Length 613;
Best Local Similarity 28.7%; Pred. No. 3.5e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 10 VFLEPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69
Db 363 VFAIPPS-FASIFLTSTKLTCLVTLDTTYD-SVTISWTRQNGEAVKTHNTNISESHPNAT 420

QY 70 YRVVSVLTVLHQDLNGKCYKCKVSNKALPAPIEKTISKAK 110
Db 421 FSAVGEASICEDDWSGERFTCTVTHDLPSPKQIISRPK 461

RESULT 14
Q96GA6 ID Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match          24.1%; Score 142; DB 4; Length 614;
Best Local Similarity 28.7%; Pred. No. 3.5e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 10 VFLEPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69
Db 364 VFAIPPS-FASIFLTSTKLTCLVTLDTTYD-SVTISWTRQNGEAVKTHNTNISESHPNAT 421

QY 70 YRVVSVLTVLHQDLNGKCYKCKVSNKALPAPIEKTISKAK 110
Db 422 FSAVGEASICEDDWSGERFTCTVTHDLPSPKQIISRPK 462

RESULT 15
Q96AA6 ID Q96AA6 PRELIMINARY; PRT; 618 AA.
AC Q96AA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 67.8 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPH, AND LYMPHOMA;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
```

Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC017356; AAH17356.1; -
 SQ Hypothetical protein.
 KW SEQUENCE 618 AA; 67758 MW; 96DBDAC7C696E0A6 CRC64;

Query Match 24.1%; Score 142; DB 4; Length 618;
Best Local Similarity 28.7%; Pred. NO. 3.5e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 10 VFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69
|| || :: :::: :||| |: | | | | | | | |
Db 368 VFAIPPS-FASIFLTKSKTCLVTDLTTDY-SVTISWTRQNGEAVKTHTNISSEHPNAT 425

Qy 70 YRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 110
 :
Dd 426 FSAVGEASTCEDDWNSSGRFTCTVTHTDLPSLKQTISRPK 466

Search completed: June 21, 2002, 08:59:34
Job time: 1633 sec

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:00:26 ; Search time 48.19 Seconds
(without alignments)
88.382 Million cell updates/sec

Title: US-09-674-857-10
Perfect score: 588
Sequence: 1 APPVAGGSPVLFPPKPKDT.....CKVSNKALPAPIETISKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	572	97.3	330	1 GCL_HUMAN	P01857 homo sapien
2	548.5	93.3	326	1 GC2_HUMAN	P01859 homo sapien
3	539	91.7	327	1 GC4_HUMAN	P01861 homo sapien
4	534	90.8	290	1 GC3_HUMAN	P01860 homo sapien
5	440	74.8	333	1 GCB_RAT	P20761 rattus norv
6	436	74.1	323	1 GC_RABIT	P01870 oryctolagus
7	436	74.1	329	1 GC3_CAVPO	P01862 cavia porce
8	433	73.6	329	1 GC3_MOUSE	P22436 mus musculu
9	433	73.6	398	1 GC3M_MOUSE	P03987 mus musculu
10	411	69.9	324	1 GCL_MOUSE	P01868 mus musculu
11	411	69.9	393	1 GC1M_MOUSE	P01869 mus musculu
12	403	68.5	335	1 GCAB_MOUSE	P01864 mus musculu
13	401	68.2	330	1 GCAA_MOUSE	P01863 mus musculu
14	401	68.2	336	1 GCB_MOUSE	P01866 mus musculu
15	401	68.2	399	1 GCAM_MOUSE	P01865 mus musculu
16	401	68.2	405	1 GCBM_MOUSE	P01867 mus musculu
17	400	68.0	329	1 GCC_RAT	P20762 rattus norv
18	389	66.2	326	1 GCL_RAT	P20759 rattus norv
19	354	60.2	322	1 GCA_RAT	P20760 rattus norv
20	164.5	28.0	428	1 EPC_HUMAN	P01854 homo sapien
21	160	27.2	429	1 EPC_RAT	P01855 rattus norv
22	153	26.0	457	1 MUC_SUNMU	P20768 suncus muri
23	144	24.5	421	1 EPC_MOUSE	P06336 mus musculu
24	142	24.1	454	1 MUCB_HUMAN	P01871 homo sapien
25	140	23.8	391	1 MUCB_HUMAN	P04220 homo sapien
26	136	23.1	454	1 MUC_MESAU	P06337 mesocricetu
27	136	23.1	455	1 MUC_MOUSE	P01872 mus musculu
28	136	23.1	476	1 MUCB_MOUSE	P01873 mus musculu
29	130	22.1	106	1 KAC_HUMAN	P01834 homo sapien
30	129.5	22.0	299	1 ALC_RABIT	P01879 oryctolagus
31	123.5	21.0	340	1 ALC2_HUMAN	P01877 homo sapien
32	123.5	21.0	353	1 ALC1_GORGO	P20758 gorilla gor
33	123.5	21.0	353	1 ALC1_HUMAN	P01876 homo sapien

ALIGNMENTS

RESULT 1

ID	GCL_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	IGHG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RT	acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RT	acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a			
RT	monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The			
RT	chymotryptic peptides of the H-chain, alignment of the tryptic			
RT	peptides and discussion of the complete structure.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary			
RT	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

P03988 oryctolagus
P04221 oryctolagus
P01874 canis famill
P20763 gallus gall
P23086 heterodontu
P23084 heterodontu
P23085 heterodontu
P01843 mus musculu
P01878 mus musculu
P01840 oryctolagus
P20765 mus spretus
P23087 heterodontu

RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RX MEDLINE=77070267; PubMed=1002129;
RA DISELFDIE BONDS.
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RX X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Delsenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
CC MARKER & THE GIM (NON-1) MARKERS.
CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35,116,198,269 & 272.
CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198,267&272.
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DR EMBL; J00228; AAC82527.1; ALT_INIT.
DR PIR; A02146; GHU
DR PDB; 1FC1; 15-JUL-92;
DR PDB; 1FC2; 15-JUL-92;
DR MIM; 147100; -
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW 3D-structure.
FT NON_TER 1 98
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 223 CH2.
FT DOMAIN 224 330 CH3.
FT DISULFID 27 83
FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT MOD_RES 330 330
FT VARIANT 97 97
FT VARIANT 239 239
FT VARIANT 241 241
FT STRAND 123 126
FT HELIX 130 134

FT TURN 136 137
FT STRAND 141 148
FT TURN 153 162
FT STRAND 163 164
FT STRAND 165 166
FT STRAND 175 178
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 206
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 240
FT TURN 241 242
FT STRAND 245 256
FT STRAND 260 266
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 312
FT TURN 313 314
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FT STRAND 320 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 97.3%; Score 572; DB 1; Length 330;
Best Local Similarity 97.3%; Pred No. 1,4e-50;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APVAGGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATK 60
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DB 114 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATK 173

QY 61 PREQYNSTYRVSVLTVLHODLNGKEYCKVSKNKPAPIEKTISKAK 110
||| : |||||
DB 174 PREQYNSTYRVSVLTVLHODLNGKEYCKVSKNKPAPIEKTISKAK 223

RESULT 2
GC2_HUMAN
ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GNIGH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
RT heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RC TISSUE=Fetal liver;
RA MEDLINE=83001943; PubMed=6811139;
RX Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
RT evolution of a gene family.";
RL Cell 29:671-679(1982).

RN RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=84235992; PubMed=6329676;
 RA Krawinkel U., Rabbitts T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 genes.";
 RL EMBO J. 1:403-407(1982).
 [3]
 RN RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 [4]
 RN RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 [5]
 RN RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 immunoglobulins gamma chains";
 RL Mol. Immunol. 16:923-925(1979).
 [6]
 RN RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RX Hofmann T., Parr D.M.;
 RT Submitted (MAR-1980) to the PIR data bank.
 [7]
 RN RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 [8]
 RN RP DISULFIDE BONDS
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 [9]
 RN RP DISULFIDE BONDS
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
 [10]
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 CC EMBL; J00230; AAB59393.1; -;
 DR PIR; A02148; G2HU.
 DR HSSP; P01857; 1PCL.
 DR MIM; 147110; -;
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF000047; Ig; 3.
 DR SMART; SM00410; IG_like; 1.
 DR SMART; SM00407; IGC1; 2.
 DR PROSITE; PS00290; IG_MHC; 2.

KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CHI.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT SITE 156 156
 FT MOD_RES 326 326
 FT VARIANT 60 60
 FT CONFLICT 109 109 /FTid=VAR_003889.
 FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
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 Query Match 93.3%; Score 548.5; DB 1; Length 336;
 Best Local Similarity 93.6%; Pred. No. 3.3e-48;
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 QY 1 APPVAGSPVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db 111 APPVA-GPVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 169
 QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAK 110
 Db 170 PREQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIETISKTK 219
 RESULT 3
 GC4_HUMAN
 ID GC4_HUMAN STANDARD; PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-4 chain C region.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83157104; PubMed=6299662;
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 1:11-18(1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE=70207560; PubMed=4192699;
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 constant region of a gamma 4 chain.";
 RL Biochem. J. 117:33-47(1970).
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; K01316; AAB59394.1; ALT_INIT.
 DR PIR; A02150; G4HU.
 DR HSSP; P01842; 7FAB.


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FT VARIANT 227 227 S -> N (IN OMM).
FT /FTID-VAR_003894.
FT MISSING (IN ZUC).
FT /FTID-VAR_003895.
FT F -> Y (IN OMM).
FT /FTID-VAR_003896.
SQ SEQUENCE 290 AA; 32331 MW; E69CBCE95705B2F46 CRC64;

Query Match 90.8%; Score 534; DB 1; Length 290;
Best Local Similarity 89.1%; Pred. No. 8.5e-47;
Matches 98; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 74 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 133
QY 61 PREQYNSTYRVSVLTVHLQDMLNGKEYKCKVSNKALPAPIEKTISKAK 110
DB 134 PREQYNSTYRVSVLTVHLQDMLNGKEYKCKVSNKALPAPIEKTISKAK 183

RESULT 5
GCB_RAT ID GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig-like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00407; IGL; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 74.8%; Score 440; DB 1; Length 333;
Best Local Similarity 70.8%; Pred. No. 3e-37;
Matches 77; Conservative 20; Mismatches 12; Indels 0; Gaps 0;

QY 2 PPVAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
DB 118 PELLGGPSVFIFFPKPKDILLISQNAKVTCCVVVDSEEDPVQFSWFWNNVEVHTAQTP 177
QY 62 REEYNSTYRVSVLTVHLQDMLNGKEYKCKVSNKALPAPIEKTISKAK 110
DB 178 REEYNSTYRVSVSNALPQHODWSGKFEKCKVSNKALPAPIEKTISKPK 226

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RESULT 6
GCB_RAT ID GCB_RAT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-1 haplotype.";
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT immunoglobulin G.";
RL Biochem. J. 116:249-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RT (in) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC -!- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC MARKERS AND REF.5 THE E15 MARKER.
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CC -----
CC EMBL; M16426; AAA31289.1; -.
DR PIR; A02161; GHRB.
DR HSP; P01857; IFC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGL; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).

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FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 O -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;
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Query Match 74.1%; Score 436; DB 1; Length 323;
Best Local Similarity 72.5%; Pred. No. 7.5e-37;
Matches 79; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

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QY 2 PPVAGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTP 61
   I : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 108 PELLGSPVFIFPPKPKDLMISRTPEVTCVVVDVSHEDPEVQFTWYINNEQVTRPPL 167
   I : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 62 REQYNSTYRVSVLTVLHODWLNKGKCKVSNKALPAPIETISKAK 110
   I : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 168 REQQFNSTIRVSTLPIHODWLNKGKCKVSNKALPAPIETISKAR 216
   I : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 7
GC2_CAVPO STANDARD; PRT; 329 AA.
ID GC2_CAVPO
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RX SEQUENCE OF 4-68.
RP MEDLINE=71058471; PubMed=5538606;
RA Birstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
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antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR: A02151; G2GP.
DR HSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202 N-LINKED (GLCNAC. . .).
FT CARBOHYD 178 178
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 74.1%; Score 436; DB 1; Length 329;
Best Local Similarity 74.3%; Pred. No. 7.6e-37;
Matches 81; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 2 PPVAGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTP 61
   I : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 113 PENLGGSPVFIFPPKPKDLMISLTPVTCVVVDVSHEDPEVQFTWFDNKPVGNAETKP 172
   I : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 62 REQYNSTYRVSVLTVLHODWLNKGKCKVSNKALPAPIETISKAK 110
   I : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 173 RVEQYNTFRVESVLPQHODWLNKGKCKVSNKALPAPIETISKTK 221
   I : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
GC3_MOUSE STANDARD; PRT; 329 AA.
ID GC3_MOUSE
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
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DR	InterPro:	IPR003006;	Ig_MHC.
DR	InterPro:	IPR003597;	Ig_C1.
DR	InterPro:	IPR003600;	Ig_Like.
DR	Pfam:	PF00047;	Ig_3
DR	SMART:	SM00410;	Ig_Like; 1.
DR	SMART:	SM00407;	IGc1; 2.
DR	PROSITE:	PS00290;	Ig_MHC; 1.
KW	Immunoglobulin domain;	Immunoglobulin C region;	Glycoprotein;
KW	Transmembrane;	Alternative splicing.	
FT	NON_TER	1	
FT	DOMAIN	1	CH1.
FT	DOMAIN	98	HINGE.
FT	DOMAIN	113	CH2.
FT	DOMAIN	114	CH3.
FT	TRANSMEM	224	POTENTIAL.
FT	TRANSMEM	346	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	363	E -> G (IN REF. 2).
FT	CONFLICT	333	E -> Q (IN REF. 2).
FT	CONFLICT	342	E -> P (IN REF. 2).
FT	CONFLICT	388	P -> F (IN REF. 2).
SQ	SEQUENCE	398 AA;	CF7F264B50A41B95 CRC64;

Query Match		73.6%;	Score 433;	DB 1;	Length 398;
Best Local Similarity		71.2%;	Pred. No. 1.9e-36;		
Matches	79;	Conservative	14;	Mismatches	16;
				Indels	2;
				Gaps	39

QY	2	PP--VAGGPSVFELFPKPKDGLMISRTPEVTCTVVVDVSHEDPEVKFNWYVDGVEVHNAKT	59
DB	112	PPGNILGGPSVFELFPKPKDALMISLTPKVTCVVVDSEDDPDVHVSNFVDNKEVHTAWT	171
QY	60	KPREQYNSTRYRVSVLTVLHDWLNGKEYCKVKSKNALPAPIETKISKAK	110
DB	172	QPREAQYNSTRFVSVALPIQHQMGRGKEFKCVKNKALPAPIERTISKPK	222

RESULT	10
GCI_MOUSE	
ID	GCI_MOUSE STANDARD; PRT; 324 AA.
AC	P01868;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	Ig gamma-1 chain C region.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RN	SEQUENCE FROM N.A.
RX	MEDLINE=80045036; PubMed=115593;
RA	Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA	Takahashi N., Mano Y.;
RT	"Cloning and complete nucleotide sequence of mouse immunoglobulin
RT	gamma 1 chain gene.";
RL	Cell 18:559-568(1979).
RL	[2]
RP	SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX	MEDLINE=8020559; PubMed=6769752;
RA	Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shmizu A.,
RA	Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT	"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
RT	cloned in a bacterial plasmid.";
RL	Gene 9:87-97(1980).
RL	[3]
RP	SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX	MEDLINE=80012837; PubMed=113776;
RA	Rogers J., Clarke P., Salser W.;
RT	"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
RT	heavy chain.";
RL	Nucleic Acids Res. 6:3305-3321(1979).
RL	[4]
RX	SEQUENCE (MYELOMA PROTEIN MOPC 21).
RP	MEDLINE=78242288; PubMed=98524.

RA Adetugbo K.;
 RT "Evolution of immunoglobulin subclasses. Primary structure of a
 RL murine myeloma gamma1 chain.";
 RN J. Biol. Chem. 253:6068-6075(1978).
 [5]
 RP DISULFIDE BONDS (MOPC 21).
 RX MEDLINE=73008889; PubMed=5073237;
 RA Svasti J., Milstein C.;
 RL "The disulphide bridges of a mouse immunoglobulin G1 protein.";
 RT Biochem. J. 126:837-850(1972).
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 CC -----
 DR EMBL; V00793; CAA24172.1; -;
 DR EMBL; V00793; CAA24173.1; -;
 DR EMBL; V00793; CAA24174.1; -;
 DR EMBL; V00793; CAA24175.1; -;
 DR EMBL; V00795; CAA24176.1; -;
 DR PIR; A02159; GIMS.
 DR HSSP; P01842; 7FAB.
 DR GlycoSuiteDB; P01868; -;
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR003006; Iq_MHC.
 DR InterPro; IPR003597; Iq_c1.
 DR Pfam; PF00047; Iq; 3.
 DR SMART; SM00407; Igc1; 2.
 DR PROSITE; PS00290; Iq_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing.
 FT NON_TER 1 97
 FT DOMAIN 1 97
 FT DOMAIN 98 110
 FT DOMAIN 111 217
 FT DOMAIN 218 324
 FT DISULFID 27 82
 FT DISULFID 102 102
 FT DISULFID 104 104
 FT DISULFID 107 107
 FT DISULFID 109 109
 FT DISULFID 138 198
 FT CARBOHYD 174 174
 FT N-LINKED (GLCNAC. . .).
 FT /FTid=CAR_000055.
 FT 244 302
 FT DISULFID 324 324
 FT MOD_RES 324 324
 FT CONFLICT 276 276
 FT CONFLICT 278 278
 FT CONFLICT N -> D (IN REF. 3).
 FT CONFLICT N -> D (IN REF. 3).
 SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;
 Query Match 69.9%; Score 411; DB 1; Length 324;
 Best Local Similarity 70.6%; Pred.No. 2.5e-34;
 Matches 72; Conservative 18; Mismatches 12; Indels 0; Gaps 0;
 QY 9 SVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 68
 Db 116 SVFIFFPKPKDVLTLTPKVTCTVVVDISKDPQFQSFVDFVDEVHTAQTPREEQFN 175
 QY 69 TVRVSVLTVLHQLWLNKEYCKYKSNKALPAPIETKISKAK 110
 Db 176 TFRSVSELPIMHQDLWLNKEFKCRVNSAFAPIETKISKTK 217
 RESULT 11
 GC1M_MOUSE STANDARD; PRT; 393 AA.
 ID GC1M_MOUSE AC P01869;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ig gamma-1 chain C region, membrane-bound form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80045036; PubMed=115593;
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RT Takahashi N., Mano Y.;
 RL "Cloning and complete nucleotide sequence of mouse immunoglobulin
 gamma 1 chain gene.";
 RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 323-393 FROM N.A.
 RX MEDLINE=82197626; PubMed=6804950;
 RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
 RT "mRNA for surface immunoglobulin gamma chains encodes a highly
 conserved transmembrane sequence and a 28-residue intracellular
 domain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
 RN [3]
 RP SEQUENCE OF 323-366 FROM N.A.
 RX MEDLINE=82115295; PubMed=6799207;
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
 RT Eisenberg D., Wall R.;
 RL "Gene segments encoding transmembrane carboxyl termini of
 immunoglobulin gamma chains.";
 RL Cell 26:19-27(1981).
 RN [4]
 RP SEQUENCE OF 1-44 FROM N.A.
 RX MEDLINE=82222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 immunoglobulin gamma chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
 CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED-
 CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
 CC SEGMENT OF MU CHAINS.
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 CC -----
 DR EMBL; V00793; CAA24172.1; -;
 DR EMBL; V00793; CAA24173.1; -;
 DR EMBL; V00793; CAA24174.1; -;
 DR PIR; B02159; GIMS.
 DR HSSP; P01842; 7FAB.
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR003006; Iq_MHC.
 DR InterPro; IPR003597; Iq_c1.
 DR Pfam; PF00047; Iq; 3.
 DR SMART; SM00407; Igc1; 2.
 DR PROSITE; PS00290; Iq_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing; Transmembrane.
 FT NON_TER 1 97
 FT DOMAIN 1 97
 FT DOMAIN 98 110
 FT DOMAIN 111 217
 FT DOMAIN 218 324
 FT DISULFID 27 82
 FT DISULFID 102 102
 FT INTERCHAIN (WITH A LIGHT CHAIN).
 FT INTERCHAIN (WITH A LIGHT CHAIN).

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FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198 N-LINKED (GLCNAC. . .).
FT CARBOHYD 174 174 POTENTIAL.
FT DISULFID 244 302 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 340 357
FT DOMAIN 358 393
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B/AICE27 CRC64;

Query Match 69.9%; Score 411; DB 1; Length 393;
Best Local Similarity 70.6%; Pred. No. 3.1e-34;
Matches 72; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

QY 9 SVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNS 68
Db 116 SVFIFFPKPKDLTITLTGPKVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNS 175

QY 69 TYRVVSVLTVLHQLDNLNGKEYCKVSKNPKALPAPIETISKAK 110
Db 176 TFRSVSELPIMHQLDNLNGKEYCKVSKNPKALPAPIETISKAK 217

RESULT 12
GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT Igg2a and Igg2ab alleles of the mouse."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain C regions of Igla and Ig1b allotypic forms."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
CC
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CC
CC EMBL; J00479; ; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_1like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; IG_1like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
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FT NON_TER 1 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 68.5%; Score 403; DB 1; Length 335;
Best Local Similarity 65.5%; Pred. No. 1.7e-33;
Matches 72; Conservative 19; Mismatches 19; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTK 60
Db 119 APDLGLGGSPVFIFFPKPKDKVLMISLSPMTVCVVVDVSEDDPDVQISWFFNNVEVHTAQ 178

QY 61 PREEOYNSYRVSVLTVLHQLDNLNGKEYCKVSKNPKALPAPIETISKAK 110
Db 179 THREDYNSTLRVVSALPIQHQQMMSGKEFKCKVNNRNLPSPIETISKPR 228

RESULT 13
GCAB_MOUSE STANDARD; PRT; 330 AA.
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-2A chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Sikorav J.-L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT Balb/c gamma 2a heavy chain messenger RNA."
RL Nucleic Acids Res. 8:3143-3155(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RT and evolution of heavy chain genes: further evidence for intervening
RT sequence-mediated domain transfer."
RL Nucleic Acids Res. 9:1365-1381(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81223894; PubMed=6787604;
RA Ollo R., Auffray C., Mochamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multigenic
RT family."
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications
RT for the evolution of immunoglobulin structure and function."
RL Eur. J. Biochem. 43:423-435(1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges."
RL Eur. J. Biochem. 30:452-462(1972).
CC
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CC EMBL; V00798; CAA24178.1; --
CC PIR; A02152; G2MSA.
CC HSSP; P01842; 7FAB.
DR DR InterPro; IPR003006; Ig_MHC.
DR DR InterPro; IPR003597; Ig_cl.
DR DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; B84361C5445A6864 CRC64;

Query Match 68.2%; Score 401; DB 1; Length 330;
Best Local Similarity 66.4%; Pred. No. 2.6e-33;
Matches 73; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 114 APNLLGGPSVFPPKIKDKVLMISLPIVTCVVVDVSEDDPDQVQISFWNNVEVHTAQTK 173

QY 61 PREEQYNSTRYVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 174 THREDYNSTRVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKPK 223

RESULT 14
GCB_MOUSE STANDARD; PRT; 336 AA.
AC P01866;
DC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2B chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (A ALLELE).
RX MEDLINE=80120716; PubMed=6756534;
RA Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
RT "Complete nucleotide sequence of immunoglobulin gamma2b chain gene
RT cloned from newborn mouse DNA.";
RL Nature 283:786-789(1980).
RN [2]
RP SEQUENCE FROM N.A. (MPC 11).
RX MEDLINE=80081501; PubMed=117548;
RA Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT gamma 2b heavy chain messenger RNA.";
RL Science 206:1299-1303(1979).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=80081502; PubMed=117549;
RA Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
RT "Sequence of the cloned gene for the constant region of murine gamma
RT 2b immunoglobulin heavy chain.";
RL Science.206:1303-1306(1979).
RN [4]
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```
RP SEQUENCE FROM N.A. (B ALLELE).
RX MEDLINE=82173203; PubMed=6803173;
RA Olio R., Rougeon F.;
RT "Mouse immunoglobulin allotypes: post-duplication divergence of gamma
RL 2a and gamma 2b chain genes.";
RN Nature 296:761-763(1982).
RN [5]
RP CARBOHYDRATE-LINKAGE SITE THR-105.
RX MEDLINE=94216359; PubMed=7512967;
RA Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,
RA Irimura T., Takahashi N., Kato K., Arata Y.;
RT "O-glycosylation in hinge region of mouse immunoglobulin G2b.";
RL J. Biol. Chem. 269:12345-12350(1994).
CC -1- PTM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS
CC MODIFIED WITH 2 SIALIC ACID RESIDUES.
CC -1- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA
CC CHAINS.
CC -1- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.
CC PIR; A02157; G2MS11.
CC HSSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 150 210
FT DISULFID 256 314
FT CARBOHYD 105 105
FT MOD_RES 336 336
FT VARIANT 163 163 Q -> R (IN B ALLELE).
FT VARIANT 194 194 T -> A (IN B ALLELE).
FT VARIANT 300 300 N -> D (IN B ALLELE).
FT VARIANT 301 301 M -> I (IN B ALLELE).
FT CONFLICT 25 25 L -> S (IN REF. 2 AND 3).
FT CONFLICT 36 36 S -> P (IN REF. 2 AND 3).
FT CONFLICT 239 239 I -> T (IN REF. 2 AND 3).
SQ SEQUENCE 336 AA; 36658 MW; 7D879662607C356E CRC64;

Query Match 68.2%; Score 401; DB 1; Length 336;
Best Local Similarity 65.5%; Pred. No. 2.7e-33;
Matches 72; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 120 APNLEGGPSVFPPKIKDKVLMISLPIVTCVVVDVSEDDPDQVQISFWNNVEVHTAQTK 179

QY 61 PREEQYNSTRYVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 180 THREDYNSTRVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIK 229

RESULT 15
GCB_MOUSE STANDARD; PRT; 399 AA.
AC P01865;
DC 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=82222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC SEGMENT OF MU CHAINS.
CC -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
CC IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
CC THE A ALLELE.
CC -----
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CC -----
DR EMBL; J00471; AAB59661.1; ALT_INIT.
DR FIR; A02154; G2MSAM.
DR HSP; P01857; IFCl.
DR MGD; MG1:96443; Igh-1.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003597; Iq-cl.
DR InterPro; IPR003600; Iq_like.
DR Pfam; PF00047; Iq; 3.
DR SMART; SM00410; Iq-like; 1.
DR SMART; SM00407; Iqcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT TRANSMEM 346 363 POTENTIAL.
FT DOMAIN 364 399 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;

Query Match 68.2%; Score 401; DB 1; Length 399;
Best Local Similarity 66.4%; Pred. No. 3.2e-33;
Matches 73; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKPKDTLMISRPETCVVVDVSHDEPKFNKYVDGVEVHNAKTK 60
DB 114 APNLLGGPSVFIFPPKIKLVMLISLPIVTCVVVDVSDPDQVQISWFNVEVHTAQTQ 173
QY 61 PREEQNSTYRVSVLTGLHODVNLGKCKYKVKSNKALPAPIETKTSKAK 110
DB 174 THREDYNSTLRVVSALPIQHQDWSGKEFKCKVNNKDLPAPIERTISKPK 223
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Search completed: June 21, 2002, 09:00:26
Job time: 1450 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:37:55 ; Search time 102.05 Seconds
(without alignments)
103.575 Million cell updates/sec

Title: US-09-674-857-10
Perfect score: 588
Sequence: 1 APPVAGGPSVFLPPPKPDKT.....CKVSNKALPAPIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	572	97.3	234	2 PT0207	Ig gamma Chain C r
2	572	97.3	255	4 S31866	Ig gamma-1 chain C
3	572	97.3	330	1 GHU	Ig gamma-1 chain C
4	572	97.3	374	2 S69339	Ig heavy chain V r
5	554	94.2	377	2 A60764	Ig gamma-3 chain C
6	554	94.2	377	2 A23511	Ig gamma-3 chain C
7	548.5	93.3	326	1 G2HU	Ig gamma-2 chain C
8	539	91.7	327	1 G4HU	Ig gamma-4 chain C
9	534	90.8	289	1 G3HUWI	Ig gamma-3 heavy c
10	468	79.6	328	2 I47160	Ig gamma-2 chain C
11	468	79.6	328	2 I47159	Ig gamma 2a chain
12	463	78.7	277	2 I47162	Ig gamma 4 chain c
13	445	75.7	470	2 S22080	Ig heavy chain pre
14	444	75.5	328	2 I47161	Ig gamma 3 chain c
15	444	75.5	328	2 I47158	Ig gamma 1 chain c
16	440	74.8	333	2 PS0018	Ig gamma-2b chain
17	436	74.1	308	2 C30554	Ig heavy chain C r
18	436	74.1	323	1 GHRB	Ig gamma chain C r
19	436	74.1	329	1 G2GP	Ig gamma-2 chain C
20	436	74.1	472	2 S31459	Ig gamma-1 chain -
21	433	73.6	329	1 G3MSC	Ig gamma-3 chain C
22	433	73.6	398	1 G3MSM	Ig gamma-3 chain C
23	411	69.9	324	1 G1MS	Ig gamma-1 chain C
24	411	69.9	393	1 G1MSM	Ig gamma-1 chain C
25	411	69.9	444	2 PC436	monoclonal antibod
26	403	68.5	335	1 G2MSAB	Ig gamma-2a chain
27	402	68.4	327	2 S05611	Ig gamma-2 chain C
28	401	68.2	330	1 G2MSA	Ig gamma-2a chain
29	401	68.2	399	1 G2MSAM	Ig gamma-2a chain

30	401	68.2	405	1 G2MSBM	Ig gamma-2b chain
31	401	68.2	469	2 S37483	Ig gamma-2a chain
32	401	68.2	474	1 G2MS11	Ig gamma-2b chain
33	400	68.0	329	2 S00847	Ig gamma-2c chain
34	393	66.8	475	2 S01321	Ig gamma-2b chain
35	391	66.5	446	2 S40295	Ig gamma-2a chain
36	389	66.2	326	2 PS0017	Ig gamma-1 chain C
37	354	60.2	322	2 PS0019	Ig gamma-2a chain
38	319	54.3	112	2 B30503	Ig gamma-2a chain
39	275	46.8	88	2 A30503	Ig gamma-2b chain
40	264	44.9	180	2 I46732	Ig gamma heavy cha
41	177	30.1	152	2 S14236	Ig gamma-1 chain C
42	165.5	28.1	426	2 I36948	Ig epsilon-chain -
43	164.5	28.0	428	1 EHHU	Ig epsilon chain C
44	161	27.4	549	2 S04845	Ig heavy chain pre
45	160	27.2	429	1 EHRT	Ig epsilon chain C

ALIGNMENTS

RESULT 1

PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C>Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 97.3%; Score 572; DB 2; Length 234;
Best Local Similarity 97.3%; Pred. No. 2.6e-50;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	APPVAGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK	60
DB	25	APELLGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK	84
QY	61	PREEQYNSTRYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAK	110
DB	85	PREEQYNSTRYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAK	134

RESULT 2

S31866
Ig gamma-1 chain C region - synthetic
C:Species: Synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C>Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filpula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FIL>
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 97.3%; Score 572; DB 4; Length 255;

Best Local Similarity 97.3%; Pred. No. 2.8e-50;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : |||||
Db 39 APPELLGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 98
|| : |||||
QY 61 PREEQYNSTYRVVSVLTVTLHODWLNKGKEYCKVSNKALPAPIEKTISKAK 110
|| : |||||
Db 99 PREEQYNSTYRVVSVLTVTLHODWLNKGKEYCKVSNKALPAPIEKTISKAK 148
|| : |||||

RESULT 3

GHG

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C>Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999

C:Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A>Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers,

A>Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of a human immunoglobulin gamma genes: implications for evolution of a

A:Reference number: S33887; MUID:83001943

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A:Reference number: A90563; MUID:71064024

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96, R', 98-135 <CUN>

A>Note: This sequence has the Glm(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A:Reference number: A90564; MUID:71064025

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154, Q', 156-165, Q', 167-176, Q', 178-194, N', 196-197, D', 199-238, E', 240,

A>Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nite),

igen Primaerstruktur.

A:Reference number: A91668; MUID:77070269

A:Contents: myeloma protein Nie

A:Accession: B91668

A:Molecule type: protein

A:Residues: 1-34, Q', 36-96, R', 98-115, Q', 117-197, D', 199-238, D', 240, L', 242-268, E', 27

A>Note: this sequence has the Glm(17) and Glm(1) markers

R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983

A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723

A:Molecule type: protein

A:Residues: 1-96, R', 98-197, D', 199-238, E', 240, M', 242-266, D', 268-271, D', 273-330 <

A>Note: this sequence has the Glm(3) and Glm(non-1) markers

R:Gall, W.E.; Edelman, G.M.

Biochemistry 9, 3188-3196, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul

A:Reference number: A90565; MUID:71064027

A:Contents: annotation; disulfide bonds

R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976

A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunog

enbromide cleavage products, and the disulfide bridges.

A:Reference number: A91667; MUID:77070267

A:Contents: annotation; disulfide bonds

C:Genetics:

A:Gene: GDB:IGHG1

A:Cross-references: GDB:120085; OMIM:147100

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1; 114/1; 224/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:137-206/Domain: immunoglobulin homology <IM2>

F:243-310/Domain: immunoglobulin homology <IM3>

F:278/Disulfide bonds: interchain (to light chain) #status experimental

F:103/Disulfide bonds: interchain (to heavy chain) #status experimental

F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental

F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 97.3%; Score 572; DB 1; Length 330;
Best Local Similarity 97.3%; Pred. No. 3.9e-50;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|| : |||||

Db 114 APPELLGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 173
|| : |||||

QY 61 PREEQYNSTYRVVSVLTVTLHODWLNKGKEYCKVSNKALPAPIEKTISKAK 110
|| : |||||

Db 174 PREEQYNSTYRVVSVLTVTLHODWLNKGKEYCKVSNKALPAPIEKTISKAK 223
|| : |||||

RESULT 4

S69339

Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000

C:Accession: S69339; S72664

R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 229, 54-60, 1995

A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A:Reference number: S69339; MUID:95262687

A:Accession: S69339

A:Molecule type: mRNA

A:Residues: 1-374 <KHA>

A:Cross-references: EMBL:X81695

R:Khamilichi, A.A.

submitted to the EMBL Data Library, September 1994

A:Reference number: S72664

A:Accession: S72664

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-140, C', 142-374 <KH2>

A:Cross-references: EMBL:X81695

C:Superfamily: immunoglobulin C region; immunoglobulin homology

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.3%; Score 548.5; DB 1; Length 326;
Best Local Similarity 93.6%; Pred. No. 9e-48;
Matches 103; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 111 APPVA-GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 169

Qy 61 PREEQYNSTYRVVSVLTVHLQDWLNGKEYCKVSKNPKALPAPIETISKAK 110
Db 170 PREEQFNSTYRVVSVLTVHLQDWLNGKEYCKVSKNPKALPAPIETISKTK 219

RESULT 8
G4HU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104
A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant r
A:Reference number: A90249; MUID:70207560
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30,81-326 <PIN>
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.7%; Score 539; DB 1; Length 327;
Best Local Similarity 91.8%; Pred. No. 8.2e-47;
Matches 101; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 111 APEFLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTK 170

Qy 61 PREEQYNSTYRVVSVLTVHLQDWLNGKEYCKVSKNPKALPAPIETISKAK 110
Db 171 PREEQFNSTYRVVSVLTVHLQDWLNGKEYCKVSKNGLPSSIEKTISKAK 220

RESULT 9
G3HUWI
Ig gamma-3 heavy chain disease proteins - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C:Accession: A90442; A92219; A90198; A93915; A02149
R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 hea
A:Reference number: A90442; MUID:81021548
A:Contents: heavy chain disease protein Wis
A:Accession: A90442
A:Molecule type: protein
A:Residues: 1-289 <FRA>
A:Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch
A:Note: this protein lacks most of the V region and all of the CH1 region. Residue 12
A:Note: the sequence of residues 42-76 was taken from the reference that follows
R:Michaelson, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplicat
A:Reference number: A92219; MUID:77118561
A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protei
A:Accession: A92219
A:Molecule type: protein
A:Residues: 12-97 <MIC>
A:Note: the hinge region in gamma-3 chains is about four times as long as in other ga
idue segment (12-28)
A:Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form in
R:Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of t
A:Reference number: A90198; MUID:77021516
A:Contents: heavy chain disease protein Zuc, partial sequence corresponding to residu
A:Accession: A90198
A:Molecule type: protein
A:Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A:Note: this protein lacks most of the V region, all of the CH1 region, and part of t
R:Alexander, A.; Steinmetz, M.; Barrिताut, D.; Frangione, B.; Franklin, E.C.; Hood,
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A:Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deleti
A:Reference number: A93915; MUID:82247835
A:Contents: heavy chain disease protein Omm
A:Accession: A93915
A:Molecule type: mRNA
A:Residues: 12-70;72-114;116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-
A:Note: a carboxyl-terminal lys is removed posttranslationally
A:Note: this sequence may represent an allelic form or another gamma chain subclass
C:Comment: The heavy chain disease protein Wis is shown.
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F:203-270/Domain: immunoglobulin homology <IMW>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 90.8%; Score 534; DB 1; Length 289;
Best Local Similarity 89.1%; Pred. No. 2.3e-46;
Matches 98; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 74 APEFLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 133

Qy 61 PREEQYNSTYRVVSVLTVHLQDWLNGKEYCKVSKNPKALPAPIETISKAK 110

Db 134 PREQQFNSTFRVSVLTILHQNLDGKEYCKVSNKALPAPIEKTISK 183
RESULT 10
147160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845
A:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845
A:Accession: I47160
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
C:Genetics:
A:Gene: IgG2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>
Query Match 79.6%; Score 468; DB 2; Length 328;
Best Local Similarity 80.8%; Pred. No. 1.2e-39;
Matches 84; Conservative 13; Mismatches 7; Indels 0; Gaps 0;
Qy 7 GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66
Db 116 GPSVFIFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 66
Qy 67 NSTYRVSVSLVTLHODWLNKGEYCKVSNKALPAPIEKTISKAK 110
Db 176 NSTYRVSVSLVTLHODWLNKGEYCKVSNKALPAPIEKTISKAK 219
RESULT 11
147159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124
C:Genetics:
A:Gene: IgG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>
Query Match 79.6%; Score 468; DB 2; Length 328;
Best Local Similarity 80.8%; Pred. No. 1.2e-39;
Matches 84; Conservative 13; Mismatches 7; Indels 0; Gaps 0;
Qy 7 GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66
Db 116 GPSVFIFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 66
Qy 67 NSTYRVSVSLVTLHODWLNKGEYCKVSNKALPAPIEKTISKAK 110
Db 176 NSTYRVSVSLVTLHODWLNKGEYCKVSNKALPAPIEKTISKAK 219
RESULT 12

147162
Ig gamma 4 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47162
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845
A:Accession: I47162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:U03782; NID:9433129; PIDN:AAA52220.1; PID:9433130
C:Genetics:
A:Gene: IgG4
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>
Query Match 78.7%; Score 463; DB 2; Length 277;
Best Local Similarity 79.8%; Pred. No. 3.2e-39;
Matches 83; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
Qy 7 GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66
Db 65 GPSVFIFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 66
Qy 67 NSTYRVSVSLVTLHODWLNKGEYCKVSNKALPAPIEKTISKAK 110
Db 125 NSTYRVSVSLVTLHODWLNKGEYCKVSNKALPAPIEKTISKAK 168
RESULT 13
S22080
Ig heavy chain precursor (B/MT 4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S22080; S06610; A31303
R:Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22080
A:Accession: S22080
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-470 <SAN>
A:Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and 9
A:Reference number: S06610; MUID:90097956
A:Accession: S06610
A:Molecule type: DNA
A:Residues: 142-470 <SYM>
A:Cross-references: EMBL:X16701
A:Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: Ig CH gamma-1
A:Introns: 98/1; 111/1; 221/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IMM>
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 75.7%; Score 445; DB 2; Length 470;
Best Local Similarity 73.4%; Pred. No. 3.9e-37;
Matches 80; Conservative 12; Mismatches 17; Indels 0; Gaps 0;
Qy 2 PPVAGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
Db 253 PELPGGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 312

67. NSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 109
 :
 176 NSTYRVSVLP IQH QD WJ L K G E F C K V N N V D L P A P I T R I S K A 218

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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:32:16 ; Search time 77.71 Seconds
(without alignments)
34.261 Million cell updates/sec

Title: US-09-674-857-9
Perfect score: 582
Sequence: 1 APPVAGPSVFLPPPKPDTL.....CKVSNKALPAPIEKTISKAK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	559	96.0	109	3	US-08-444-644-30
2	559	96.0	109	4	US-08-232-246A-30
3	559	96.0	432	3	US-08-477-460B-2
4	559	96.0	432	3	US-08-379-516-2
5	559	96.0	432	4	US-09-329-916-2
6	559	96.0	432	4	US-08-485-372A-2
7	559	96.0	432	4	US-09-409-006A-2
8	559	96.0	432	5	PCT-US93-07422-2
9	559	96.0	530	3	US-08-477-460B-4
10	559	96.0	530	3	US-08-379-516-4
11	559	96.0	530	4	US-09-329-916-4
12	559	96.0	530	4	US-08-485-372A-4
13	559	96.0	530	4	US-09-409-006A-4
14	559	96.0	530	5	PCT-US93-07422-4
15	558	95.9	116	2	US-08-232-539D-55
16	558	95.9	212	1	US-08-430-633-4
17	558	95.9	212	2	US-08-620-694A-4
18	558	95.9	212	2	US-08-936-854-4
19	558	95.9	212	3	US-09-022-255-4
20	558	95.9	212	3	US-09-022-696-4
21	558	95.9	212	3	US-09-022-253-4
22	558	95.9	212	3	US-09-022-260-4
23	558	95.9	212	4	US-09-022-259-4
24	558	95.9	212	4	US-09-022-257-4
25	558	95.9	232	2	US-08-595-043A-50
26	558	95.9	235	4	US-09-131-247-6
27	558	95.9	254	2	US-08-284-391B-33

28	558	95.9	254	4	US-09-218-950-33	Sequence 33, Appl
29	558	95.9	331	1	US-09-178-869-2	Sequence 2, Appl
30	558	95.9	347	1	US-07-940-861-43	Sequence 43, Appl
31	558	95.9	347	1	US-08-459-512-43	Sequence 43, Appl
32	558	95.9	347	2	US-08-459-657-43	Sequence 43, Appl
33	558	95.9	347	2	US-08-460-132-43	Sequence 43, Appl
34	558	95.9	347	4	US-08-466-465-8	Sequence 8, Appl
35	558	95.9	347	5	PCT-US92-02050-43	Sequence 43, Appl
36	558	95.9	360	4	US-09-180-100-11	Sequence 11, Appl
37	558	95.9	371	1	US-08-236-311-7	Sequence 7, Appl
38	558	95.9	371	3	US-08-457-918-7	Sequence 22, Appl
39	558	95.9	376	4	US-09-180-100-22	Sequence 4, Appl
40	558	95.9	387	1	US-08-470-299-4	Sequence 16, Appl
41	558	95.9	388	4	US-09-131-247-16	Sequence 14, Appl
42	558	95.9	389	4	US-09-131-247-14	Sequence 3, Appl
43	558	95.9	396	2	US-08-784-512-3	Sequence 3, Appl
44	558	95.9	396	4	US-09-176-228-3	Sequence 8, Appl
45	558	95.9	424	4	US-09-333-593A-8	

ALIGNMENTS

RESULT 1
US-08-444-644-30
; Sequence 30, Application US/08444644
; Patent No. 601555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear


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1 1LEX:
2 INFORMATION FOR SEQ ID NO: 2:
3 SEQUENCE CHARACTERISTICS:
4 LENGTH: 432 amino acids
5 TYPE: amino acid
6 STRANDEDNESS: unknown
7 TOPOLOGY: unknown
8 MOLECULE TYPE: protein
9 ORIGINAL SOURCE:
10 ORGANISM: homo sapien
11

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US-08-477-460B-4 ; Sequence 4, Application US/08477460B
; Patent No. 6034223
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals

```

; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,460B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
;
US-08-477-460B-4

Query Match 96.0%; Score 559; DB 3; Length 530;
Best Local Similarity 94.5%; Pred. No. 8.1e-57;
Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKP 60
    |||||
Db 315 APPVAGPSVLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNKYVDGVVHNAKTKP 374

QY 61 REQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
    |||||
Db 375 REQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 423

RESULT 10
US-08-379-516-4
; Sequence 4, Application US/08379516
; Patent No. 6083478
; GENERAL INFORMATION:
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
; FILE REFERENCE: 41215-A-PCT-US
; CURRENT APPLICATION NUMBER: US/08/379,516
; CURRENT FILING DATE: 1996-06-10
; EARLIER APPLICATION NUMBER: PCT/US93/07422
; EARLIER FILING DATE: 1993-08-06
; EARLIER APPLICATION NUMBER: 07/927,931
; EARLIER FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 9

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-379-516-4

Query Match 96.0%; Score 559; DB 3; Length 530;
Best Local Similarity 94.5%; Pred. No. 8.1e-57;
Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKP 60
    |||||
Db 315 APPVAGPSVLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNKYVDGVVHNAKTKP 374

QY 61 REQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
    |||||
Db 375 REQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 423

RESULT 11
US-09-329-916-4
; Sequence 4, Application US/09329916
; Patent No. 6177549
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; FILE REFERENCE: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/329,916
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,460
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
;
US-09-329-916-4

Query Match 96.0%; Score 559; DB 4; Length 530;

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Best Local Similarity 94.5%; Pred. No. 8.1e-57;
Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 315 APPVAGPSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 374
QY 61 REEQYNSTYRVVSVLTVLDHQLNGKREYKCKVSNKALPAPIEKTISKAK 109
Db 375 REEQFNSTFRVSVLTVVHQLNGKREYKCKVSNKGLPAPIEKTISKTK 423

RESULT 12

US-08-485-372A-4
; Sequence 4, Application US/08485372A
; Patent No. 6187748
; GENERAL INFORMATION:
; APPLICANT: Beaudry, Gary A.
; APPLICANT: Madon, Paul J.
; TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,372A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,227
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37690-II-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte

US-08-485-372A-4

Query Match 96.0%; Score 559; DB 4; Length 530;
Best Local Similarity 94.5%; Pred. No. 8.1e-57;
Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 315 APPVAGPSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 374
QY 61 REEQYNSTYRVVSVLTVLDHQLNGKREYKCKVSNKALPAPIEKTISKAK 109
Db 375 REEQFNSTFRVSVLTVVHQLNGKREYKCKVSNKGLPAPIEKTISKTK 423

RESULT 13

US-09-409-006A-4
; Sequence 4, Application US/09409006A
; Patent No. 6342586
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-09-409-006A-4

Query Match 96.0%; Score 559; DB 4; Length 530;
Best Local Similarity 94.5%; Pred. No. 8.1e-57;
Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 315 APPVAGPSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 374
QY 61 REEQYNSTYRVVSVLTVLDHQLNGKREYKCKVSNKALPAPIEKTISKAK 109
Db 375 REEQFNSTFRVSVLTVVHQLNGKREYKCKVSNKGLPAPIEKTISKTK 423

RESULT 14

PCT-US93-07422-4
; Sequence 4, Application PC/TUS9307422
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 08:36:09 ; Search time 224.82 Seconds
(without alignments)
53.852 Million cell updates/sec

Title: US-09-674-857-9
Perfect score: 582
Sequence: 1 APPVAGPSVFLFPKPKDTL.....CKVSNKALPAPIETISKAK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	567	97.4	109	21	Mutated CH2 sequen
2	560.5	96.3	368	20	Rat Thy-1-human Ig
3	560.5	96.3	368	20	Human Thy-1-human
4	560.5	96.3	444	21	Humanised anti-CD2
5	559	96.0	109	14	Undefined ORF2 enc
6	559	96.0	217	21	Amino acid sequenc
7	559	96.0	217	22	Human IgG2. Homo
8	559	96.0	217	22	Human IgG2 Fc regi
9	559	96.0	326	22	Human immunoglobul
10	559	96.0	381	20	Human IL-2/Ig fusi
11	559	96.0	432	13	CD4-gamma2 chimeri

12	559	96.0	432	15	CD4-gamma 2 chimera
13	559	96.0	432	21	Human CD4-gamma 2
14	559	96.0	432	22	Human CD4-gamma2 c
15	559	96.0	432	22	CD4-gamma2 chimeri
16	559	96.0	442	22	Humanised 323/A3 (
17	559	96.0	443	20	Human IgG2 chain C
18	559	96.0	451	21	The heavy chain of
19	559	96.0	461	21	Humanised 323/A3 (
20	559	96.0	462	21	Human immunoglobul
21	559	96.0	463	21	The heavy chain of
22	559	96.0	463	21	The heavy chain of
23	559	96.0	463	21	The heavy chain of
24	559	96.0	463	21	The heavy chain of
25	559	96.0	464	21	The heavy chain of
26	559	96.0	464	21	The heavy chain of
27	559	96.0	475	18	Soluble B7-1-Ig.
28	559	96.0	530	13	CD4-IgG2 chimeric
29	559	96.0	530	21	CD4-IgG2 chimeric
30	559	96.0	530	22	Human CD4-IgG2 chi
31	559	96.0	530	22	CD4-IgG2 chimeric
32	558	95.9	116	20	Human IgG1 Fc gamma
33	558	95.9	212	16	Immunoglobulin G1
34	558	95.9	212	17	Human immunoglobul
35	558	95.9	212	17	Human IgG1 Fc regi
36	558	95.9	212	19	Human immunoglobul
37	558	95.9	212	20	IgG1 Fc protein us
38	558	95.9	212	20	Human IgG1 Fc prot
39	558	95.9	212	21	Human IgG1 Fc regi
40	558	95.9	212	21	Human immunoglobul
41	558	95.9	212	21	Human immunoglobul
42	558	95.9	212	21	Fc region of human
43	558	95.9	212	22	Fc region of human
44	558	95.9	212	22	Human immunoglobul
45	558	95.9	224	8	Sequence of human

ALIGNMENTS

RESULT 1
AA54996
ID AA54996 standard; protein; 109 AA.
XX
AC AA54996;
XX
DT 17-FEB-2000 (first entry)
XX
DE Mutated CH2 sequence G1deltaab.
KW Binding molecule; CH2 sequence; complement dependent lysis; Fc gammaRIIB;
KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
KW autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
KW neonatal alloimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
KW sickle cell anaemia; coronary artery occlusion.
OS Synthetic.
XX
XX WO9958572-A1.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-CB01441.
XX
PR 08-MAY-1999; 98GB-0009951.
XX
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI Armour KL, Clark MR, Williamson LM;
XX

DR WPI; 2000-039075/03.
 XX Immunoglobulin-derived binding molecules that do not activate
 PT complement or trigger cytotoxic activities and maintaining desirable
 PT immunoglobulin properties -
 XX
 XX Claim 12; Fig 17; 81pp; English.
 PS
 CC This sequence represents the mutated CH2 molecule Gideltaab, and is a
 CC binding molecule of the invention. The recombinant binding molecule
 CC is capable of binding a target molecule without triggering complement
 CC dependent lysis, or the cell-mediated destruction of the target
 CC comprises: (a) a binding domain capable of binding a target molecule; and
 CC (b) an effector domain that is homologous to all or part of a constant
 CC domain of a human immunoglobulin G (IgG) heavy chain. The binding
 CC molecule is used to bind a target molecule (especially FcgammaRIIb
 CC causing inhibition of B cell activation, mast cell degranulation or
 CC phagocytosis). The binding molecule can be used to prevent or inhibit the
 CC binding of a second binding molecule, e.g. an antibody, to the target
 CC molecule. The binding molecule is useful for the treatment of
 CC graft-vs-host disease, organ transplant rejection, bone-marrow transplant
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
 CC autoimmune thrombocytopenia and arthritis), alloimmunity
 CC (e.g. foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
 CC coronary artery occlusion). The binding molecules do not activate
 CC complement or trigger cytotoxic activities through FcgammaR and desirable
 CC IgG properties have been retained. The polypeptides do not contain
 CC non-human amino acids, and are therefore likely to have reduced
 CC immunogenicity. Further, they still bind Protein A, which is consistent
 CC with being able to cross the human placenta through interaction with FcRn
 CC (neonatal Fc receptor).
 XX
 SQ Sequence 109 AA;
 Query Match 97.4%; Score 567; DB 21; Length 109;
 Best Local Similarity 97.2%; Pred. No. 2.4e-49;
 Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTP 60
 DB 1 appvagsvflppkpkdtlmisrtpevtcvvvdshedpevkfnwvdygvevhnatktp 60
 QY 61 REEQYNSTYRVSVTLVTHQDWLNGKEYCKVSNKALPAPIETISKAK 109
 DB 61 reeqynstyrsvsvtlvthqdwlngkeyckvsnknglpssiektiskak 109
 RESULT 2
 AAY31788
 ID AAY31788 standard; Protein; 368 AA.
 XX
 AC AAY31788;
 XX
 DT 06-DEC-1999 (first entry)
 XX
 DE Rat Thy-1-human IgG constant region fusion protein.
 XX
 KW Thy-1; rat; human; IgG; angiogenesis; cancer; tumour;
 KW rheumatoid arthritis; atherosclerosis; therapy.
 XX
 OS Chimeric - Rattus sp.
 OS Chimeric - Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "Thy-1 signal peptide"
 FT Protein 18..368
 FT /label= "mature Thy-1Ig, specifically claimed in
 FT Claim 8"
 XX

PN W09945951-A2.
 XX
 PD 16-SEP-1999.
 XX
 PF 11-MAR-1999; 99WO-US05256.
 XX
 PR 11-MAR-1998; 98US-0077524.
 XX
 PA (HARD) HARVARD COLLEGE.
 PA (HABE/) HABER C.
 XX
 PI Haber E, Shaw S, Jain MK, Lee W;
 XX WPI: 1999-561618/47.
 DR N-PSDB; AAX87979.
 XX
 PT Inhibiting Thy-1 expression in endothelial cell, useful for inhibiting
 PT angiogenesis -
 XX
 PS Claim 8; Page 45-46; 47pp; English.
 CC The present sequence represents a fusion protein, the mature
 CC portion of which is claimed, comprising the rat Thy-1 extracellular
 CC region (see also AAY31786) and the constant region (hinge, CH2, CH3)
 CC of human IgG1. The fusion protein was transiently expressed in COS
 CC cells transfected with an expression plasmid containing a chimeric
 CC DNA (see AAX87979). A claimed method for inhibiting angiogenesis in
 CC a mammal comprises administering a compound that inhibits Thy-1
 CC associated proliferation of an endothelial cell. This compound is
 CC preferably the extracellular region of rat or human Thy-1. The
 CC method is used in the treatment of a mammal having a tumour (e.g.
 CC by reducing vascularisation), atherosclerosis or rheumatoid
 CC arthritis, the lesions of which may be associated with
 CC neovascularisation (all claimed). Another claimed method for
 CC inhibiting angiogenesis involves administering a Thy-1 antisense
 CC nucleic acid or a Thy-1-specific antibody linked to a cytotoxic
 CC agent. A method for promoting angiogenesis involves administering
 CC a compound that increases Thy-1 expression in an endothelial cell
 CC such as a chimeric protein comprising the Thy-1 extracellular
 CC fragment and the constant region of an immunoglobulin.
 XX
 SQ Sequence 368 AA;
 Query Match 96.3%; Score 560.5; DB 20; Length 368;
 Best Local Similarity 93.9%; Pred. No. 4.6e-48;
 Matches 107; Conservative 1; Mismatches 1; Indels 5; Gaps 1;
 QY 1 APPVA-----GPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
 DB 148 sppsapellggpsvflppkpkdtlmisrtpevtcvvvdshedpevkfnwvdygvevhn 207
 QY 56 AKTKPREQYNSTYRVSVTLVTHQDWLNGKEYCKVSNKALPAPIETISKAK 109
 DB 208 aktkpreeqynstyrsvsvtlvthqdwlngkeyckvsnknglpssiektiskak 261
 RESULT 3
 AAY31789
 ID AAY31789 standard; Protein; 368 AA.
 XX
 AC AAY31789;
 XX
 DT 06-DEC-1999 (first entry)
 XX
 DE Human Thy-1-human IgG constant region fusion protein.
 XX
 KW Thy-1; human; IgG; angiogenesis; cancer; tumour;
 KW rheumatoid arthritis; atherosclerosis; therapy.
 XX
 OS Chimeric - Homo sapiens.
 XX
 XX Key Location/Qualifiers

FT	Peptide	1..19
FT	FT	/note= "Thy-1 signal peptide"
FT	Protein	18..368
FT	FT	/note= "Thy-1-Ig fusion, specifically claimed in Claim 8"
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PX	WO9945951-A2.	
XX		
PD	16-SEP-1999.	
XX		
PF	11-MAR-1999;	99WO-USO5256.
XX		
PR	11-MAR-1998;	98US-0077524.
XX	(HARD) HARVARD COLLEGE.	
PA	(HABE/) HABER C.	
XX		
PI	Haber E, Shaw S, Jain MK, Lee W;	
XX		
DR	WPI; 1999-561618/47.	
XX	N-PSDB; AAX87980.	
PT	Inhibiting Thy-1 expression in endothelial cell, useful for inhibiting angiogenesis -	
XX		
PS	Claim 8; Page 46-47; 47pp; English.	
CC	The present sequence represents a fusion protein, the mature region of which is claimed, comprising the human Thy-1 extracellular region (see AAY31787) and the constant region (hinge, CH2, CH3) of human IgG1. A claimed method for inhibiting angiogenesis in a mammal comprises administering a compound that inhibits Thy-1 associated proliferation of an endothelial cell. The compound is preferably the extracellular region of rat or human Thy-1. The method is used in the treatment of a mammal having a tumour (e.g. by reducing vascularisation), atherosclerosis or rheumatoid arthritis, the lesions of which may be associated with neovascularisation (all claimed). Another claimed method for inhibiting angiogenesis involves administering a Thy-1 antisense nucleic acid or a Thy1-specific antibody linked to a cytotoxic agent. A method for promoting angiogenesis involves administering a compound that increases Thy-1 expression in an endothelial cell such as a chimeric protein comprising the Thy-1 extracellular fragment and the constant region of an immunoglobulin.	
XX		
SQ	Sequence	368 AA;
Query Match . 96.3%; Score 560.5; DB 20; Length 368;		
Best Local Similarity 93.9%; Pred. No. 4.e-48;		
Matches 107; Conservative 1; Mismatches 1; Indels 5; Gaps		
QY	1 APPVA-----GPSVFLEPPKPKDPLMLSRPEVTCTVVVDYSHEDPVKFNWYDGVGVHN 55	
	: :	
Db	148 spspasellgpsvflfpkpkdtlmsrpevtctvvvdvshepdkfnwvydgvgevhnn 207	
QY	56 AKTKPREQYNSTRVVSVLTVLHQDLWGNGKEYCKVSNKALPAPIEKTIISKAK 109	
Db	208 aktkpreqynstryrvsvltvlhqdlwgngkeyckvsnkalpapiektiskak 261	
RESULT	4	
ID	AAY32263	
XX	AAAY32263 standard; Protein; 444 AA.	
AC		
XX	AAAY32263;	
DT		
XX	15-FEB-2000 (first entry)	
DE		
XX	Humanised anti-CD23 Mab C11 heavy chain.	
KW	CD23; FCERI; Ige receptor; monoclonal antibody; C11; mouse; human;	
KW	monoclonal antibody; chimeric antibody; humanised antibody;	
KW	complementarity determining region; CDR; autoimmune disease;	

QY . 1 APPVAGPSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 600

KW Human; erythropoietin; EPO; antianemic; nephrotrophic; anti-HIV;
 KW vaccine; haemostatic; immunoglobulin G2; IgG2; EPO deficient disease;
 KW anaemia; renal failure; Human Immunodeficiency Virus; HIV;
 KW haematopoietic growth factor.
 OS Homo sapiens.
 XX WO200136489-A2.
 XX PD 25-MAY-2001.
 XX PF 03-NOV-2000; 2000WO-EP10843.
 XX PR 12-NOV-1999; 99US-0164855.
 XX PA (MERE) MERCK PATENT GMBH.
 XX PI Hartmann A, Brandt S, Rieke E, Sobel C, Lo K, Way JC, Gillies S;
 XX WPI; 2001-367563/38.
 XX Novel modified erythropoietin forms such as fusion proteins, comprising
 XX Fc portion of an immunoglobulin molecule and a target molecule having
 XX the biological activity of erythropoietin forms
 XX Example 1; Page 24; 58pp; English.
 XX The present sequence is human immunoglobulin G2 (IgG2) constant region
 XX mature protein. IgG2 forms a fusion protein with human erythropoietin
 XX (EPO). EPO has improved biological activity and an extended serum half
 XX life greater than 20 hours. The present invention relates to modified
 XX EPO forms such as fusion proteins comprising a Fc portion of an
 XX immunoglobulin (Ig) molecule and an EPO molecule (Fc-EPO). The Fc portion
 XX is fused covalently through its C-terminus directly or indirectly to the
 XX EPO molecule, and where the Fc portion as well as EPO portion may be
 XX modified or mutated. The invention also relates to non-fused EPO
 XX molecules which have a pattern of cysteines or disulphide bonding which
 XX is distinct from human or animal EPO. Pharmaceutical compositions
 XX containing EPO are useful in the treatment of EPO deficient diseases such
 XX as anaemia, renal failure, HIV infection, blood loss and chronic disease
 XX that can be treated with haematopoietic growth factor.
 XX SQ Sequence 326 AA;
 Query Match 96.0%; Score 559; DB 22; Length 326;
 Best Local Similarity 94.5%; Pred. No. 5.6e-48;
 Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 Db 111 appvagsvflfppkpkdtlmisrtpevtcvvvdvshedpevgfnwyvdgvevhnatktp 170
 QY 61 REEQYNSTYRWVSVLTVLHODWLNKGKEYCKVSNKALPAPIETISKAK 109
 Db 171 reeqfnstfrvsvltvvhqdwlngkeyckvsnkglpapietisktk 219
 RESULT 10
 AAY06895
 ID AAY06895 standard; Protein; 381 AA.
 XX AC AAY06895;
 XX DT 01-JUL-1999 (first entry)
 XX DE Human IL-2/Ig fusion protein.
 XX Fusion protein; vaccine; cytokine; immunoglobulin; autoimmune disease;
 KW infectious disease; inflammatory disease; neoplastic disease; cancer;
 KW immunologic disease; immune response; malaria; tuberculosis; hepatitis;
 KW AIDS; influenza; interleukin; IL-2; Ig; human.
 OS Homo sapiens chimeric.

OS Homo sapiens.
 XX Key Location/Qualifiers
 FT Protein 1..153
 FT Protein /note= "interleukin-2 (IL-2)"
 FT Protein 154..381
 FT Protein /note= "immunoglobulin G"
 PN WO9916466-A2.
 XX PD 08-APR-1999.
 XX PF 29-SEP-1998; 98WO-US20321.
 XX PR 12-DEC-1997; 97US-0990180.
 XX PR 29-SEP-1997; 97US-0060338.
 XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX PI Barouch DH, Letvin NL;
 XX WPI; 1999-254931/21.
 XX N-PSDB; AAX34598.
 XX New vaccine compositions
 XX Claim 16; Fig 10A-E; 66pp; English.
 XX The invention relates to vaccine compositions comprising a vaccine and a
 XX timed-release formulation of a cytokine or cytokine/immunoglobulin fusion
 XX protein or plasmid. The formulation or device releases the cytokine
 XX protein or plasmid at one or more temporal points subsequent to vaccine
 XX administration. The vaccines can be used for treating an autoimmune
 XX disease, an infectious disease, an inflammatory disease, a neoplastic
 XX disease, or an immunologic disease in an individual. The vaccines can be
 XX used to elicit immune responses against diseases such as AIDS, malaria,
 XX tuberculosis, hepatitis C, hepatitis B, cancer or influenza. The methods
 XX can provide for enhancement of one or more immunologic parameters such as
 XX an antibody response, a cellular proliferative response as well as
 XX cytotoxic T-lymphocyte levels. In addition the Ig can increase the
 XX circulating half life of the cytokine. The present sequence represents
 XX a human interleukin-2 (IL-2)/Ig fusion protein.
 XX SQ Sequence 381 AA;
 Query Match 96.0%; Score 559; DB 20; Length 381;
 Best Local Similarity 94.5%; Pred. No. 6.8e-48;
 Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 Db 166 appvagsvflfppkpkdtlmisrtpevtcvvvdvshedpevgfnwyvdgvevhnatktp 225
 QY 61 REEQYNSTYRWVSVLTVLHODWLNKGKEYCKVSNKALPAPIETISKAK 109
 Db 226 reeqfnstfrvsvltvvhqdwlngkeyckvsnkglpapietisktk 274
 RESULT 11
 AAR26782
 ID AAR26782 standard; Protein; 432 AA.
 XX AC AAR26782;
 XX DT 06-FEB-1993 (first entry)
 XX DE CD4-gamma2 chimeric heavy chain homodimer.
 XX homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;
 KW chimeric; increased serum half life; HIV infection; AIDS; ss.
 OS Homo sapiens chimeric.

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XX FH Key Location/Qualifiers
FT Domain 1..216
FT /label= CD4
FT Domain 217..325
FT /label= CH2
FT Domain 326..433
FT /label= CH3
XX WO9213947-A.
XX 20-AUG-1992.
XX 10-FEB-1992; 92WO-US01143.
XX 08-FEB-1991; 91US-0653684.
XX (PROG-) PROGENICS PHARM INC.
XX Beaudry GA, Maddon PJ;
XX WPI; 1992-300034/36.
XX N-PSDB; AAQ28088.
XX CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for
XX treatment, prevention and diagnosis of HIV infection
XX Claim 2; Fig 3; 90pp; English.
XX This sequence represents a CD4-gamma2 chimeric heavy chain homodimer.
XX It was produced by expression of the coding mutagenised cDNA
XX (produced as described in AAQ28088) in Dhfr-CHO cells. The protein is
XX efficiently assembled intracellularly and effectively secreted from
XX mammalian cells pref. CHO, COS, or myeloma cells as a homodimer,
XX enabling high recovery and purification from the medium of cells
XX expressing it. It possesses increased serum half-life and has increased
XX avidity for HIV cf. heavy chain dimers. It can inhibit HIV infection of
XX CD4+ cells and block the spread of HIV infection within a patient.
XX Attachment to a detectable marker makes it useful in an assay for HIV
XX or SIV infection, and it can also be linked to toxins, eg Diphtheria,
XX Pseudomonas exotoxin A (domains I or II) or the deglycosylated A-chain
XX of ricin.
XX Sequence 432 AA;

Query Match 96.0%; Score 559; DB 13; Length 432;
Best Local Similarity 94.5%; Pred. No. 7.9e-48;
Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 217 appvagsvflpppkdktlmistrpevtcvvvdvshedpevgfnwvvgdevhnaaktp 276
QY 61 REQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
Db 277 reeqfnstfrvsvltvvhqdwlngkeyckckvsnkglpapiektisktk 325

RESULT 12
AAR46678
ID AAR46678 standard; Protein; 432 AA.
XX AAR46678;
AC AAR46678;
XX 08-AUG-1994 (first entry)
XX CD4-gamma 2 chimeric heavy chain.
XX CD4; gamma; heavy chain; chimeric; chimeraic; immunoconjugate; HIV;
XX human immunodeficiency virus; radionuclide; toxin; therapy;
XX treatment; imaging; detection; targeting.
XX

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OS Homo sapiens.
XX Key Location/Qualifiers
XX FH 1..204
XX FT /label= CD4 Region.
XX FT 205..216
XX FT /label= Hinge Region.
XX FT 217..325
XX FT /label= CH2 Region.
XX FT 326..432
XX FT /label= CH3 Region.
XX WO9403191-A.
XX 17-FEB-1994.
XX 06-AUG-1993; 93WO-US07422.
XX 07-AUG-1992; 92US-0927931.
XX (PROG-) PROGENICS PHARM INC.
XX Allaway GP, Maddon PJ;
XX WPI; 1994-065392/08.
XX N-PSDB; AAQ57750.
XX Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2
XX immunoconjugates - used to kill HIV-infected cells and to image
XX and stage HIV infection
XX Disclosure; Figure 3; 142pp; English.
XX A CD4-gamma 2 chimeric heavy chain homodimer is linked to a non-
XX peptidyl toxin or a gamma radiation-emitting radionuclide of low to
XX moderate cytotoxicity. The resulting immunoconjugate comprising the
XX toxin can be used to kill HIV infected cells and to treat HIV
XX infected subjects to reduce the population of HIV infected cells.
XX It can also be used to reduce the likelihood of infection. The
XX immunoconjugate comprising the radionuclide can be used to image HIV
XX infected tissue, to calculate the stage of HIV infection or the
XX efficacy of an anti-HIV treatment using the imaging technique and
XX for determining the prognosis of an HIV infected subject.
XX Sequence 432 AA;

Query Match 96.0%; Score 559; DB 15; Length 432;
Best Local Similarity 94.5%; Pred. No. 7.9e-48;
Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Db 217 appvagsvflpppkdktlmistrpevtcvvvdvshedpevgfnwvvgdevhnaaktp 276
QY 61 REQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
Db 277 reeqfnstfrvsvltvvhqdwlngkeyckckvsnkglpapiektisktk 325

RESULT 13
AAY85079
ID AAY85079 standard; Protein; 432 AA.
XX AAY85079;
AC AAY85079;
XX 19-JUN-2000 (first entry)
XX Human CD4-gamma 2 chimeric heavy chain homodimer amino acid sequence.
XX CD4-gamma 2 chimeric heavy chain homodimer; immunoconjugate; treatment;
XX cytotoxic radionuclide; cell surface glycoprotein; prevent; infection;
XX cellular immune response interaction mediator; HIV interaction;

```

KW staging; prognosis; envelope glycoprotein burden; human.
 XX Homo sapiens.
 OS US6034223-A.
 PN 07-MAR-2000.
 PD 07-JUN-1995; 95US-0477460.
 PF 07-AUG-1992; 92US-0927931.
 PR 06-AUG-1993; 93WO-US07422.
 PR 03-FEB-1995; 95US-0379516.
 XX (PROG-) PROGENICS PHARM INC.
 PA Allaway GP, Maddon PJ;
 PI WPI: 2000-269502/23.
 DR N-PSDB; AAZ98855.
 DR New immunoconjugate, used to treat, prevent or image human immune
 PT deficiency virus infection, comprises radionuclide attached to
 PT heterotetramer of CD4-immunoglobulin chimeras
 XX Disclosure; Fig 3; 58pp; English.
 PS This sequence represents the human CD4-gamma 2 chimeric heavy chain
 XX homodimer amino acid sequence. The invention relates to an
 CC immunoconjugate comprising a cytotoxic radionuclide and a heterotetramer
 CC of two heavy chains and two light chains. The cytotoxic radionuclide is
 CC linked to either the heavy chains or the light chains, or to all four
 CC chains, directly or through a bifunctional chelator. Both heavy chains
 CC are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by vector
 CC CD4-Ig2HC-prcCMV (ATCC 75193) and both light chains are chimeric
 CC CD4-kappa chains encoded by vector CD4-kLC-prcCMV (ATCC 75194). CD4 is a
 CC non-polymorphic cell surface glycoprotein that is expressed on the
 CC surface of helper T lymphocytes, cells of the monocyte/macrophage lineage
 CC and dendritic cells. CD4 associates with major histocompatibility complex
 CC (MHC) class II molecules on the surface of antigen presenting cells to
 CC mediate efficient cellular immune response interactions. In humans CD4 is
 CC the target of interaction with the human immunodeficiency virus HIV. The
 CC immunoconjugate is used to kill cells infected with HIV, and for treating
 CC (for staging or prognosis of infection, and for assessing efficacy of
 CC treatments). The immunoconjugate is also used to determine the HIV
 CC envelope glycoprotein burden, once determined, this information is used
 CC in the staging and prognosis of HIV infected patients. The
 CC immunoconjugate should be active against all strains of HIV (since the
 CC CD4-gp120 interaction is essential for infection). The heterotetramers
 CC are assembled intracellularly and secreted efficiently from mammalian
 CC cells, allowing high recovery and purification from the culture medium.
 CC They have longer half-life in serum and greater avidity than heavy chain
 XX dimers.
 SQ Sequence 432 AA;

Query Match 96.0%; Score 559; DB 21; Length 432;
 Best Local Similarity 94.5%; Pred. No. 7.9e-48;
 Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 DB 217 appvagsvflfppkpkdtlmisrtpevtcvvvdvshedpevqfnwydgvvhnaktkp 276
 QY 61 REEQYNSTRYVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAK 109
 DB 277 reeqnstrfyrsvsvltvvhqdwlngkeyckvsnkalgpapiektisktk 325
 RESULT 14
 AAB80883

ID AAB80883 standard; Protein; 432 AA.
 XX AAB80883;
 AC 29-MAY-2001 (first entry)
 XX Human CD4-gamma2 chimeric heavy chain homodimer.
 DE Human; Anti-HIV; CD4-IgG2 chimeric heterotetramer;
 KW immunoglobulin gamma 2.
 XX Homo sapiens.
 OS US6187748-B1.
 XX 13-FEB-2001.
 PD 07-JUN-1995; 95US-0485372.
 PF 08-FEB-1991; 91US-0653684.
 PR 10-FEB-1992; 92WO-US01143.
 PR 08-DEC-1992; 92US-0960440.
 XX (PROG-) PROGENICS PHARM INC.
 PA Maddon PJ, Beaudry GA;
 PI WPI: 2001-264981/27.
 DR N-PSDB; AAF77829.
 DR Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell,
 XX or treating a subject having CD4+ cells infected with HIV involves
 PT using CD4-IgG2 chimeric heterotetramer to form a complex with the HIV -
 PT Disclosure; Fig 3; 55pp; English.
 PS The present invention relates to a method for inhibiting infection of a
 CC CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2
 CC chimeric heterotetramer to form a complex with the HIV (CD4 - cluster of
 CC differentiation 4; IgG2 - immunoglobulin gamma 2). CD4 is a cell surface
 CC glycoprotein that is expressed primarily on the surface of T cells. In
 CC man, CD4 is the target of interaction with HIV. The heterotetramer has
 CC two heavy and two light chains which are encoded by expression vectors
 CC CD4-IgG2HC-prcCMV (V1) and CD4-kLC-prcCMV (V2), respectively. The method
 CC is used to inhibit infection of a CD4+ cell by a HIV and to prevent CD4+
 CC cells of a subject from becoming infected with HIV. The method is also
 CC useful for treating a subject having CD4+ cells infected with HIV. The
 CC present sequence is human fusion protein: CD4-gamma2 chimeric heavy chain
 CC homodimer. This sequence was used in the method of the present invention.
 XX Sequence 432 AA;
 SQ

Query Match 96.0%; Score 559; DB 22; Length 432;
 Best Local Similarity 94.5%; Pred. No. 7.9e-48;
 Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 DB 217 appvagsvflfppkpkdtlmisrtpevtcvvvdvshedpevqfnwydgvvhnaktkp 276
 QY 61 REEQYNSTRYVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAK 109
 DB 277 reeqnstrfyrsvsvltvvhqdwlngkeyckvsnkalgpapiektisktk 325
 RESULT 15
 AAB67322
 ID AAB67322 standard; Protein; 432 AA.
 XX AAB67322;
 AC 23-APR-2001 (first entry)
 DT

XX CD4-gamma2 chimeric heavy chain homodimer protien.
DE
XX
XX Immunconjugate; chelator; chimeric; HIV;
KW human immunodeficiency virus.
XX
XX Homo sapiens.
OS
XX
XX US6177549-B1.
PN
XX
XX 23-JAN-2001.
PD
XX
XX 10-JUN-1999; 99US-0329916.
PF
XX
XX 07-JUN-1995; 95US-0477460.
PR
XX 07-AUG-1992; 92US-0927931.
PR
XX 06-AUG-1993; 93US-0379516.
PR
XX 06-AUG-1993; 93WO-US07422.
XX
XX (PROG-) PROGENICS PHARM INC.
PA
XX
XX Maddon PJ, Allaway GP;
PI
XX
XX WPI; 2001-158582/16.
DR
XX
XX Immunconjugate for treating human immunodeficiency virus-infected
PT subject, consists of cytotoxic radionuclide linked to heterotetramer
PT comprising two chimeric CD4-IgG2 heavy chains and two chimeric
PT CD4-kappallight chains -
PT
XX
XX Disclosure; Fig 3; 43pp; English.
PS
XX
XX The present invention relates to an immunoconjugate, comprising a
CC cytotoxic radionuclide linked, directly or via a bifunctional
CC chelator, to a heterotetramer having two chimeric CD4-IgG2 heavy
CC chains encoded by an expression vector CD4-IgG2HC-pRCMV and
CC two chimeric CD4-kappa light chains encoded by an expression vector
CC CD4-KLC-pRCMV. The invention is useful for killing human
CC immunodeficiency virus (HIV)-infected cells, for the treatment and
CC prevention of infection with HIV.
XX
XX
SQ Sequence 432 AA;

Query Match 96.0%; Score 559; DB 22; Length 432;
Best Local Similarity 94.5%; Pred. No. 7.9e-48;
Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 APPVAGSVFLPFPKPKDTLMISRTPEVTCVVYVDSHEDPEVKFNMYVDGVEVHNAKTKP 60
Db 217 appvagsvflfppkpkdtlmisrtpevtcvvdshepvevqfnwvvdgvevhnaktkp 276
QY 61 REEQNSTYRVSVSLVTLVHQDWLNGKEYCKVSNKALPAPIEKTISKAK 109
Db 277 reeqnstfrvsvltvwhqdwlngkeyckvsnkglpapiektistktk 325

Search completed: June 21, 2002, 08:36:09
Job time: 323 sec

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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:59:33 ; Search time 176.89 Seconds

(without alignments)
106.600 Million cell updates/sec

Title: US-09-674-857-9

Perfect score: 582

Sequence: 1 APPVAGSVFLFPKPKDTL.....CKVSNKALPAPIEKTISKAK 109

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	558	95.9	701	4 Q96PQ8	Q96PQ8 homo sapien
2	454	78.0	337	6 Q95M34	Q95M34 equus cabal
3	411	70.6	437	11 Q9R1A4	Q9R1A4 mus musculus
4	411	70.6	463	11 Q99LC4	Q99LC4 mus musculus
5	391	67.2	473	11 Q9D8L4	Q9D8L4 mus musculus
6	386	66.3	473	11 Q91Z05	Q91Z05 mus musculus
7	383	65.8	468	11 Q99L31	Q99L31 mus musculus
8	383	65.8	473	11 Q99L25	Q99L25 mus musculus
9	142	24.4	375	4 Q9BSZ1	Q9BSZ1 homo sapien
10	142	24.4	597	4 Q9QB8	Q9QB8 homo sapien
11	142	24.4	597	4 Q9BU10	Q9BU10 homo sapien
12	142	24.4	597	4 Q96BB9	Q96BB9 homo sapien
13	142	24.4	613	4 Q96EY0	Q96EY0 homo sapien
14	142	24.4	614	4 Q96GA6	Q96GA6 homo sapien
15	142	24.4	618	4 Q96AA6	Q96AA6 homo sapien
16	130.5	22.4	684	13 Q90544	Q90544 ginglymosto

17	123.5	21.2	384	4 Q9UP60	Q9UP60 homo sapien
18	123.5	21.2	416	4 Q9NPP6	Q9NPP6 homo sapien
19	123.5	21.2	494	4 Q96K68	Q96K68 homo sapien
20	123.5	21.2	496	4 Q96KX8	Q96KX8 homo sapien
21	123.5	21.2	496	4 Q96DK0	Q96DK0 homo sapien
22	119.5	20.5	500	4 Q9BRV0	Q9BRV0 homo sapien
23	118.5	20.4	130	11 Q9D8W4	Q9D8W4 mus musculus
24	118.5	20.4	233	11 Q91V32	Q91V32 m adult mal
25	114	19.6	211	11 Q91X10	Q91X10 mus musculus
26	114	19.6	233	11 Q91WS9	Q91WS9 mus musculus
27	114	19.6	234	11 Q91WF8	Q91WF8 mus musculus
28	114	19.6	235	11 Q91W12	Q91W12 mus musculus
29	114	19.6	238	11 Q9SM37	Q9SM37 mus musculus
30	113.5	19.5	486	11 Q91Z07	Q91Z07 mus musculus
31	113.5	19.5	487	11 Q99KA4	Q99KA4 mus musculus
32	112.5	19.3	233	4 Q96I69	Q96I69 homo sapien
33	112.5	19.3	235	11 Q99M11	Q99M11 mus musculus
34	112.5	19.3	236	4 Q96E61	Q96E61 homo sapien
35	112.5	19.3	479	11 Q99M22	Q99M22 mus musculus
36	112.5	19.3	484	11 Q99LA6	Q99LA6 mus musculus
37	112	19.2	214	11 Q9R1A5	Q9R1A5 mus musculus
38	111.5	19.2	479	11 Q91WP5	Q91WP5 mus musculus
39	111.5	19.2	481	11 Q91WT3	Q91WT3 mus musculus
40	111.5	19.2	481	11 Q91WT1	Q91WT1 mus musculus
41	111.5	19.2	482	11 Q91X92	Q91X92 mus musculus
42	111.5	19.2	488	11 Q91WR1	Q91WR1 mus musculus
43	110.5	19.0	426	11 Q9DCD9	Q9DCD9 mus musculus
44	110.5	19.0	480	11 Q91XE1	Q91XE1 mus musculus
45	101	17.4	1215	5 Q9V787	Q9V787 drosophila

ALIGNMENTS

RESULT 1

Q96PQ8 PRELIMINARY; PRT; 701 AA.

AC Q96PQ8: 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21477448; PubMed=11593034;

RA Hu Z., Garen A.;

RT "Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).

DR EMBL; AF272774; AAK58686.1; .

SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 95.9%; Score 558; DB 4; Length 701;
Best Local Similarity 93.0%; Pred. No. 6e-53;
Matches 106; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
|| : |||||
Db 481 PCPAPELGGPSVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 540

QY 56 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
|||||
Db 541 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 594

RESULT 2

Q95M34 PRELIMINARY; PRT; 337 AA.

ID Q95M34

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AC Q95M34:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IMMUNOGLOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
DE (FRAGMENT).
GN IGHC1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP .SEQUENCE FROM N.A.
RA Wagner B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP .SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B.; Overesch G.; Sheoran A.; Holmes M.; Richards C.;
RA Leibold W.; Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199;105-119(1998).
DR EMBL; AJ300675; CAC44624.1; -.
FT NON_TER 1
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 78.0%; Score 454; DB 6; Length 337;
Best Local Similarity 75.5%; Pred. No. 7e-42;
Matches 80; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

QY 4 VAGPSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
Db 123 LGGSVFIAPPNKDTLMITRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 182
QY 64 QYNSTYRVSVLTQHQDNLGKPKCKVSKNPKALPAPIETISKAK 109
Db 183 QFNSTYRVSVLTQHQDNLGKPKCKVSKNPKALPAPIETISKAK 228

RESULT 3
Q9RIA4
ID Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP .SEQUENCE FROM N.A.
RA Wilde K.G.; Yu X.; Ekramoddoullah A.K.M.; Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; Ig_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 70.6%; Score 411; DB 11; Length 463;
Best Local Similarity 70.6%; Pred. No. 5.6e-37;
Matches 72; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

QY 8 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 67
Db 255 SVFIFFPKPKDVLITLTPKVTCTVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 314
QY 68 TYRVVSVLTVLHODWLNKGEYKCKVSKNPKALPAPIETISKAK 109
Db 315 TFRSVSELPIMHQDWLNKGEYKCKVSKNPKALPAPIETISKAK 356

RESULT 5
Q9D8L4
ID Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DE 1810060009RIK PROTEIN.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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Query Match 70.6%; Score 411; DB 11; Length 437;
Best Local Similarity 70.6%; Pred. No. 5.2e-37;
Matches 72; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

QY 8 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 67
Db 229 SVFIFFPKPKDVLITLTPKVTCTVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 288
QY 68 TYRVVSVLTVLHODWLNKGEYKCKVSKNPKALPAPIETISKAK 109
Db 289 TFRSVSELPIMHQDWLNKGEYKCKVSKNPKALPAPIETISKAK 330

RESULT 4
Q99LC4
ID Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP .SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igc1; 2.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; Ig_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 70.6%; Score 411; DB 11; Length 463;
Best Local Similarity 70.6%; Pred. No. 5.6e-37;
Matches 72; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

QY 8 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 67
Db 255 SVFIFFPKPKDVLITLTPKVTCTVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 314
QY 68 TYRVVSVLTVLHODWLNKGEYKCKVSKNPKALPAPIETISKAK 109
Db 315 TFRSVSELPIMHQDWLNKGEYKCKVSKNPKALPAPIETISKAK 356

RESULT 5
Q9D8L4
ID Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DE 1810060009RIK PROTEIN.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl L., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00406; Ig; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 67.2%; Score 391; DB 11; Length 473;
Best Local Similarity 63.2%; Pred. No. 9.2e-35;
Matches 72; Conservative 18; Mismatches 18; Indels 6; Gaps 1;

QY 2 PPVA-----GPSVFELPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
Db 253 PCPAAPDLLGGPSVFPPPKIKDVLMSLSPKVTCTVVDVSEDDPDVQISWFWNNVEVHT 312

QY 56 AKTKPREQNSTYRVSVLTVLHODWLNKGCKVSKNKPAPIETKTSKAK 109
Db 313 AQQTTHREDYNSTRVVSALPIQHDWMSGKFKCKVNNRNPALPIETKTSKPR 366

RESULT 6
QY 6 QNSTYRVVSALPIQHDWLNKGCKVSKNKPAPIETKTSKAK 109
ID Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE HYPOTHETICAL 51.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

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Query Match 66.3%; Score 386; DB 11; Length 473;
Best Local Similarity 66.3%; Pred. No. 3.3e-34;
Matches 69; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

QY 6 GPSVFELPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQ 65
Db 263 GPSVFELPPPKIKDVLMSLTPKVTCTVVDVSEDDPDVQISWFWNNVEVHTAQTHREDY 322

QY 66 NSTYRVVSALPIQHDWLNKGCKVSKNKPAPIETKTSKAK 109
Db 323 NSTYRVVSALPIQHDWMSGKFKCKVNNKDLPSPIETKTSKIK 366

RESULT 7
QY 66 NSTYRVVSALPIQHDWLNKGCKVSKNKPAPIETKTSKAK 109
ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00406; Ig; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 65.8%; Score 383; DB 11; Length 468;
Best Local Similarity 66.0%; Pred. No. 6.9e-34;
Matches 70; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 63
Db 256 LGGPSVFELPPPKIKDVLMSLSPKVTCTVVDVSEDDPDVQISWFWNNVEVHTAQTHRE 315

QY 64 QNSTYRVVSALPIQHDWLNKGCKVSKNKPAPIETKTSKAK 109
Db 316 DYNSTRVVSALPIQHDWMSGKFKCKVNNKALPAPIETKTSKPK 361

RESULT 8
QY 64 QNSTYRVVSALPIQHDWLNKGCKVSKNKPAPIETKTSKAK 109
ID Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.

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RA	Strausberg R.;
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC003888; AAH03888.1; -
DR	HSSP; P01842; 7FAB
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR003597; Ig.cl.
DR	InterPro; IPR003600; Ig_like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig; 4.
DR	SMART; SM00409; Ig; 2.
DR	SMART; SM00407; Igcl; 3.
DR	SMART; SM00406; Ig; 1.
DR	SMART; SM00410; Ig_like; 1.
DR	PROSITE; P500290; IG_MHC; UNKNOWN_1.
SQ	SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

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Query Match      65.8%; Score 383; DB 11; Length 473;
Best Local Similarity 66.0%; Pred. No. 7e-34;
Matches 70; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

QY      4 VAGSVFLFPKPKDTLMIISTPEVTCVVVDVSHEDPEVKFNWYVDGVEFVNAKTKPREE 63
      : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      261 LGGSVFIFFPKIKDVLMIISLSPMTCVVVDVSEDDPDVQISWFVNNVEVLTAQQTTHRE 320

QY      64 QYNSTYRVWSVLTVLVHODWLNKGKEYKCVSKNKPALPAPIEKTIISRAK 109
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      321 DYNSTLRVWSALP:TOHQDWSMGKGFCKKVNKNKALPAPIERTISRPK 366

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RESULT	9
Q9BSZ1	
ID	PRELIMINARY; PRT; 375 AA.
OC	Q9BSZ1;
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (rEMBLrel. 17, Last sequence update)
DE	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	HYPOTHETICAL 41.3 KDA PROTEIN.
OS	homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute-
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
OX	NCHI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lymph, LYMPHOMA;
RA	Strausberg R.;
RL	Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
DR	EMBL; BC004476; AAHQ4476.1; -.
DR	HSP; P01857; 1FC1.
DR	InterPro; IPR003597; Ig_c1.
DR	InterPro; IPR003600; Ig_like.
DR	InterPro; IPR003006; Ig_MHC.
DR	Pfam; PF00047; Ig; 3.
DR	SMART; SM00407; IGc1; 3.
DR	SMART; SM00410; IG_Like; 1.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW	Hypothetical protein.
SQL	SEQUENCE 375 AA; 41314 MW; BIA0A0998F473619 CRC64:

Query Match	24.4%;	Score 142;	DB 4;	Length 375;
Best Local Similarity	28.7%;	Pred. No. 1 8e-07;		
Matches	29;	Conservative 26;	Mismatches 44;	Indels 2; Gaps 2;
QY	9	VFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGEVHNNAKT	KPREEQYNST	68
		: : : : : : : : : : : : : : : :		
D _b	146	VFAIPSP-FASIFLTKSTKLTLCLVTDLTTVD-SVTISWTRQNGEAVATHINISESHENAT		203
QY	69	YRVYSVLTVLHQDWLNCKKEYKKCVSKNALPAPIEKTSKAK		109
		: :		
D _b	204	FSAVGASTICEDDNWSGERETCTVTHTDLSPLKQTISRPK		244

RESULT	10
Q9BQB8	
ID	Q9BQB8 PRELIMINARY; PRT; 597 AA.
AC	Q9BQB8;
DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
OS	Homo sapiens (Human);
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute-
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=RHABDOWYOSARCOMA;
RA	Strausberg R.;
RL	Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RL	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=LYMPHOMA;
RA	Strausberg R.;
RL	Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL	EMBL; BC006180; AAH06180.1; -;
EMBL	EMBL; BC001872; AAH01872.1; -;
DR	HSP; P01825; 7FAB.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR003597; Ig.cl.
DR	InterPro; IPR003600; Ig_like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; ig; 5.
DR	SMART; SM00409; IG; 2.
DR	SMART; SM00407; IGcl; 4.
DR	SMART; SM00406; IGV; 1.
DR	SMART; SM00410; IG_like; 1.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_3.
DR	SEQUENCE 597 AA; 65300 MW; 2DAFAD50AG375851 CRC64;
SQL	

Query Match	24.43;	Score 142;	DB 4;	Length 597;
Best Local Similarity	28.7%;	Pred. No. 3.3e-07;		
Matches	29;	Conservative 26;	Mismatches 44;	Indels 2;
Gaps	2;			

RESULT	11
Q9BU10	
ID	Q9BU10 PRELIMINARY;
AC	PRT; 597 AA.
DT	01-JUN-2001 (TRENBLrel. 17, Created)
DT	01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE	01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE	HYPOTHETICAL 65.3 KDA PROTEIN.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea
ON	NCBI_TaxId=9606;
OX	[1]
RN	SEQUENCE FROM N.A.
RC	TISSUE=Lymph, LYMPHOMA;
RA	Strausberg R.;
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ datab
DR	EMBL; BC002963; AA02963.1; -
DR	HSP; F01825; 7/FAB.
DR	InterPro; IPR003599; Iq.

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DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 5.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGcl; 4.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IG_Like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 24.4%; Score 142; DB 4; Length 597;
Best Local Similarity 28.7%; Pred. No. 3.3e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 9 VFLEPPPKDTLMISRPETVCVVVDVSHEDPEVKFKNWYDGVGVHNAKTKPREEQYNST 68
DB 368 VFAIPPS-FASIFTKTKLCLVTDLTYYD-SVTISWTRONGEAVKTHTNISESHPNAT 425
QY 69 YRVYSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAK 109
DB 426 FSAVGEASICDDNWSGERFCTCTVHTDLPFLKQTISRPK 466

RESULT 12
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOHETICAL 65.0 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RW EMBL; BC015760; AAH15760.1; -.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 24.4%; Score 142; DB 4; Length 597;
Best Local Similarity 28.7%; Pred. No. 3.3e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 9 VFLEPPPKDTLMISRPETVCVVVDVSHEDPEVKFKNWYDGVGVHNAKTKPREEQYNST 68
DB 368 VFAIPPS-FASIFTKTKLCLVTDLTYYD-SVTISWTRONGEAVKTHTNISESHPNAT 425
QY 69 YRVYSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAK 109
DB 426 FSAVGEASICDDNWSGERFCTCTVHTDLPFLKQTISRPK 466

RESULT 13
Q96EYO PRELIMINARY; PRT; 613 AA.
AC Q96EYO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR WGC:20337).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;

Db 426 FSAVGEASICEDDWNSEGFCTVTHTDLPSPKQTIISRPK 466

Search completed: June 21, 2002, 08:59:33
Job time: 1632 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:00:25 ; Search time 48.19 Seconds

(without alignments)
87.579 Million cell updates/sec

Title: US-09-674-857-9

Perfect score: 582

Sequence: 1 APPVAGPSVFLPPPKPDL.....CKVSNKALPAPIETISKAK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	559	96.0	326	1 GC2_HUMAN	P01859 homo sapien
2	558	95.9	330	1 GC1_HUMAN	P01857 homo sapien
3	526	90.4	327	1 GC4_HUMAN	P01861 homo sapien
4	519	89.2	290	1 GC3_HUMAN	P01860 homo sapien
5	432	74.2	329	1 GC2_CAVPO	P01862 cavia porce
6	429	73.7	333	1 GCB_RAT	P02061 rattus norv
7	428	73.5	323	1 GC_RABIT	P01870 oryctolagus
8	425.5	73.1	329	1 GC3_MOUSE	P22436 mus musculu
9	425.5	73.1	398	1 GC3M_MOUSE	P03987 mus musculu
10	411	70.6	324	1 GC1_MOUSE	P01868 mus musculu
11	411	70.6	393	1 GC1M_MOUSE	P01869 mus musculu
12	396	68.0	329	1 GCC_RAT	P20762 rattus norv
13	391	67.2	335	1 GCAB_MOUSE	P01864 mus musculu
14	389	66.8	326	1 GC1_RAT	P20759 rattus norv
15	387	66.5	330	1 GCAA_MOUSE	P01863 mus musculu
16	387	66.5	399	1 GCAM_MOUSE	P01865 mus musculu
17	386	66.3	406	1 GCB_MOUSE	P01866 mus musculu
18	386	66.3	435	1 GCBM_MOUSE	P01867 mus musculu
19	354	60.8	322	1 GCAB_MOUSE	P20760 rattus norv
20	164.5	28.3	428	1 EPC_HUMAN	P01854 homo sapien
21	160	27.5	429	1 EPC_RAT	P01855 rattus norv
22	153	26.3	457	1 MUC_SUNMU	P20768 suncus muri
23	144	24.7	421	1 EPC_MOUSE	P06336 mus musculu
24	143	24.6	391	1 MUCB_HUMAN	P04220 homo sapien
25	142	24.4	454	1 MUC_HUMAN	P01871 homo sapien
26	138	23.7	106	1 KAC_HUMAN	P01834 homo sapien
27	136	23.4	454	1 MUC_MESAU	P06337 mesocricetu
28	136	23.4	455	1 MUC_MOUSE	P01872 mus musculu
29	136	23.4	476	1 MUCM_MOUSE	P01873 mus musculu
30	131.5	22.6	299	1 ALC_RABIT	P01879 oryctolagus
31	124	21.3	458	1 ALC_MOUSE	P03988 oryctolagus
32	124	21.3	479	1 MUCM_RABIT	P04221 oryctolagus
33	123.5	21.2	340	1 ALC2_HUMAN	P01877 homo sapien

34	123.5	21.2	353	1 ALC1_GORGO	P20758 gorilla gor
35	123.5	21.2	353	1 ALC1_HUMAN	P01876 homo sapien
36	121.5	20.9	450	1 MUC_CANFA	P01874 canis famill
37	120	20.6	103	1 LAC_CHICK	P20763 gallus gall
38	118.5	20.4	105	1 LAC1_MOUSE	P01843 mus musculu
39	115.5	19.8	105	1 LAC5_MOUSE	P20765 mus spretus
40	115.5	19.8	393	1 HVC3_HETFR	P23086 heterodontu
41	114	19.6	106	1 KAC_MOUSE	P01837 mus musculu
42	113.5	19.5	370	1 HVC1_HETFR	P23084 heterodontu
43	112.5	19.3	344	1 ALC_MOUSE	P01878 mus musculu
44	111.5	19.2	105	1 LAC5_MOUSE	P20764 mus musculu
45	111	19.1	103	1 KAC4_RABIT	P01840 oryctolagus

ALIGNMENTS

RESULT 1	
GC2_HUMAN	
ID GC2_HUMAN	STANDARD; PRT; 326 AA.
AC P01859;	
DT 21-JUL-1986	(Rel. 01, Created)
DT 21-JUL-1986	(Rel. 01, Last sequence update)
DT 16-OCT-2001	(Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.	
GN IGHG2.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE OF 2-326 FROM N.A.	
RX MEDLINE=82197621; PubMed=6804948;	
RA Ellison J.W., Hood L.E.;	
RT "Linkage and sequence homology of two human immunoglobulin gamma	
RT heavy chain constant region genes."	
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).	
RN [2]	
RP SEQUENCE OF 88-115 FROM N.A.	
RC TISSUE=Fetal liver;	
RX MEDLINE=83001943; PubMed=6811139;	
RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;	
RT "Structure of human immunoglobulin gamma genes: implications for	
RT evolution of a gene family."	
RL Cell 29:671-679(1982).	
RN [3]	
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.	
RC TISSUE=Fetal liver;	
RX MEDLINE=84235992; PubMed=6329676;	
RA Krawinkel U., Rabbitts T.H.;	
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma	
RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass	
RT genes."	
RL EMBO J. 1:403-407(1982).	
RN [4]	
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).	
RX MEDLINE=81007873; PubMed=6774012;	
RA Wang A.-C., Tung E., Fudenberg H.H.;	
RT "The primary structure of a human IgG2 heavy chain: genetic,	
RT evolutionary, and functional implications."	
RL J. Immunol. 125:1048-1054(1980).	
RN [5]	
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).	
RX MEDLINE=80001357; PubMed=113060;	
RA Connell G.E., Parr D.M., Hofmann T.;	
RT "The amino acid sequences of the three heavy chain constant region	
RT domains of a human IgG2 myeloma protein."	
RL Can. J. Biochem. 57:758-767(1979).	
RN [6]	
RP SEQUENCE OF 238-275 (ZIE).	
RX MEDLINE=80114419; PubMed=118920;	
RA Hofmann T., Parr D.M.;	
RT "A note of the amino acid sequence of residues 381-391 of human	

immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
[7]
REVIEWS TO 25; 59; 60 AND 264-268 (ZIE).
Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank.
[8]
SEQUENCE OF 1-121 (DOT).
MEDLINE=95255298; PubMed=7737190;
Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
"Characterization of the two unique human anti-flavin monoclonal
immunoglobulins.";
Eur. J. Biochem. 228:886-893(1995).
[9]
DISULFIDE BONDS.
MEDLINE=72033500; PubMed=4940472;
Milstein C., Frangione B.;
"Disulfide bridges of the heavy chain of human immunoglobulin G2.";
Biochem. J. 121:217-225(1971).
[10]
DISULFIDE BONDS.
MEDLINE=69064124; PubMed=5782707;
Frangione B., Milstein C., Pink J.R.L.;
"Structural studies of immunoglobulin G.";
Nature 221:145-148(1969).

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EMBL; J00230; AAB59393.1; -
PIR; A02148; G2HU.
HSP; P01857; 1FC1.
MIM; 147110; -
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003597; Ig_C1.
InterPro: IPR003600; Ig_Like.
Pfam: PF00047; Ig; 3.
SMART; SM00410; Ig_Like; 1.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region.
NON_TER 1 1
DOMAIN 1 98 CH1.
DOMAIN 99 110 HINGE.
DOMAIN 111 219 CH2.
DOMAIN 220 326 CH3.
DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
DISULFID 27 83
DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 140 200
DISULFID 246 304
SITE 156 156
MOD_RES 326 326
VARIANT 60
AT OR NEAR THE COMPLEMENT-BINDING SITE.
REMOVED POST-TRANSLATIONALLY (PROBABLE).
S -> A (IN MYELOMA PROTEINS TIL & ZIE).
/FTid=VAR_003889.
C -> S (IN REF. 3).
CONFLICT 109 109
SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;

Query Match 96.0%; Score 559; DB 1; Length 326;
Best Local Similarity 94.5%; Pred. No. 4e-49; 2; Indels 0; Gaps 0;
Matches 103; Conservative 4; Mismatches 0;
1 APPVAGPSVFLPPPKDITLMSRTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
|||||
111 APPVAGPSVFLPPPKDITLMSRTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 170
|||||
61 REEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKSKAK 109
|||||
171 REEQFNSTFRVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETKSKTK 219
|||||

Db 111 APPVAGPSVFLPPPKDITLMSRTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 170
QY 61 REEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKSKAK 109
Db 171 REEQFNSTFRVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIETKSKTK 219
RESULT 2
GCL_HUMAN
ID GCL_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a
monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
chymotryptic peptides of the H-chain, alignment of the tryptic
peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
IgG1 immunoglobulin (myeloma protein Nie). I: Purification and
characterization of the protein, the L- and H-chains, the
cyanogen bromide cleavage products, and the disulfide bridges.";

RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Delsenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -!- MISCELLANEOUS: NIE HAS THE GLM(17) ALLOTYPIC MARKER, 97-K, & THE
CC GLM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GLM(3)
CC MARKER & THE GLM (NON-1) MARKERS.
CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35,116,198,269 & 272.
CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198,267&272.
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CC -----
DR EMBL; J00228; AAC82527.1; ALT_INIT.
DR PIR; A02146; GHU.
DR PDB; 1FC1; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR MIM; 147100; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; Ig_c1; 2.
DR PROSITE; PS00290; Ig_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98
FT DOMAIN 99 110
FT DOMAIN 111 223
FT DOMAIN 224 330
FT DISULFID 27 83
FT DISULFID 103 103
FT DISULFID 109 109
FT DISULFID 112 112
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 330
FT MOD_RES 330 330
FT VARIANT 97 97
FT VARIANT 239 239
FT VARIANT 241 241
FT STRAND 123 126
FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164
FT STRAND 165 166
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FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
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FT STRAND 215 219
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FT STRAND 230 234
FT HELIX 238 240
FT TURN 241 242
FT STRAND 245 256
FT STRAND 260 268
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 95.9%; Score 558; DB 1; Length 330;
Best Local Similarity 93.0%; Pred No. 5,1e-49;
Matches 106; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
II : |||||
DB 110 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 169

QY 56 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
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DB 170 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223

RESULT 3
GC4_HUMAN
ID GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-4 chain C region.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
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CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; G4HU.
DR HSP; P01842; 7FAB.


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FT VARIANT      227      227      S -> N (IN OMM).
FT VARIANT      227      227      /FTIG-VAR_003894.
FT VARIANT      227      227      MISSING (IN ZUC).
FT VARIANT      279      279      /FTIG-VAR_003895.
FT VARIANT      279      279      F -> Y (IN OMM).
FT VARIANT      279      279      /FTIG-VAR_003896.
FT SEQUENCE     290 AA; 32331 MW; E69CBC95705B2F46 CRC64;

Query Match      89.2%; Score 519; DB 1; Length 290;
Best Local Similarity 89.6%; Pred. No. 3.7e-45;
Matches 95; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKPRPEE 63
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
78 LGGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKPREQ 137

QY 64 QYNSTYRVVSVLTVLDHQLNKGKCKVSNKALPAPIEKTISKAK 109
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
138 QFNSTYRVVSVLTVLDHQLNKGKCKVSNKALPAPIEKTISKTK 183

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the
half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
```

```
RL Biochemistry 10:26-31(1971).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match      74.2%; Score 432; DB 1; Length 329;
Best Local Similarity 73.6%; Pred. No. 2.5e-36;
Matches 81; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

QY 2 PP--VAGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTK 59
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
112 PPENLGSPSVFIIPPKDLMISLTPRVTCVVVDVSDPEVQFTWFDVKNKPVGNAETK 171

QY 60 PREEQNSTYRVVSVLTVDHQLNKGKCKVSNKALPAPIEKTISKAK 109
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
172 PRVEQNTTFRVESVLPVLDHQLNKGKCKVSNKALPAPIEKTISKTK 221

RESULT 6
GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
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FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 73.7%; Score 429; DB 1; Length 333;
Best Local Similarity 70.8%; Pred. No. 5e-36;
Matches 75; Conservative 20; Mismatches 11; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
DB 121 LGGPSVFIPPPKDKILLISQNAKVTCCVVVDSEEDPDVQFSFVNVVEVHTAQTQPRE 180

QY 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
DB 181 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 226

RESULT 7
GC_RABBIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-1 haplotype.";
RL Immunogenetics 18:387-397(1983).
RN [2]
SEQUENCE OF 1-128.
RP MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
SEQUENCE OF 88-266 FROM N.A.
RP MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
SEQUENCE OF 132-161.
RP MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT immunoglobulin G.";
RL Biochem. J. 116:249-259(1970).
RN [5]
SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (In) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC -!- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC MARKERS AND REF.5 THE E15 MARKER.
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DR EMBL; M16426; AAA31289.1; -
DR PIR; A02161; GHRB
DR HSSP; P01857; LFCL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IgC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 73.5%; Score 428; DB 1; Length 323;
Best Local Similarity 71.8%; Pred. No. 6.1e-36;
Matches 79; Conservative 13; Mismatches 16; Indels 2; Gaps 1;

QY 2 PP-VAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
DB 107 PPELLGGPSVFIPLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 166

QY 60 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
DB 167 LREQQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 216

RESULT 8
GC3_MOUSE STANDARD; PRT; 329 AA.
ID P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
-----
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DR	InterPro:	IPR003006;	Ig_MHC.
DR	InterPro:	IPR003597;	Ig_C1.
DR	InterPro:	IPR003600;	Ig_Like.
DR	Pfam:	PF00047;	Ig_3.
DR	SMART:	SM00410;	Ig_Like; 1.
DR	SMART:	SM00407;	IGC1; 2.
DR	KPOSITE:	PS00290;	IG_MHC; 1.
KW	Immunoglobulin domain;	Immunoglobulin C region;	Glycoprotein;
KW	Transmembrane;	Alternative splicing.	
FT	NON_TER	1	1
FT	DOMAIN	1	97
FT	DOMAIN	98	113
FT	DOMAIN	114	223
FT	DOMAIN	224	327
FT	TRANSMEM	346	362
FT	DOMAIN	363	398
FT	CONFLICT	333	333
FT	CONFLICT	342	342
FT	CONFLICT	388	388
FT	SEQUENCE	398 AA;	CF7F264B50A41B95 CRC64;
QY	Query Match	73.1%;	Score 425.5; DB 1; Length 398;
DB	Best Local Similarity	70.3%;	Pred No. 1.4e-35;
DB	Matches	78; Conservative	14; Mismatches 16; Indels 3; Gaps
QY	2 PP----	VAGPSPVFLPPPKDPTLMSRTPEVTCTVVVDVSHEDPYKFNMYDGVVEVHNAKT 58	
DB	112 PPGNILGSPSVFI	PPPKDPMISLPKTCVVVDVSEDDPDVHSVDFVNKEVHTAWT 171	
QY	59 KPREEQNSTYRVVSUTVLHQDWLNKEKYCKVSNKALPAPIEKTTSKAK 109		
DB	172 QPREAQNSTFRVVSALPIQHODWMRGKFKCVNNKALPAPIERTSKPK 222		
RESULT	10		
GCI_MOUSE	ID	GCI_MOUSE	STANDARD; PRT; 324 AA.
AC	P01868;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	30-MAY-2000 (Rel. 39, Last annotation update)		
DE	Ig gamma-1 chain C region.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=80045036; PubMed=115593;		
RA	Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,		
RA	Takahashi N., Mano Y.;		
RT	"cloning and complete nucleotide sequence of mouse immunoglobulin		
RT	gamma 1 chain gene.";		
RL	Cell 18:559-568(1979).		
RL	[2]		
RN	SEQUENCE OF 76-324 FROM N.A. (MVELOMA PROTEIN MOPC 31C).		
RX	MEDLINE=80202559; PubMed=6769752;		
RA	Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,		
RA	Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;		
RT	"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences		
RT	cloned in a bacterial plasmid.";		
RL	Gene 9:87-97(1980).		
RN	[3]		
RN	SEQUENCE OF 70-327 FROM N.A. (MVELOMA PROTEIN MOPC 21).		
RX	MEDLINE=80012837; PubMed=113776;		
RA	Rogers J., Clarke P., Salsner W.;		
RT	"Sequence analysis of cloned cDNA encoding part of an immunoglobulin		
RT	heavy chain.";		
RL	Nucleic Acids Res. 6:3305-3321(1979).		
RN	[4]		
RX	SEQUENCE (78242288); PubMed=98524;		
RX	MEDLINE=78242288; PubMed=98524;		


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FT DISULFID 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138
FT CARBOHYD 174
FT DISULFID 244
FT TRANSMEM 340
FT DOMAIN 358
FT SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;

Query Match 70.6%; Score 411; DB 1; Length 393;
Best Local Similarity 70.6%; Pred. No. 3.9e-34;
Matches 72; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

QY 8 SVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYGVGVEVHNKATKPRREQYNS 67
Db 116 SVFIPEPKPKDVLITLTPKVTCTVVVDISKDDPEVQFSWFVDDVEVHTAQTPREQFNS 175

QY 68 TYRVSVLVTLVHODWLNKREYCKVSNKALPAPIEKTISKAK 109
Db 176 TFRSVSELPIMHODWLNKREYCKRVNSAAPPAPIEKTISKTK 217

RESULT 12
GCC_RAT
ID GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galfrè P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RT region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
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CC -----
DR EMBL; X07189; CAA30169.1;
DR PIR; S00847; S00847.
DR HSP; P01857; IFC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 1 97
FT DOMAIN 98 113
FT DOMAIN 114 222
FT DOMAIN 223 329
FT DISULFID 15 15
FT DISULFID 27 82
FT DISULFID 111 111
FT DISULFID 113 113
FT DISULFID 143 203
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FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 68.0%; Score 396; DB 1; Length 329;
Best Local Similarity 68.0%; Pred. No. 1e-32;
Matches 70; Conservative 18; Mismatches 15; Indels 0; Gaps 0;

QY 7 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYGVGVEVHNKATKPRREQYN 66
Db 120 PSVFIPEPKPKDILMITLTPKVTCTVVVDSEEPDQVQFSWFVDNVRVFTAQTPHEEQLN 179

QY 67 STYRVSVLVTLVHODWLNKREYCKVSNKALPAPIEKTISKAK 109
Db 180 GTFRVSVTLTHIQHODWMSKEFKCKVNNKDLPSPIEKTISKPR 222

RESULT 13
GCAB_MOUSE
ID GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT IgG2a and IgG2b alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain C regions of Igla and Ig1b allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
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CC -----
DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSP; P01857; IFC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 67.2%; Score 391; DB 1; Length 335;
Best Local Similarity 63.2%; Pred. No. 3.4e-32;
Matches 72; Conservative 18; Mismatches 18; Indels 6; Gaps 1;
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QY 2 PPVA-----GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
  |||  |||||:|||||  |||||  |||||:|||||  |||||  |||||  |||||  |||||
Db 115 PPCAAPDLGGPSVFIPPPKIKDVLMSLSPMTVCVVVDVSDDDPDVQISWEVNNVEVHT 174
  |||  |||||:|||||  |||||  |||||:|||||  |||||  |||||  |||||  |||||
QY 56 AKTKPREEQNSRYRVSVLTVLHODWLNKYEKCKVSNKALPAPIETKTSKAK 109
  |||  |||||:|||||  |||||  |||||:|||||  |||||  |||||  |||||  |||||
Db 175 AQTQTHREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNRNPALSPIEKTSKPR 228
  |||  |||||:|||||  |||||  |||||:|||||  |||||  |||||  |||||  |||||
RESULT 14
GCL_RAT
ID GCL_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DOMAIN 1 97
FT CH1.
FT DOMAIN 98 112
FT HINGE.
FT DOMAIN 113 219
FT CH2.
FT DOMAIN 220 326
FT CH3.
FT DISULFID 27 82
FT DISULFID 102 102
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT DISULFID 176 176
FT CARBOHYD N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 66.8%; Score 389; DB 1; Length 326;
Best Local Similarity 68.0%; Pred. No. 5.2e-32;
Matches 68; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

QY 8 SVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQNS 67
  |||  |||||:|||||  |||||  |||||:|||||  |||||  |||||  |||||  |||||
Db 118 SVFIFFPKPKDVLITLTPKVTCTVVVDVSDDDPEVDFSVFVDDVHTAQTRPPPEQFNS 177
  |||  |||||:|||||  |||||  |||||:|||||  |||||  |||||  |||||  |||||
QY 68 TYRVSVSLTVLHODWLNKYEKCKVSNKALPAPIETKTSK 107
  |||  |||||:|||||  |||||  |||||:|||||  |||||  |||||  |||||  |||||
Db 178 TFRSVSELPILHODWLNKTRFKCKVTSAAFPPIETKTSK 217
  |||  |||||:|||||  |||||  |||||:|||||  |||||  |||||  |||||  |||||
RESULT 15
GCAA_MOUSE
ID GCAA_MOUSE STANDARD; PRT; 330 AA.
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-2A chain C region, A allele.

Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Sikorav J.-L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
  Balb/c gamma 2a heavy chain messenger RNA.";
RL Nucleic Acids Res. 8:3143-3155(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
  and evolution of heavy chain genes; further evidence for intervening
  sequence-mediated domain transfer.";
RL Nucleic Acids Res. 9:1365-1381(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=8122394; PubMed=6787604;
RA Ollo R., Auffray C., Morchamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
  suggests that exons can be exchanged between genes in a multigenic
  family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
  immunoglobulin:amino-acid sequence of the FC fragment. Implications
  for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
  immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462(1972).
CC -----
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  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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  -----
DR EMBL; V00798; CAA24178.1; -.
DR PIR; A02152; G2MSA.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG-like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15
FT INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT DISULFID 330 330
FT MOD_RES 330 AA; 36389 MW; B8A361C5445A6864 CRC64;
SQ SEQUENCE 330 AA; 36389 MW; B8A361C5445A6864 CRC64;
  REMOVED POST-TRANSLATIONALLY.
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:37:55 ; Search time 102.05 Seconds
(without alignments)
102.633 Million cell updates/sec

Title: US-09-674-857-9
Perfect score: 582
Sequence: 1 APPVAGSVLFPKPKDTL.....CKVSNKALPAPIEKTISKAK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-71:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	560	96.2	234	2 PT0207	Ig gamma chain C r
2	559	96.0	326	1 G2HU	Ig gamma-2 chain C
3	558	95.9	255	4 S31866	Ig gamma-1 chain C
4	558	95.9	330	1 GHU	Ig gamma-1 chain C
5	558	95.9	374	2 S69339	Ig heavy chain V r
6	539	92.6	377	2 A60764	Ig gamma-3 chain C
7	539	92.6	377	2 A23511	Ig gamma-3 chain C
8	526	90.4	327	1 G4HU	Ig gamma-4 chain C
9	519	89.2	289	1 G3HUWI	Ig gamma-3 heavy c
10	468	80.4	328	2 I47160	Ig gamma-2a chain
11	468	80.4	328	2 I47159	Ig gamma 2a chain
12	463	79.6	277	2 I47162	Ig gamma 4 chain c
13	452	77.7	328	2 I47161	Ig gamma 3 chain c
14	452	77.7	328	2 I47158	Ig gamma 1 chain c
15	434	74.6	470	2 S22080	Ig heavy chain pre
16	432	74.2	329	1 G2GP	Ig gamma-2 chain C
17	429	73.7	333	2 PS0018	Ig gamma-2b chain
18	428	73.5	323	1 GHRB	Ig gamma chain C r
19	425.5	73.1	329	1 G3MSC	Ig gamma-3 chain C
20	425.5	73.1	398	1 G3MSM	Ig gamma-3 chain C
21	425	73.0	308	2 C30554	Ig heavy chain C r
22	425	73.0	472	2 S31459	Ig gamma-1 chain -
23	411	70.6	324	1 G1MS	Ig gamma-1 chain C
24	411	70.6	393	1 G1MSM	Ig gamma-1 chain C
25	411	70.6	444	2 PC4436	monoclonal antibody
26	403	69.2	327	2 S06611	Ig gamma-2 chain C
27	396	68.0	329	2 S00847	Ig gamma-2c chain
28	391	67.2	335	1 G2MSAB	Ig gamma-2a chain
29	389	66.8	326	2 PS0017	Ig gamma-1 chain C

30	387	66.5	330	1 G2MSA	Ig gamma-2a chain
31	387	66.5	399	1 G2MSAM	Ig gamma-2a chain
32	387	66.5	469	2 S37483	Ig gamma-2a chain
33	386	66.3	405	1 G2MSBM	Ig gamma-2b chain
34	386	66.3	474	1 G2MS11	Ig gamma-2b chain
35	378	64.9	475	2 S01321	Ig gamma-2b chain
36	377	64.8	446	2 S40295	Ig gamma-2a chain
37	354	60.8	322	2 PS0019	Ig gamma-2a chain
38	319	54.8	112	2 B30503	Ig gamma-2a chain
39	275	47.3	88	2 A30503	Ig gamma-2b chain
40	264	45.4	180	2 I46732	Ig gamma heavy Cha
41	177	30.4	152	2 S14236	Ig gamma-1 chain C
42	165.5	28.4	426	2 I36948	Ig epsilon-chain -
43	164.5	28.3	428	1 EHHU	Ig epsilon chain C
44	161	27.7	549	2 S04845	Ig heavy chain pre
45	160	27.5	429	1 EHRT	Ig epsilon chain C

ALIGNMENTS

RESULT 1

PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C>Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
A:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 96.2%; Score 560; DB 2; Length 234;
Best Local Similarity 93.9%; Pred. No. 1.9e-49;
Matches 107; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

QY	2	PPVA-----GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
DB	21	PPCAAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 80
QY	56	AKTKPREQYNSTYRVVSVLTVLDHQLAKGKEYCKVSKNKPAPIEKTISKAK 109
DB	81	AKTKPREQYNSTYRVVSVLTVLDHQLAKGKEYCKVSKNKPAPIEKTISKAK 134

RESULT 2
G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C>Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain
A:Reference number: A93906; MUID:82197621
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, an
A:Reference number: A92809; MUID:81007873
A:Contents: myeloma protein Til
A:Accession: A92809

A:Molecule type: protein
A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G
A:Reference number: A93132; MUID:80114419
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation: Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500
A:Contents: annotation: myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124
A:Contents: annotation: Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:1CHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
haIn disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.0%; Score 559; DB 1; Length 326;
Best Local Similarity 94.5%; Pred. No. 3.5e-49;
Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
DB 111 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 170

QY 61 REEQNSTYRVSVLTVLVHQLDNLNGKEYCKVSNKALPAPIETISKAK 109
DB 171 REEQNSTYRVSVLTVLVHQLDNLNGKEYCKVSNKALPAPIETISKAK 219

RESULT 3
S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866

R:Filpula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene produc
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FIL>
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 95.9%; Score 558; DB 4; Length 255;
Best Local Similarity 93.0%; Pred. No. 3.3e-49;
Matches 106; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 55
DB 35 PCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 94

QY 56 AKTKPREQNSTYRVSVLTVLVHQLDNLNGKEYCKVSNKALPAPIETISKAK 109
DB 95 AKTKPREQNSTYRVSVLTVLVHQLDNLNGKEYCKVSNKALPAPIETISKAK 148

RESULT 4
GHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C:Accession: A93433; S36861; S33887; B90563; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: EMBL:Z17370
A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R:Itakashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: Implications for evolution of
A:Reference number: S33887; MUID:83001943
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:Cross-references: EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A:Reference number: A90563; MUID:71064024
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96,'R',98-135 <CUN>
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A:Reference number: A90564; MUID:71064025
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein

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A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match          95.9%; Score 558; DB 2; Length 374;
Best Local Similarity 93.0%; Pred. No. 5.3e-49;
Matches 106; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

QY  2 PP-----VAGPSVFLPPPKDPTLMISRPEVTCVVVDVSHEDPEVKFNNYVDGVEVHN 55
    || : |||||
Db  154 PPCPAPELLGGPSVFLFPPPKDPTLMISRPEVTCVVVDVSHEDPEVKFNNYVDGVEVHN 213
    |||||

QY  56 AKTKPREQNSYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIETKTSKAK 109
    |||||
Db  214 AKTKPREQNSYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIETKTSKAK 267

RESULT 6
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 con
A:Reference number: A60764; MUID:90007613
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain; immunoglobulin homology <IMX>

Query Match          92.6%; Score 539; DB 2; Length 377;
Best Local Similarity 94.3%; Pred. No. 4.5e-47;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY  4 VAGPSVFLFPKPKDPTLMISRPEVTCVVVDVSHEDPEVKFNNYVDGVEVHNKTPREE 63
    : |||||
Db  165 LGGPSVFLFPKPKDPTLMISRPEVTCVVVDVSHEDPEVKFNNYVDGVEVHNKTPREE 224
    |||||

QY  64 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIETKTSKAK 109
    |||||
Db  225 QYNSTFRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKTSK 270
    |||||

RESULT 7
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Port, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:
A:Reference number: A23511; MUID:86148507
A:Accession: A23511
A:Molecule type: DNA

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```
I47162
Ig gamma 4 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47162
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845
A:Accession: I47162
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C:Genetics:
A:Gene: IgG4
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 463; DB 2; Length 277;
Best Local Similarity 79.8%; Pred. No. 1.6e-39;
Matches 83; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 6 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 GPSAFIFPPKPKDMLISRTPKVTCVVVDVSDENPEVQFSWYVDGVEVHTAQRPRKEQF 124
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 66 NSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAK 109
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 125 NSTYRVSVLPIQHODWLNKGEYCKVSNKALPAPIEKTISKAK 168
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
I47161
Ig gamma 3 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47161
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845
A:Accession: I47161
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128
C:Genetics:
A:Gene: IgG3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 77.7%; Score 452; DB 2; Length 328;
Best Local Similarity 79.0%; Pred. No. 2.6e-38;
Matches 83; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 114 VAGPSVFIFPPKPKDMLISQTPVTCVVVDVSKHAHQFSWYVDGVEVHTAETRPKEE 173
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 64 QNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAK 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 174 QFNSTYRVSVLPIQHODWLNKGEYCKVSNKALPAPIEKTISKAK 218
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
I47158
Ig gamma 1 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47158
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```
I47160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A:Reference number: I47158; MUID:95015845
A:Accession: I47160
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C:Genetics:
A:Gene: IgG2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 468; DB 2; Length 328;
Best Local Similarity 80.8%; Pred. No. 6.3e-40;
Matches 84; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 6 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 116 GPSVFIFPPKPKDMLISRTPTQVTCVVVDVSDENPEVQFSWYVDGVEVHTAQRPRKEQF 175
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 66 NSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAK 109
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 176 NSTYRVSVLPIQHODWLNKGEYCKVSNKALPAPIEKTISKAK 219
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RESULT 11
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A:Reference number: I47158; MUID:95015845
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C:Genetics:
A:Gene: IgG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 468; DB 2; Length 328;
Best Local Similarity 80.8%; Pred. No. 6.3e-40;
Matches 84; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 6 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 65
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Db 116 GPSVFIFPPKPKDMLISRTPTQVTCVVVDVSDENPEVQFSWYVDGVEVHTAQRPRKEQF 175
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 66 NSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAK 109
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 176 NSTYRVSVLPIQHODWLNKGEYCKVSNKALPAPIEKTISKAK 219
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RESULT 12
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R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: 147158; MUID:95015845
A:Accession: 147158
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
C:Genetics:
A:Gene: IgG1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Search completed: June 21, 2002, 08:37:55
Job time: 429 sec

Query Match 77.7%; Score 452; DB 2; Length 328;
Best Local Similarity 79.0%; Pred. No. 2.6e-38;
Matches 83; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

Qy 4 VAGPSVFLPPPKDMLMSRTPVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63

Db 114 VAGPSVFIFPPKPKDTLMISPTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 173

Qy 64 QYNSTYRVSVLTVTLQHDWLNGLKPKCKVSKNKPAPLPIETSKA 108

Db 174 QFNSTYRVSVLTPIQHDWLNGLKPKCKVSKNKPAPLPIETSKA 218

RESULT 15

S22080
Ig heavy chain precursor (B/Mt.4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S22080; S06610; A31303
R:Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22080
A:Accession: S22080
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-470 <SAN>
A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2
A:Reference number: S06610; MUID:90097956
A:Accession: S06610
A:Molecule type: DNA
A:Residues: 142-470 <SYM>
A:Cross-references: EMBL:X16701
A>Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: Ig CH gamma-1
A:Introns: 98/1; 111/1; 221/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IMM>
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 74.6%; Score 434; DB 2; Length 470;
Best Local Similarity 72.7%; Pred. No. 2.7e-36;
Matches 80; Conservative 11; Mismatches 17; Indels 2; Gaps 1;

Qy 2 PP--VAGPSVFLPPPKDMLMSRTPVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59

Db 252 PPELPGGSPSVFIFPPKPKDTLMISPTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 311

Qy 60 PREQYNSTYRVSVLTVTLQHDWLNGLKPKCKVSKNKPAPLPIETSKA 109

Db 312 PREQYNSTYRVSVLTPIQHDWLNGLKPKCKVSKNKPAPLPIETSKA 361

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:32:16 ; Search time 77.71 Seconds
(without alignments)
34.575 Million cell updates/sec

Title: US-09-674-857-8
Perfect score: 585
Sequence: 1 APELLGSPSVFLPPPKDPT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2.6/ptodata/2/1aa/5A_COMB.pep: *
2: /cgn2.6/ptodata/2/1aa/5B_COMB.pep: *
3: /cgn2.6/ptodata/2/1aa/6A_COMB.pep: *
4: /cgn2.6/ptodata/2/1aa/6B_COMB.pep: *
5: /cgn2.6/ptodata/2/1aa/PTCUS_COMB.pep: *
6: /cgn2.6/ptodata/2/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	98.5	468	4	US-09-485-737B-67 Sequence 67, Appl
2	576	98.5	711	4	US-09-485-737B-90 Sequence 90, Appl
3	571	97.6	110	3	US-08-444-644-21 Sequence 21, Appl
4	571	97.6	110	4	US-08-232-246A-21 Sequence 21, Appl
5	571	97.6	116	2	US-08-232-539D-55 Sequence 55, Appl
6	571	97.6	212	1	US-08-430-633-4 Sequence 4, Appl
7	571	97.6	212	2	US-08-620-694A-4 Sequence 4, Appl
8	571	97.6	212	3	US-08-936-854-4 Sequence 4, Appl
9	571	97.6	212	2	US-09-022-255-4 Sequence 4, Appl
10	571	97.6	212	3	US-09-022-696-4 Sequence 4, Appl
11	571	97.6	212	3	US-09-022-253-4 Sequence 4, Appl
12	571	97.6	212	3	US-09-022-260-4 Sequence 4, Appl
13	571	97.6	212	4	US-09-022-259-4 Sequence 4, Appl
14	571	97.6	212	4	US-09-022-257-4 Sequence 4, Appl
15	571	97.6	232	2	US-08-595-043A-50 Sequence 50, Appl
16	571	97.6	235	4	US-09-131-247-6 Sequence 6, Appl
17	571	97.6	254	2	US-08-284-391B-33 Sequence 33, Appl
18	571	97.6	254	4	US-09-218-950-33 Sequence 33, Appl
19	571	97.6	316	4	US-09-178-869-4 Sequence 4, Appl
20	571	97.6	331	4	US-09-178-869-2 Sequence 2, Appl
21	571	97.6	347	1	US-07-940-861-43 Sequence 43, Appl
22	571	97.6	347	1	US-08-459-512-43 Sequence 43, Appl
23	571	97.6	347	2	US-08-459-657-43 Sequence 43, Appl
24	571	97.6	347	2	US-08-460-132-43 Sequence 43, Appl
25	571	97.6	347	4	US-08-466-465-8 Sequence 8, Appl
26	571	97.6	347	5	PCT-US92-02050-43 Sequence 43, Appl
27	571	97.6	360	4	US-09-180-100-11 Sequence 11, Appl

28	571	97.6	371	1	US-08-236-311-7	Sequence 7, Appl
29	571	97.6	371	3	US-08-457-918-7	Sequence 7, Appl
30	571	97.6	376	4	US-09-180-100-22	Sequence 22, Appl
31	571	97.6	387	1	US-08-470-299-4	Sequence 4, Appl
32	571	97.6	388	4	US-09-131-247-16	Sequence 16, Appl
33	571	97.6	389	4	US-09-131-247-14	Sequence 14, Appl
34	571	97.6	396	2	US-08-784-1043-3	Sequence 3, Appl
35	571	97.6	396	4	US-09-176-228-3	Sequence 3, Appl
36	571	97.6	424	4	US-09-333-593A-8	Sequence 8, Appl
37	571	97.6	424	5	PCT-US95-03866-12	Sequence 12, Appl
38	571	97.6	424	5	PCT-US95-03866-14	Sequence 14, Appl
39	571	97.6	437	5	PCT-US96-10043-11	Sequence 11, Appl
40	571	97.6	442	5	PCT-US96-10043-9	Sequence 9, Appl
41	571	97.6	446	3	US-08-397-411-7	Sequence 7, Appl
42	571	97.6	449	1	US-08-458-516-13	Sequence 13, Appl
43	571	97.6	449	3	US-08-897-236-23	Sequence 23, Appl
44	571	97.6	449	4	US-09-679-397-2	Sequence 2, Appl
45	571	97.6	451	2	US-08-887-352B-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-485-737B-67
; Sequence 67, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-67

Query Match 98.5%; Score 576; DB 4; Length 468;
Best Local Similarity 98.2%; Pred. No. 6.6e-61;
Matches 108; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 APELLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 251 APELLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 310
QY 61 PREEQYNSTRYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTISKAK 110
Db 311 PREEQYNSTRYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTISKAK 360

RESULT 2
US-09-485-737B-90
; Sequence 90, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,

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; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

Query Match          98.5%; Score 576; DB 4; Length 711;
Best Local Similarity 98.2%; Pred. No. 1.2e-60;
Matches 108; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APELLGPGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Db 251 APELLGPGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   |||||
QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110
   |||||
Db 311 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTTISKAK 360
   |||||

RESULT 3
US-08-444-644-21
; Sequence 21, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
```

```
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-444-644-21

Query Match          97.6%; Score 571; DB 3; Length 110;
Best Local Similarity 97.3%; Pred. No. 3.8e-61;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGPGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   |||||
Db 1 APELLGPGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
   |||||
QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAK 110
   |||||
Db 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTTISKAK 110
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RESULT 4
US-08-232-246A-21
; Sequence 21, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
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; LEN3TH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-21

Query Match 97.6%; Score 571; DB 4; Length 110;
Best Local Similarity 97.3%; Pred. No. 3.8e-61;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Db 1 APELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110
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Db 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETTSKAK 110
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RESULT 5

US-08-232-539D-55
; Sequence 55, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:

; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-232-539D-55

Query Match 97.6%; Score 571; DB 2; Length 116;
Best Local Similarity 97.3%; Pred. No. 4e-61;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Db 6 APELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 65
QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110
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Db 66 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETTSKAK 115
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RESULT 6

US-08-430-633-4
; Sequence 4, Application US/08430633
; Patent No. 5726286
; GENERAL INFORMATION:

; APPLICANT: ALDERSON, MARK
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: COHEN, JEFFREY
; APPLICANT: COMEAU, MICHAEL
; APPLICANT: FARRAH, THERESA
; APPLICANT: SPRIGGS, MELANIE
; TITLE OF INVENTION: Isolated Epstein-Barr Virus BzLF2 Proteins
; TITLE OF INVENTION: That Bind MHC Class II Beta Chains
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,633
; FILING DATE: 28-APR-1995
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/235,397
; FILING DATE: 04/28/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2612
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: IgG1 FC
US-08-430-633-4

Query Match 97.6%; Score 571; DB 1; Length 212;
Best Local Similarity 97.3%; Pred. No. 9.1e-61;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|||||
Db 14 APELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
|||||

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110
|||||
Db 74 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETTSKAK 123
|||||

```

RESULT 7
US-08-620-694A-4
; Sequence 4, Application US/08G20694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: NO. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US98 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US98 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: 1961 FC
US-08-620-694A-4

Query Match 97.6%; Score 571; DB 2; Length 212;
Best Local Similarity 97.3%; Pred. No. 9.1e-61;
Matches 107; Conservative 1; Mismatches 2; Indels 0

QY 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNA
|||||
Db 14 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNA
|||||
QY 61 PREEQYNSTYRNVSVLTVLHODWLNGKEYCKVSNKGLPSPSIKTKAK 110
|||||
Db 74 PREEQYNSTYRNVSVLTVLHODWLNGKEYCKVSNKALPAPIKTKAK 123
|||||

RESULT 8
US-08-936-854-4
; Sequence 4, Application US/08936854
; Patent No. 5925734
; GENERAL INFORMATION:

```

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating S
 SOFTWARE: Microsoft Word for Apple,
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/022,255
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/620,694
 FILING DATE: 21 MARCH 1996
 APPLICATION NUMBER: USSN 08/538,765
 FILING DATE: 7 AUGUST 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/410,535
 FILING DATE: 23 MARCH 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,695
 REFERENCE/DOCKET NUMBER: 2617-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 212 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Human
 IMMEDIATE SOURCE:
 CLONE: IgG1 FC
 US-09-022-255-4

```

Query Match      97.6%; Score 571; DB 3; Length 212;
Best Local Similarity 97.3%; Pred. No. 9,1e-61;
Matches 107; Conservative 1; Mismatches 2; Indels

Qy      1  APELLGGPSVFLPPKPKDLMISRTPEVTCVVVDVSDHEDPEVKFNWYVDGVEVRH
      |||
      |||
      |||
Db      14  APELLGGPSVFLPPKPKDLMISRTPEVTCVVVDVSDHEDPEVKFNWYVDGVEVRH
      |||
      |||
      |||

Qy      61  PREQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKSAK 110
      |||
      |||
      |||
Db      74  PREQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKSAK 123
      |||
      |||
      |||

```

```

RESULT 10
US-09-022-696-4
; Sequence 4, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: yao, zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
;

```

```

> COUNTRY: USA
> ZIP: 98101
> COMPUTER READABLE FORM:
> MEDIUM TYPE: Floppy disk
> COMPUTER: Apple Power Macintosh
> OPERATING SYSTEM: Apple Operating System 7.5.5
> SOFTWARE: Microsoft Word for Apple, Version 6.0.1
> CURRENT APPLICATION DATA:
> APPLICATION NUMBER: US/09/022,696
> FILING DATE:
> CLASSIFICATION:
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: 08/620,694
> FILING DATE:
> CLASSIFICATION:
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: USN 08/410,535
> FILING DATE: 23 MARCH 1995
> CLASSIFICATION:
> ATTORNEY/AGENT INFORMATION:
> NAME: Perkins, Patricia Anne
> REGISTRATION NUMBER: 34,695
> REFERENCE/DOCKET NUMBER: 2617-B
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: (206)587-0430
> TELEFAX: (206)
> INFORMATION FOR SEQ ID NO: 4:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 212 amino acids
> TYPE: amino acid
> STRANDEDNESS: not relevant
> TOPOLOGY: linear
> MOLECULE TYPE: protein
> ORIGINAL SOURCE:
> ORGANISM: Human
> IMMEDIATE SOURCE:
> CLONE: IgG1 Fc
>
US-09-022-696--4
>
Query Match 97.6%; Score 571; DB 3; Length 212;
Best Local Similarity 97.3%; Pred. No. 9.1e-61;
Matches 107; Conservative 1; Mismatches 2; Indels

Qy 1 APELLGGPSVFLPPKPKDTLMTSRTEVTCVVVDVSHEDPEVKFNWYVDGVEVH
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 14 APELLGGPSVFLPPKPKDTLMTSRTEVTCVVVDVSHEDPEVKFNWYVDGVEVH
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPAPIEKTIKAK 123
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
US-09-022-253--4
> Sequence 4, Application US/09022253
> Patent No. 6096305
> GENERAL INFORMATION:
> APPLICANT: Iao, zhengbin
> APPLICANT: Spriggs, Melanie
> APPLICANT: Fanslow, William
> TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
> NUMBER OF SEQUENCES: 10
> CORRESPONDENCE ADDRESS:
> ADDRESSEE: Immunex Corporation
> STREET: 51 University Street
> CITY: Seattle
> STATE: WA
> COUNTRY: USA
> ZIP: 98101
> COMPUTER READABLE FORM:
> MEDIUM TYPE: Floppy disk
> COMPUTER: Apple Power Macintosh

```

```

RESULT 11
US-09-022-253-4
; Sequence 4, Application us/09022253
; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh

```


Query Match 97.6%; Score 571; DB 2; Length 232;
 Best Local Similarity 97.3%; Pred. No. 1e-60;
 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNWYDVGVEVHNAKTK	60
Db	16	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNWYDVGVEVHNAKTK	75
QY	61	PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK	110
Db	76	PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK	125

Search completed: June 21, 2002, 08:32:16
 Job time: 90 sec

Result No.	Score	Query Match	Length	DB	ID	Description
1	576	98.5	468	20	AAW85689	D9D10 heavy chain
2	576	98.5	711	20	AAW85692	MOTAbII fusion pro
3	571	97.6	110	13	AAW37680	Human immunoglobul
4	571	97.6	110	14	AAW41684	Undefined ORF2 enc
5	571	97.6	116	20	AAW42621	Human IgG1 Fc gamma
6	571	97.6	212	16	AAW87023	Immunoglobulin G1
7	571	97.6	212	17	AAW37264	Human immunoglobul
8	571	97.6	212	17	AAW02305	Human IgG1 Fc regi
9	571	97.6	212	19	AAW47354	Human immunoglobul
10	571	97.6	212	20	AAW23637	IgG1 Fc protein us
11	571	97.6	212	20	AAW92411	Human IgG1 Fc prot

```
PF 14-AUG-1998; 98WO-EP05165.
XX
PR 18-JUN-1998; 98EP-0870139.
PR 18-AUG-1997; 97EP-0870122.
XX
PA (INNO-) INNOGENETICS NV.
XX
XX Buyse M, Sablon E;
XX
DR WPI; 1999-180969/15.
DR N-PSDB; AAX08631.
XX
XX New engineered antibodies which bind and neutralise interferon-gamma
PT - useful for prevention and treatment of septic shock, cachexia,
PT immune diseases and skin disorders
XX
PS Disclosure; Fig 9; 134pp; English.
XX
XX New antibodies which bind and neutralise interferon-gamma (IFN
CC gamma) can be used as a medicant, for preventing or treating
CC septic shock, cachexia, immune diseases including multiple sclerosis
CC and Crohn's disease and skin disorders including bullous,
CC inflammatory and neoplastic dermatoses. The antibody is selected
CC from a single chain antibody (scFv), a chimeric antibody or diabody
CC comprising the humanised variable domain of the monoclonal mouse
CC anti-IFN gamma antibody D9D10; a multivalent antibody; or a ruminant
CC gamma levels in a sample. Two fusion cDNA genes encoding heavy and
CC light chain fusion proteins of the humanised D9D10 antibody were
CC constructed. The light chain comprised cDNA encoding the mouse D9D10
CC leader sequence, the humanised D9D10 light chain and a human
CC immunoglobulin kappa light chain constant region. The heavy chain
CC comprised cDNA encoding the mouse D9D10 light chain leader sequence
CC followed by the humanised D9D10 heavy chain variable domain and a
CC human IgG1 heavy chain constant domain in which the C1q-complement
CC binding site had been mutated. Four overlapping synthetic
CC oligonucleotides (AAX08585-88) were used to construct the D9D10 light
CC chain leader sequence. This was then subsequently amplified using two
CC primers (AAX08589, AAX08590) to generate PCR-V fragment. The humanised
CC heavy chain variable domain was amplified from pGEM-T-Vhh using two
CC primers (AAX08591, AAX08592) to generate PCR-VI fragment. The two
CC fragments had a base pair overlap and were fused together using
CC primers (AAX08593, AAX08594) and then cloned into pGEM-T to give
CC pGEMldrVhh. The human heavy chain constant domain was amplified
CC with two primers (AAX08595, AAX08596) and cloned into pGEM-T to give
CC pGEM-T-Ch. Two separate PCR amplifications were then performed
CC using pGEM-T-Ch as a template. The primers used were AAX08598, AAX08599
CC to generate PCR-VIII fragment and AAX08597, AAX08600 to generate PCR-IX
CC fragment. These were then overlapped and fused using primers AAX08599,
CC AAX08600 and the resulting PCR-X fragment inserted into pGEMldrVhh to
CC generate the complete heavy chain fusion DNA in a vector designated
CC pGEMHd9D10H. For a description of the construction of the light chain
CC fusion cDNA see GENESeq records AAX08573-X08584.
XX
XX Sequence 468 AA;
XX
Query Match 98.5%; Score 576; DB 20; Length 468;
Best Local Similarity 98.2%; Pred. No. 4.4e-52;
Matches 108; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 APELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 251 apellggpsvflfpkpkdtlmisrptevtcvvvdvshedpevkfnwvydvgevhnaatk 310
QY 61 PREEOYNSTRYVSVLTVLHDLWLNKEYKCKVSNKGLPSSIEKTIKAK 110
DB 311 preeynstryrsvsvltvlhqdwlngkeykckvsnkalpasiektiskak 360
RESULT 2
AAX085692
ID AAW85692 #standard; Protein; 711 AA.
```

```
XX
AC AAW85692;
XX
DT 12-AUG-1999 (first entry)
XX
DE MoTabII fusion protein.
XX
XX Antibody; humanised; variable region; heavy chain; light chain;
KW interferon gamma; IFN; treatment; prevention; septic shock; cachexia;
KW immune disease; multiple sclerosis; Crohn's disease; skin
KW disorders; inflammation; neoplasia; dermatitis; monoclonal
KW antibody; diabody; scFv; multivalent; ruminant.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH FT Peptide 1..20
FT FT Domain /label= Mouse_D9D10_light_chain_signal_peptide
FT FT 21..137 /note= "Humanised heavy chain variable domain of
FT D9D10"
FT Domain 138..467
FT /note= "Human IgG1 heavy chain constant domain"
FT Misc-difference 458
FT /note= "Leu added by cloning strategy"
FT Region 459..472
FT /label= Gly(3)Ser_linker
FT Domain 473..711
FT /label= Humanised_D9D10_ScFv
XX
XX WO9909055-A2.
PN
XX
XX 25-FEB-1999.
XX
XX 14-AUG-1998; 98WO-EP05165.
XX
XX 18-JUN-1998; 98EP-0870139.
XX 18-AUG-1997; 97EP-0870122.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Buyse M, Sablon E;
XX
XX WPI; 1999-180969/15.
XX N-PSDB; AAW85692.
XX
XX New engineered antibodies which bind and neutralise interferon-gamma
PT - useful for prevention and treatment of septic shock, cachexia,
PT immune diseases and skin disorders
XX
XX Disclosure; Fig 20; 134pp; English.
XX
XX New antibodies which bind and neutralise interferon-gamma (IFN
CC gamma) can be used as a medicant, for preventing or treating
CC septic shock, cachexia, immune diseases including multiple sclerosis
CC and Crohn's disease and skin disorders including bullous,
CC inflammatory and neoplastic dermatoses. The antibody is selected
CC from a single chain antibody (scFv), a chimeric antibody or diabody
CC comprising the humanised variable domain of the monoclonal mouse
CC anti-IFN gamma antibody D9D10; a multivalent antibody; or a ruminant
CC gamma levels in a sample.
XX
XX Sequence 711 AA;
XX
Query Match 98.5%; Score 576; DB 20; Length 711;
Best Local Similarity 98.2%; Pred. No. 7.4e-52;
Matches 108; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 APELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 251 apellggpsvflfpkpkdtlmisrptevtcvvvdvshedpevkfnwvydvgevhnaatk 310
```

QY 61 PREEQNSTYRVVSVTLVHLDWLNCKEYKCKVSNKGLPSSIEKTISKAK 110
 |||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 311 preeqynstyrsvvsvtlvhqdwlngkeyckvsnkalpasiektiskak 360

RESULT 3
 AAR27680
 ID AAR27680 standard; Protein; 110 AA.
 XX
 AC AAR27680;
 XX
 DT 10-MAR-1993 (first entry)
 XX
 DE Human immunoglobulin IgG1 CH2 region.
 XX
 KW Isoallotype; IgG1 G1m(1,2,17); anti-allotype response;
 KW humanised Ab.
 XX
 OS Homo sapiens.
 XX
 PN WO9216562-A.
 PD 01-OCT-1992.
 XX
 PF 12-MAR-1992; 92WO-CB00445.
 XX
 PR 12-MAR-1991; 91GB-0005245.
 XX
 PA (LYNX-) LYNXVALE LTD.
 XX
 PI Clark MR;
 DR WPI; 1992-349162/42.
 XX
 PT Humanised antibodies having modified allotypic determinant -
 PT useful for matching allotypes in therapy with decreased
 PT likelihood of causing undesirable immune responses
 XX
 PS Disclosure; Fig 4c; 57pp; English.
 XX
 CC In humans, IgG1 may exist as either of two allotypes at site 1, 2
 CC or 17. The inventor's propose eliminating these allotypes by
 CC amino acid changes to agree with the sequences of IgG2, IgG3 and
 CC IgG4. None of the allotype sites (1, 2 and 17) are located within
 CC the CH2 domain. New "isoallotypes" should be suitable for therapeutic
 CC use in all patients. See AAR27678-R27681.
 XX
 SQ Sequence 110 AA;

Query Match 97.6%; Score 571; DB 13; Length 110;
 Best Local Similarity 97.3%; Pred. No. 2.5e-52;
 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPPPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 apellgppsflfppkpkdtlmisrtpetvcvvdvshedpevkfnwydgvghnaktk 60

QY 61 PREEQNSTYRVVSVTLVHLDWLNCKEYKCKVSNKGLPSSIEKTISKAK 110
 |||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 preeqynstyrsvvsvtlvhqdwlngkeyckvsnkalpasiektiskak 110

RESULT 4
 AAR41684
 ID AAR41684 standard; Protein; 110 AA.
 XX
 AC AAR41684;
 XX
 DT 20-OCT-1993 (first entry)
 XX
 DE Undefined ORF2 encoded by PAH4602.

XX Polymerase chain reaction; primer; PCR; amplify; murine; heavy;
 KW light; chain; variable; constant; region; anti-human; transferrin;
 KW receptor; antibody; brain; capillary; endothelial cell; conjugate;
 KW neuropharmacological; diagnostic; agent; tumour; AIDS; stroke;
 KW epilepsy; Parkinsons disease; Alzheimers disease.
 XX
 OS Synthetic.
 XX
 PN WO9310819-A.
 PD 10-JUN-1993.
 XX
 PF 24-NOV-1992; 92WO-US10206.
 XX
 PR 26-NOV-1991; 91US-0800458.
 XX
 PA (ALKE-) ALKERMES INC.
 XX
 PI Friden PM;
 XX
 DR WPI; 1993-196742/24.
 DR N-PSDB; AAQ43844.
 XX
 PT Antibody conjugates specific for transferrin receptor - used
 PT for diagnosis and treatment of cancer, AIDS and neurological
 PT disorders
 XX
 PS Disclosure; Fig 11K; 151pp; English.
 XX
 CC The sequences given in AAR41682-85 are encoded by the expression vector,
 CC PAH4602. This vector contains open reading frames encoding the heavy
 CC chain variable region (VH) of the antibody 128.1, an ampicillin
 CC resistance gene and a histidine (histidinol) selection marker.
 CC Transcription of the VH gene is from the VH promoter of the murine
 CC 27.44 gene. The vector also includes a heavy chain immunoglobulin
 CC enhancer and the human gamma1 constant region (CH). The VH region of
 CC 128.1 was isolated by polymerase chain reaction and cloned into plasmid
 CC PAH4274. This was achieved by digesting the plasmid and the product
 CC with EcoRV and NheI. The VH gene was inserted in-frame with the human
 CC gamma1 CH region CH at the 3' end of the VH-J region by means of a NheI
 CC site. 128.1 is an anti-human transferrin receptor antibody which binds
 CC to the transferrin receptor on brain capillary endothelial cells. This
 CC antibody may be used in a conjugate in which it is linked to a neuro-
 CC pharmaceutical or diagnostic agent. The conjugate may be used to treat
 CC or prevent neurological disorders eg. brain tumours, AIDS, stroke,
 CC epilepsy, Parkinsons and Alzheimers disease. It may also be used for
 CC diagnostic methods.
 XX
 SQ Sequence 110 AA;

Query Match 97.6%; Score 571; DB 14; Length 110;
 Best Local Similarity 97.3%; Pred. No. 2.5e-52;
 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPPPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTK 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 apellgppsflfppkpkdtlmisrtpetvcvvdvshedpevkfnwydgvghnaktk 60

QY 61 PREEQNSTYRVVSVTLVHLDWLNCKEYKCKVSNKGLPSSIEKTISKAK 110
 |||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 preeqynstyrsvvsvtlvhqdwlngkeyckvsnkalpasiektiskak 110

RESULT 5
 AAY42621
 ID AAY42621 standard; protein; 116 AA.
 XX
 AC AAY42621;
 XX
 DT 10-JAN-2000 (first entry)
 XX

```

DE  Human IgG1 Fc gamma2 region.
XX
KW  Immunoglobulin E; IgE; antagonist; Fc epsilon RI receptor; human; bds;
KW  receptor-binding; binding determinant sequence; anti-IgE antibody;
KW  allergic disease.
XX
XX  Homo sapiens.
OS
XX
PN  US5965709-A.
XX
XX  US5965709-A.
XX
PD  12-OCT-1999.
XX
XX  21-APR-1994; 94US-0232539.
XX
XX  14-AUG-1991; 91US-0744768.
PR
XX  07-JAN-1994; 94US-0178583.
XX
XX  (GETH ) GENENTECH INC.
PA
XX  Jardieu PM, Presta LG;
PI
XX  WPI; 1999-579941/49.
XX
XX  Immunoglobulin E variants as peptide antagonists useful for raising and
PT  screening anti-immunoglobulin E (IgE) antibodies, in the isolation and
PT  purification of Fc epsilon RI receptor and in the treatment of allergic
PT  diseases -
XX
PS  Example 2; Column 61-62; 37pp; English.
XX
XX  The invention provides immunoglobulin E (IgE) antagonists comprising one
CC  or more of the Fc epsilon RI receptor-binding determinant sites of human
CC  IgE. The antagonists include IgE variants comprising an immunoglobulin
CC  template and binding determinant sequences (bds) Cbds, EFbds and the
CC  sequence shown in AA42581. The Cbds (CD loop binding determinant
CC  sequence) are selected from the sequences shown in AA42587-442577 and
CC  the EFbds (EF loop binding determinant sequence) are selected from
CC  sequences shown in AA42578-442580. The variants are useful in raising
CC  and screening anti-IgE antibodies, in the isolation and purification of
CC  Fc epsilon RI receptor and in the treatment and prophylaxis of allergic
CC  diseases.
XX
XX  Sequence 116 AA;
SQ
Query Match 97.6%; Score 571; DB 20; Length 116;
Best Local Similarity 97.3%; Pred. No. 2.7e-52;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 APELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 6 apellggpsvflfppkpkdtlmisrtpvctcvvvdvshedpevkfnwvydgvvhnakt 65
QY 61 PREEQYNSTYRVVSVLTVTLQDWLNCKEYKCKVSNKGLPSSIEKTIKAK 110
DB 66 preeqynstyrvvsvltvhlqdwlngkeykckvsknalpapiektiskak 115
RESULT 6
AAR87023
ID AAR87023 standard; protein; 212 AA.
XX
AC AAR87023;
XX
XX 11-JUN-1996 (first entry)
XX
XX Immunoglobulin G1 Fc region.
XX
KW BZLF2; Epstein-Barr virus; EBV; C-type lectin; beta chain; MHC; antigen;
KW major histocompatibility complex; immunoglobulin; cytotoxic T cell;
KW autoimmune disease; myasthenia gravis; multiple sclerosis; allergy;
KW systemic lupus erythematosus; organ transplant rejection; asthma; IL-7;
KW tissue transplant rejection; therapy; cancer; viral disease; mouse;

```

```

KW  interleukin-7.
XX
XX  Homo sapiens.
XX
PN  WO9530015-A2.
XX
XX  09-NOV-1995.
XX
XX  28-APR-1995; 95WO-US05348.
PF
XX  28-APR-1994; 94US-0235397.
PR
XX  (IMV ) IMMUNEX CORP.
XX  (UMOR ) UNIV MISSOURI.
PA  (USSH ) US NAT INST OF HEALTH.
XX
XX  Alderson M, Armitage RJ, Cohen JI, Comeau MR, Farrah TM;
PI  Hutt-fletcher LM, Spriggs MK;
PI  WPI; 1995-393086/50.
XX
XX  Epstein-Barr virus BZLF2 fusion proteins - used for treating e.g.
PT  auto-immune disease, transplant rejection, allergy, asthma, cancer
PT  or viral infection.
XX
PS  Example 1; Page 38-39; 51pp; English.
XX
XX  This sequence represents the human immunoglobulin G1 Fc region, and was
CC  used in creating a BZLF2-immunoglobulin Fc fusion protein (BZLF2/FC).
CC  BZLF2 is a Epstein-Barr virus (EBV) protein. To create BZLF2/FC, this
CC  sequence, the leader sequence of mouse interleukin-7 (IL-7) (see
CC  AAR87021), a flag octapeptide (see AAR87022) and a flexible linker (see
CC  AAR87024) are joined to the extracellular domain (residues 34 to 223) of
CC  the BZLF2 sequence (see AAR87020). The BZLF2/FC fusion protein
CC  containing this sequence is referred to in claim 4. BZLF2 proteins are
CC  members of the C-type lectin family. The C-type lectin domain is found
CC  in type II membrane proteins. The BZLF2 protein is capable of binding
CC  the beta chain of a major histocompatibility complex (MHC) class II
CC  antigen. Fusion proteins with an oligomerising zipper domain (OZD),
CC  instead of an immunoglobulin Fc region, can also be created. BZLF2
CC  proteins inhibit antigen-specific antibody formation, proliferation of
CC  blood mononuclear cells and cytotoxic T cell responses. They also
CC  exhibit superantigen-like activity. The proteins can be used for
CC  treating or preventing autoimmune diseases such as myasthenia gravis,
CC  multiple sclerosis and systemic lupus erythematosus. Also, for treating
CC  organ or tissue transplant rejection and for treating or preventing
CC  allergy or asthma. They can be used for treating cancer and viral
CC  disease, especially EBV infection.
XX
XX  Sequence 212 AA;
SQ
Query Match 97.6%; Score 571; DB 16; Length 212;
Best Local Similarity 97.3%; Pred. No. 5.6e-52;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 APELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 14 apellggpsvflfppkpkdtlmisrtpvctcvvvdvshedpevkfnwvydgvvhnakt 73
QY 61 PREEQYNSTYRVVSVLTVTLQDWLNCKEYKCKVSNKGLPSSIEKTIKAK 110
DB 74 preeqynstyrvvsvltvhlqdwlngkeykckvsknalpapiektiskak 123
RESULT 7
AAR97264
ID AAR97264 standard; protein; 212 AA.
XX
AC AAR97264;
XX
XX 14-FEB-1997 (first entry)
XX

```

DE Human immunoglobulin G1 Fc region.
 XX
 KW HVS14; major histocompatibility complex; MHC; Class II; allergy;
 KW binding protein; inhibition; antigen presentation; superantigen;
 KW treatment; cancer; viral disease; immunoglobulin; IgG1; Fc region;
 KW fusion protein.
 XX
 OS Homo sapiens.
 XX
 PN WO9617939-A1.
 XX
 XX 13-JUN-1996.
 XX
 XX 07-DEC-1995; 95WO-US15948.
 XX
 XX 06-JUN-1995; 95US-0485549.
 XX
 XX 07-DEC-1994; 94US-0351901.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX
 XX Alderson M, Armitage R, Spriggs M, Yao Z;
 XX
 XX WPI; 1996-287183/29.
 XX
 XX Isolated Herpes virus Saimiri 14 proteins - useful for treating
 PT autoimmune disorders, transplant rejection, allergy, asthma, cancer
 PT or viral disease
 XX
 XX Claim 4; Page 32; 45pp; English.
 XX
 XX The present sequence is a human immunoglobulin G1 Fc region, which
 CC can form a claimed fusion protein with the Herpesvirus saimiri
 CC (HVS) major histocompatibility complex (MHC) Class II binding
 CC protein, HVS14. The fusion protein can be used to treat cancer or
 CC viral disease, as HVS14 inhibits antigen presentation, or acts as
 CC a superantigen.
 XX
 XX Sequence 212 AA;

Query Match 97.6%; Score 571; DB 17; Length 212;
 Best Local Similarity 97.3%; Pred. No. 5.6e-52;
 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 DB 14 apellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwvydgvgevhnaatk 73

QY 61 PREEQYNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
 DB 74 preeqynstyrvvsvltvhlqdwlngkeykckvsnkalpapietkiskak 123

RESULT 8
 AAW02305
 ID AAW02305 standard; Protein; 212 AA.
 XX
 AC AAW02305;
 XX
 XX 05-DEC-1996 (first entry)
 XX
 XX Human IgG1 Fc region.
 XX
 XX IgG1; interleukin-17 receptor; IL-17R.
 XX
 XX Homo sapiens.
 XX
 XX WO9629408-A1.
 XX
 XX 26-SEP-1996.
 XX
 XX 21-MAR-1996; 96WO-US04018.
 XX

PR 07-AUG-1995; 95US-0538765.
 PR 23-MAR-1995; 95US-0410535.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX
 XX Fanslow WC, Spriggs MK, Yao Z;
 XX
 XX WPI; 1996-443184/44.
 XX
 XX DNA encoding interleukin-17 receptor - useful for regulating immune
 PT and inflammatory responses, or to suppress graft rejection
 PT
 XX Example 1; Page 33; 52pp; English.
 XX
 XX The human IgG1 Fc region (AAW02305) can be used as a fusion partner
 CC for interleukin-17 receptor (IL-17R) proteins (see also AAW04184-85),
 CC allowing purification of recombinant IL-17R using protein A or
 CC protein G affinity chromatography. Fusions between Fc and HVS13
 CC (see also AAW02387), a viral homologue of IL-17, and between Fc
 CC and murine CTLA8 (AAW02386) were used to identify cells that
 CC express the murine IL-17R. Selected murine thymoma EL4 cells
 CC were used as a source of murine IL-17R cDNA (AAT33800).
 XX
 XX Sequence 212 AA;

Query Match 97.6%; Score 571; DB 17; Length 212;
 Best Local Similarity 97.3%; Pred. No. 5.6e-52;
 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 DB 14 apellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwvydgvgevhnaatk 73

QY 61 PREEQYNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
 DB 74 preeqynstyrvvsvltvhlqdwlngkeykckvsnkalpapietkiskak 123

RESULT 9
 AAW47354
 ID AAW47354 standard; protein; 212 AA.
 XX
 AC AAW47354;
 XX
 XX 01-JUN-1998 (first entry)
 XX
 XX Human immunoglobulin G1 Fc fragment.
 XX
 XX EBV; B2LF2; beta-chain; major histocompatibility complex; MHC;
 KW class II; antigen; prevention; treatment; autoimmune disease;
 KW transplant rejection; allergy; asthma; super-antigen; IgG1;
 KW Epstein-Barr virus; human; immunoglobulin G1; Fc fragment.
 XX
 XX Homo sapiens.
 XX
 XX US5726286-A.
 XX
 XX 10-MAR-1998.
 XX
 XX 28-APR-1995; 95US-0430633.
 XX
 XX 28-APR-1995; 95US-0430633.
 XX
 XX 28-APR-1994; 94US-0235397.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX
 XX Alderson M, Armitage RJ, Cohen JI, Comeau MR, Farrah TM;
 PI Hutt-Fletcher LM, Spriggs MK;
 XX
 XX WPI; 1998-192827/17.
 XX
 XX Epstein-Barr virus protein - binds to major histocompatibility

CC The present sequence represents a protein used to create fusion proteins
CC with the Epstein-Barr virus BZLF2 proteins of the invention. The BZLF2
CC protein is capable of binding to a beta chain of a Class II major
CC histocompatibility complex antigen to inhibit an antigen-specific


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XX      SQ      Sequence      212 AA;
Query Match      97.6%; Score 571; DB 20; Length 212;
Best Local Similarity 97.3%; Pred. No. 5.6e-52;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1      APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
      |||
      14      apelligpsvflfppkpkdtlmisrtpevtcvvdvshedpevkfnwvdgvevhnaktk 73
      |||

QY      61      PREEQNSTYRVVSVLTVTLHQLDMLNGKEYKCKVSNKGLPSSIEKTTISKAK 110
      |||
      74      preeqnstyrvvsvltvltlhqdwlngkeyckvsnkalpapiektiskak 123

RESULT 12
AAY9937
ID      AAY9937 standard; Protein; 212 AA.
XX
AC      AAY9937;
XX
DT      10-JAN-2001 (first entry)
XX
DE      Human IgG1 Fc region.
XX
KW      IL-17R; CTLA-8; Interleukin 17; Herpesvirus saimiri; HVS 13;
KW      human; antibody; immune suppression.
XX
OS      Homo sapiens.
XX
PN      US6072037-A.
XX
PD      06-JUN-2000.
XX
PF      12-FEB-1998; 98US-0022696.
XX
PR      21-MAR-1996; 96US-0620694.
PR      23-MAR-1995; 95US-0410535.
PR      07-AUG-1995; 95US-0538765.
XX
PA      (IMMV ) IMMUNEX CORP.
XX
PI      Fanslow WC, Spriggs MK, Yao Z;
XX
WPI; 2000-411206/35.
XX
PT      Antibodies immunoreactive with interleukin-17 receptor protein useful
PT      in interfering with receptor binding to CTLA-8, as components of
PT      diagnostic or research assays or in affinity purification of the
PT      receptor -
XX
XX      Disclosure; Column 31-32; 25pp; English.
XX
CC      The present invention relates to a novel receptor that binds Interleukin
CC      17 (IL-17, also known as CTLA-8) and a Herpesvirus saimiri homolog,
CC      HVS13. The receptor is a type I transmembrane protein which is referred
CC      to as IL-17R. Murine thymoma EL4 cells were found to express a
CC      receptor for IL-17. An EL4 mammalian expression library was screened
CC      and a cDNA encoding the receptor was identified (see AAA61238). The cDNA
CC      was used to isolate DNA encoding human IL-17R by cross species
CC      hybridisation. The human IL-17R cDNA and protein are described in
CC      AAA61240 and AAY99941. The present sequence is a human IgG1 Fc region
CC      that may be used with IL-17R to make a fusion protein. Soluble forms of
CC      the receptor may be used to regulate immune responses, for example to
CC      suppress rejection of organ grafts. Antibodies to IL-17R consisting of
CC      amino acids 1-322 of murine IL-17R or 1-320 of human IL-17R may be
CC      useful as components of diagnostic or research assays. Such antibodies
CC      may also be used in affinity purification of the receptor.
XX
SQ      Sequence      212 AA;

Query Match      97.6%; Score 571; DB 21; Length 212;
Best Local Similarity 97.3%; Pred. No. 5.6e-52;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1      APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
      |||
      14      apelligpsvflfppkpkdtlmisrtpevtcvvdvshedpevkfnwvdgvevhnaktk 73
      |||

QY      61      PREEQNSTYRVVSVLTVTLHQLDMLNGKEYKCKVSNKGLPSSIEKTTISKAK 110
      |||
      74      preeqnstyrvvsvltvltlhqdwlngkeyckvsnkalpapiektiskak 123

RESULT 13
AAY97182
ID      AAY97182 standard; Protein; 212 AA.
XX
AC      AAY97182;
XX
DT      04-DEC-2000 (first entry)
XX
DE      Human immunoglobulin G1 Fc region.
XX
KW      IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
KW      HVS13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KW      anti-asthmatic; immunoglobulin G1; Fc region.
XX
OS      Homo sapiens.
XX
PN      US6096305-A.
XX
PD      01-AUG-2000.
XX
PF      11-FEB-1998; 98US-0022253.
XX
PR      21-MAR-1996; 96US-0620694.
PR      23-MAR-1995; 95US-0410535.
PR      07-AUG-1995; 95US-0538765.
XX
PA      (IMMV ) IMMUNEX CORP.
XX
PI      Fanslow WC, Spriggs MK, Yao Z;
XX
WPI; 2000-523862/47.
XX
PT      Suppressing rejection of a grafted syngeneic or allogeneic organ or
PT      tissue in a graft recipient for organ transplantation involves
PT      transfecting the organ or tissue with DNA encoding soluble
PT      interleukin-17R receptor
XX
XX      Example 1; Column 31-32; 27pp; English.
XX
CC      A novel interleukin-17 receptor (IL-17R) was identified by screening a
CC      cDNA library from T cell thymoma EL4 cells, which were identified as
CC      binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
CC      region and soluble IL-17 (CTLA-8) protein or a homologous
CC      Herpesvirus saimiri (HSV) protein, designated HVS13. Suppressing
CC      rejection of a grafted syngeneic or allogeneic organ or tissue in a graft
CC      recipient involves transfecting the organ or tissue to be transplanted
CC      with DNA encoding soluble IL-17R, so that expression of IL-17R by the
CC      engrafted organ or tissue results in suppression of rejection. Soluble
CC      IL-17R fragments comprise residues 1-322 of the murine IL-17R, residues
CC      1-320 of the human IL-17R, and fragments of the extracellular domain
CC      that bind IL-17. The method is useful for regulating an immunoresponse,
CC      for suppressing rejection of grafted organs or tissues in the recipient
CC      and for treating or preventing diseases like allergy, asthma and
CC      autoimmune diseases.
XX
SQ      Sequence      212 AA;

Query Match      97.6%; Score 571; DB 21; Length 212;

```

Best Local Similarity 97.3%; Pred. No. 5.6e-52; Mismatches 2; Indels 0; Gaps 0; Matches 107; Conservative 1;

QY 1 APELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFKNWYDGVGVHNAKTK 60
|||||
Db 14 apellgspsvflfppkpkdtlmisrtpetvcvvdvshedpevkfnwydgvvhnaktk 73

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
|||||
Db 74 preeqnystyrsvvsvltvlhqdwlngkeykckvsnkalpapiektiskak 123

RESULT 14

AA97250
ID AAY97250 standard; Protein; 212 AA.

XX AC AAY97250;

DT 04-DEC-2000 (first entry)

DE Human immunoglobulin G1 Fc region.

XX IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
KW HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KW anti-asthmatic; immunoglobulin G1; Fc region.

OS Homo sapiens.

XX US6100235-A.

PN 23-MAR-1996; 96US-0620694.

XX 08-AUG-2000. 95US-0410535.

XX 11-FEB-1998; 98US-0022260.

XX 21-MAR-1996; 96US-0620694.

PR 23-MAR-1995; 95US-0410535.

PR 07-AUG-1995; 95US-0538765.

XX (IMMV) IMMUNEX CORP.

XX Fanslow WC, Spriggs MK, Yao Z;

PI WPI; 2000-548298/50.

XX Regulating, treating or preventing immune or inflammatory response in a
PT mammal, especially organ or graft rejection, allergy or asthma,
PT comprises administering interleukin-17 receptors

XX Example 1; Column 31-32; 26pp; English.

XX A novel interleukin-17 receptor (IL-17R) was identified by screening a
CC cDNA library from T cell thymoma EL4 cells, which were identified as
CC binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
CC region and soluble IL-17 (CTLA-8) protein or a homologous
CC Herpesvirus saimiri (HSV) protein, designated HSV13. Regulating an
CC immune or inflammatory response in a mammal comprises administering
CC soluble IL-17R. Soluble IL-17R fragments comprise residues 1-322 of the
CC murine IL-17R, residues 1-320 of the human IL-17R, and fragments of the
CC extracellular domain that bind IL-17. The method is useful for regulating
CC an immunoresponse, for treating or preventing diseases like allergy,
CC asthma and autoimmune diseases, and for suppressing rejection of grafted
CC organs or tissues in the recipient.

XX Sequence 212 AA;

Query Match 97.6%; Score 571; DB 21; Length 212;

Best Local Similarity 97.3%; Pred. No. 5.6e-52; Mismatches 2; Indels 0; Gaps 0; Matches 107; Conservative 1;

QY 1 APELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFKNWYDGVGVHNAKTK 60
|||||

Db 14 apellgspsvflfppkpkdtlmisrtpetvcvvdvshedpevkfnwydgvvhnaktk 73

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
|||||
Db 74 preeqnystyrsvvsvltvlhqdwlngkeykckvsnkalpapiektiskak 123

RESULT 15

AA03809
ID AAB03809 standard; Protein; 212 AA.

XX AC AAB03809;

DT 13-OCT-2000 (first entry)

DE Fc region of human immunoglobulin G1.

XX Interleukin-17 receptor; IL-17R; CTLA8; antiinflammatory; antiallergic;
KW immunosuppressive; organ rejection; graft rejection; autoimmune disease;
KW allergy; asthma; IgG1; immunoglobulin G1; human.

OS Homo sapiens.

PN US6072033-A.

PD 06-JUN-2000.

XX 11-FEB-1998; 98US-0022255.

XX 21-MAR-1996; 96US-0620694.

PR 23-MAR-1995; 95US-0410535.

PR 07-AUG-1995; 95US-0538765.

XX (IMMV) IMMUNEX CORP.

XX Fanslow WC, Spriggs MK, Yao Z;

PI WPI; 2000-411205/35.

XX Interleukin-17 receptor protein useful for regulating immune functions
PT and for preventing or treating organ or graft rejection, autoimmune
PT disease, allergy or asthma in human
XX Example 1; Column 31-32; 26pp; English.

XX This invention relates to an isolated and purified interleukin-17
CC receptor (IL-17R). A soluble IL-17 protein (CTLA8) and a herpesvirus
CC siamiri (HSV13) open reading frame (homologous to CTLA8) were expressed
CC as fusion proteins comprising an immunoglobulin Fc region, and used to
CC screen for the expression of the IL-17R. The screening identified the
CC novel receptor of the invention. IL-17R is a type I transmembrane
CC protein that exhibits antiinflammatory, immunosuppressive, antiasthmatic
CC and antiallergic activities, and is an inhibitor of T cell proliferation
CC and activation. IL-17R can be used to regulate immune functions, and is
CC useful for preventing or treating organ or graft rejection, autoimmune
CC disease, allergy or asthma. The present sequence represents the Fc region
CC of human immunoglobulin G1 (IgG1). This fragment of IgG1 forms part of
CC the IL-17 fusion protein used to identify IL-17R.

XX Sequence 212 AA;

Query Match 97.6%; Score 571; DB 21; Length 212;

Best Local Similarity 97.3%; Pred. No. 5.6e-52; Mismatches 2; Indels 0; Gaps 0; Matches 107; Conservative 1;

QY 1 APELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFKNWYDGVGVHNAKTK 60
|||||

Db 14 apellgspsvflfppkpkdtlmisrtpetvcvvdvshedpevkfnwydgvvhnaktk 73

QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
|||||

Db 74 preeqnystyrsvvsvltvlhqdwlngkeykckvsnkalpapiektiskak 123

Search completed: June 21, 2002, 08:36:09
Job time: 323 sec

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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:59:32 ; Search time 176.89 Seconds
(without alignments)
107.578 Million cell updates/sec

Title: US-09-674-857-8
Perfect score: 585
Sequence: 1 APELLGGPSVFLPPPKPKDT.....CKVSNKGLPSSIEKTSKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_19.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriaph.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571	97.6	701	4 Q96PQ8	Q96PQ8 homo sapien
2	472	80.7	337	6 Q95M34	Q95M34 equus caball
3	405	69.2	473	11 Q9D8L4	Q9D8L4 mus musculus
4	400	68.4	473	11 Q91Z05	Q91Z05 mus musculus
5	396.5	67.8	437	11 Q9R1A4	Q9R1A4 mus musculus
6	396.5	67.8	463	11 Q99LC4	Q99LC4 mus musculus
7	392	67.0	468	11 Q99L31	Q99L31 mus musculus
8	392	67.0	473	11 Q99L25	Q99L25 mus musculus
9	138	23.6	375	4 Q9BSZ1	Q9BSZ1 homo sapien
10	138	23.6	597	4 Q9BQB8	Q9BQB8 homo sapien
11	138	23.6	597	4 Q9BU10	Q9BU10 homo sapien
12	138	23.6	597	4 Q9GBB9	Q9GBB9 homo sapien
13	138	23.6	613	4 Q96EY0	Q96EY0 homo sapien
14	138	23.6	614	4 Q96GA6	Q96GA6 homo sapien
15	138	23.6	618	4 Q96AA6	Q96AA6 homo sapien
16	122.5	20.9	684	13 Q90544	Q90544 ginglymosto

17	121.5	20.8	130	11 Q9D8W4	Q9D8W4 mus musculus
18	121.5	20.8	233	11 Q91V32	Q91V32 m adult mal
19	119.5	20.4	384	4 Q9UP60	Q9UP60 homo sapien
20	119.5	20.4	416	4 Q9NPP6	Q9NPP6 homo sapien
21	119.5	20.4	494	4 Q96K68	Q96K68 homo sapien
22	119.5	20.4	496	4 Q96KX8	Q96KX8 homo sapien
23	119.5	20.4	496	4 Q96DK0	Q96DK0 homo sapien
24	116.5	19.9	235	11 Q99M11	Q99M11 mus musculus
25	115.5	19.7	500	4 Q9BRV0	Q9BRV0 homo sapien
26	114.5	19.6	233	4 Q96I69	Q96I69 homo sapien
27	114.5	19.6	236	4 Q96E61	Q96E61 homo sapien
28	112.5	19.2	486	11 Q91Z07	Q91Z07 mus musculus
29	112.5	19.2	487	11 Q99KA4	Q99KA4 mus musculus
30	111.5	19.1	479	11 Q99M22	Q99M22 mus musculus
31	111.5	19.1	484	11 Q99LA6	Q99LA6 mus musculus
32	110.5	18.9	479	11 Q91WP5	Q91WP5 mus musculus
33	110.5	18.9	481	11 Q91WT3	Q91WT3 mus musculus
34	110.5	18.9	481	11 Q91WT1	Q91WT1 mus musculus
35	110.5	18.9	482	11 Q91X92	Q91X92 mus musculus
36	110.5	18.9	488	11 Q91WR1	Q91WR1 mus musculus
37	109.5	18.7	426	11 Q9DCD9	Q9DCD9 mus musculus
38	109.5	18.7	480	11 Q91XE1	Q91XE1 mus musculus
39	105	17.9	211	11 Q91XLO	Q91XLO mus musculus
40	103	17.6	233	11 Q91WS9	Q91WS9 mus musculus
41	103	17.6	234	11 Q91WF8	Q91WF8 mus musculus
42	103	17.6	235	11 Q91W12	Q91W12 mus musculus
43	103	17.6	238	11 Q99M37	Q99M37 mus musculus
44	103	17.6	1215	5 Q9V787	Q9V787 drosophila
45	101	17.3	214	11 Q9R1A5	Q9R1A5 mus musculus

ALIGNMENTS

RESULT 1

Q96PQ8	PRELIMINARY;	PRT;	701 AA.
ID Q96PQ8			
AC Q96PQ8			
DT 01-DEC-2001 (Tremblrel. 19, Created)			
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=21477448; PubMed=11593034;			
RA Hu Z., Garen A.;			
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor			
RT cells for immunotherapy in mouse models of prostatic cancer.";			
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).			
DR EMBL; AF272774; AAK58686.1; -.			
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;			

Query Match 97.6%; Score 571; DB 4; Length 701;
Best Local Similarity 97.3%; Pred. No. 9.3e-55;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1	APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60		
DB 485	APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 544		

QY 61	PREEQNSYRVSVLTVLHQDLNGKGYKCKVSNKGLPSSIEKTSKAK 110		
DB 545	PREEQNSYRVSVLTVLHQDLNGKGYKCKVSNKGLPSSIEKTSKAK 594		

RESULT 2
Q95M34
ID Q95M34 PRELIMINARY; PRT; 337 AA.


```
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 67.8%; Score 396.5; DB 11; Length 437;
Best Local Similarity 65.1%; Pred. No. 1.2e-35;
Matches 71; Conservative 20; Mismatches 15; Indels 3; Gaps 1;

QY 2 PELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
Db 225 PEV---SSVFIFFPKPKDVLITLTTPKVTCTVVVDVSHEDPEVQFVDFVDDVEVHTAQTQ 281
||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 62 REQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 110
||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 282 REQFNSTFRSVSELPIMHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 330
||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:

RESULT 6
Q99LC4 PRELIMINARY; PRT; 463 AA.
ID Q99LC4
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BEC30783 CRC64;
```

```
Query Match 67.8%; Score 396.5; DB 11; Length 463;
Best Local Similarity 65.1%; Pred. No. 1.3e-35;
Matches 71; Conservative 20; Mismatches 15; Indels 3; Gaps 1;

QY 2 PELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
Db 251 PEV---SSVFIFFPKPKDVLITLTTPKVTCTVVVDVSHEDPEVQFVDFVDDVEVHTAQTQ 307
||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 62 REQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 110
||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 308 REQFNSTFRSVSELPIMHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 356
||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:

RESULT 7
Q99L31 PRELIMINARY; PRT; 468 AA.
ID Q99L31
AC Q99L31;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 67.0%; Score 392; DB 11; Length 468;
Best Local Similarity 65.5%; Pred. No. 4e-35;
Matches 72; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 252 APNLLGGPSVFIFFPKIKDVLISLSPMVTCTVVVDVSHEDDPDQVQISFVNVEVLTATQ 311
||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
QY 61 PREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAK 110
||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 312 THREDYNSTLRVVSALPIQHDWMSGKFEKCKVNNKALPAPIERTISKPK 361
||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:

RESULT 8
Q99L25 PRELIMINARY; PRT; 473 AA.
ID Q99L25
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
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RA	Strausberg R.;
RL	Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC003888; AAH03888.1; --
DR	HSSP; P01842; 7FAB.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR003597; Ig-cl.
DR	InterPro; IPR003600; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig_4.
DR	SMART; SM00409; Ig_2.
DR	SMART; SM00407; Igcl; 3.
DR	SMART; SM00406; Igv; 1.
DR	SMART; SM00410; IG_like; 1.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ	SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match	67.0%; Score 392; DB 11; Length 473;
Best Local Similarity	65.5%; Pred. No. 4.le-35;
Matches	72; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

QY	1	APELLGGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVGVEVINAKTK	60
Dd	257	APNLGGPSVFPPKIKDLVISLSPMWTCVVVDSEDDPDVQISWFRNNVELTAQTQ	316
QY	61	PREEQYNSTRYVSVLTVLHDPLNGKEYCKVSNKGLPSSIEKTISKAK	110
Dd	317	TREYDNTSLRVVSALPTIQHODWMSGKEFKCVNKNALPAPIERTISKPK	366

RESULT	9
Q9BSZ1	PRELIMINARY; PRT; 375 AA.
ID	Q9BSZ1 AC Q9BSZ1;
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	HYPOTHEtical 41.3 KDa PROTEIN.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_Taxid=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lymph, LYMPHOMA;
RA	Strausberg R.;
RL	Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC004476; AAH04476.1; --
DR	HSSP; P01857; LFC1
DR	InterPro; IPR003597; Ig-cl.
DR	InterPro; IPR003600; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	Pfam; PF00047; Ig_3.
DR	SMART; SM00407; Igcl; 3.
DR	SMART; SM00410; IG_like; 1.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW	Hypothetical protein.
SQ	SEQUENCE 375 AA; 41314 MW; B1A0A0998F473619 CRC64;

Query Match	23.6%; Score 138; DB 4; Length 375;
Best Local Similarity	28.7%; Pred. No. 4.5e-07;
Matches	29; Conservative 25; Mismatches 45; Indels 2; Gaps 2;

QY	10	VLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVGVEVINAKTKPREEQYST	69
Dd	146	VFAIPPS-FASIFLTSTKLTLCLVTLDITYD-SVTISWRONGEAVKTTNISHPNAT	203
QY	70	YRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTISKAK	110
Dd	204	FSAVGASICDDWNDSGERFTCTVTHTDLPSPKQTSRPK	244

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC017356; AAH17356.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;

Query Match 23.6%; Score 138; DB 4; Length 618;
 Best Local Similarity 28.7%; Pred. NO. 8.3e-07;
 Matches 29; Conservative 25; Mismatches 45; Indels 2; Gaps 2;
 QY 10 VFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69
 Db 368 VFAIPPS-FASIFLTAKSTKLTCLVTDLTYY-SVLIWTRQNGEAVKTHTNISESHPNAT 425
 QY 70 YRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
 Db 426 FSAVGEASICEDDWSGERFTCTVTHDLPSPKQTIISRPK 466

Search completed: June 21, 2002, 08:59:33
 Job time: 1632 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:00:25 ; Search time 48.19 Seconds
(without alignments)
88.382 Million cell updates/sec

Title: US-09-674-857-8
Perfect score: 585
Sequence: 1 APELLGSPVFLPPPKPDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	571	97.6	330	1 GCL_HUMAN	P01857 homo sapien
2	565	96.6	327	1 GC4_HUMAN	P01861 homo sapien
3	533	91.1	290	1 GC3_HUMAN	P01860 homo sapien
4	529	90.4	326	1 GC2_HUMAN	P01859 homo sapien
5	445	76.1	333	1 GCB_RAT	P20761 rattus norv
6	435	74.4	323	1 GC_RABIT	P01870 oryctolagus
7	432	73.8	329	1 GC2_CAVPO	P01862 cavia porce
8	419	71.6	329	1 GC3_MOUSE	P22436 mus musculu
9	419	71.6	398	1 GC3M_MOUSE	P03987 mus musculu
10	405	69.2	335	1 GCAB_MOUSE	P01864 mus musculu
11	401	68.5	330	1 GCBA_MOUSE	P01863 mus musculu
12	401	68.5	399	1 GCAM_MOUSE	P01865 mus musculu
13	400	68.4	329	1 GCC_RAT	P20762 rattus norv
14	400	68.4	336	1 GCB_MOUSE	P01866 mus musculu
15	400	68.4	405	1 GCBM_MOUSE	P01867 mus musculu
16	396.5	67.8	324	1 GCL_MOUSE	P01868 mus musculu
17	396.5	67.8	393	1 GCIM_MOUSE	P01869 mus musculu
18	380	65.0	326	1 GCL_RAT	P20759 rattus norv
19	339	57.9	322	1 GCA_RAT	P20760 rattus norv
20	166.5	28.5	428	1 EPC_HUMAN	P01854 homo sapien
21	153	26.2	429	1 EPC_RAT	P01855 rattus norv
22	153	26.2	457	1 MUC_SUNMU	P20768 suncus muri
23	138	23.6	421	1 EPC_MOUSE	P06336 mus musculu
24	138	23.6	454	1 MUC_HUMAN	P01871 homo sapien
25	137.5	23.5	299	1 ALC_RABIT	P01879 oryctolagus
26	136	23.2	391	1 MUCB_HUMAN	P04220 homo sapien
27	132	22.6	106	1 KAC_HUMAN	P01834 homo sapien
28	129	22.1	454	1 MUC_MESAU	P06337 mesocricetu
29	129	22.1	455	1 MUC_MOUSE	P01872 mus musculu
30	129	22.1	476	1 MUCM_MOUSE	P01873 mus musculu
31	127	21.7	103	1 LAC_CHICK	P20763 gallus gall
32	125	21.4	450	1 MUC_CANFA	P01874 canis famil
33	121.5	20.8	105	1 LAC1_MOUSE	P01843 mus musculu

34	121.5	20.8	105	1 LAC5_MUSSP	P20765 mus spretus
35	120	20.5	458	1 MUC_RABIT	P03988 oryctolagus
36	119.5	20.4	479	1 MUCM_RABIT	P04221 oryctolagus
37	119.5	20.4	340	1 ALC2_HUMAN	P01877 homo sapien
38	119.5	20.4	353	1 ALC1_GORGO	P20758 gorilla gor
39	119.5	20.4	353	1 ALC1_HUMAN	P01876 homo sapien
40	117.5	20.1	105	1 LAC5_MOUSE	P20764 mus musculu
41	111.5	19.1	344	1 ALC_MOUSE	P01878 mus musculu
42	111.5	19.1	393	1 HVC3_HETER	P23086 heterodontu
43	110.5	18.9	213	1 ILL1_HUMAN	P15814 homo sapien
44	109.5	18.7	105	1 LAC_HUMAN	P01842 homo sapien
45	109.5	18.7	370	1 HVC1_HETER	P23084 heterodontu

ALIGNMENTS

RESULT 1					
GCL_HUMAN					
ID	GCL_HUMAN	STANDARD;	PRT;	330 AA.	
AC	P01857;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Ig gamma-1 chain C region.				
GN	IGHG1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=82274238; PubMed=6287432;				
RA	Ellison J.W., Berson B.J., Hood L.E.;				
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."				
RL	Nucleic Acids Res. 10:4071-4079(1982).				
RN	[2]				
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).				
RX	MEDLINE=71064024; PubMed=5489771;				
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,				
RT	Waxdal M.J., Edelman G.M.;				
RL	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."				
RN	Biochemistry 9:3161-3170(1970).				
RP	[3]				
RX	SEQUENCE OF 136-329 (EU).				
RA	MEDLINE=71064025; PubMed=5530842;				
RT	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,				
RL	Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."				
RN	Biochemistry 9:3171-3181(1970).				
RP	[4]				
RX	SEQUENCE (MYELOMA PROTEIN NIE).				
RA	MEDLINE=77070269; PubMed=826475;				
RT	Ponstingl H., Hilschmann N.;				
RL	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."				
RN	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).				
RP	[5]				
RX	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.				
RA	MEDLINE=83289131; PubMed=6884994;				
RT	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;				
RL	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."				
RN	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).				
RP	[6]				
RX	DISULFIDE BONDS.				
RA	MEDLINE=71064027; PubMed=4923144;				
RT	Gall W.E., Edelman G.M.;				
RL	"The covalent structure of a human gamma G-immunoglobulin. X.				

RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196(1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9 and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -I- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, & THE
 CC G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE G1M(3)
 CC MARKER & THE G1M (NON-1) MARKERS.
 CC -I- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35, 116, 198, 269 & 272.
 CC -I- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -I- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198, 267 & 272.
 CC -----
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 DR EMBL; J00228; AAC82527.1; ALT_INIT.
 DR PIR; A02146; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR MIM; 147100; -
 DR InterPro; IPR003006; Ig-MHC.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003600; Ig-like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; Ig-like; 1.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS00290; IG-MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C' region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103
 FT DISULFID 109 109 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT VARIANT 241 241
 FT STRAND 123 126
 FT HELIX 130 134

FT TURN 136 137
 FT STRAND 141 148
 FT STRAND 158 162
 FT TURN 163 164
 FT STRAND 165 166
 FT STRAND 175 178
 FT STRAND 183 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 206
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 240
 FT TURN 241 242
 FT STRAND 245 256
 FT STRAND 260 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 324
 SQ SEQUENCE 330 AA; 3770EE106C2FA33D CRC64;
 Query Match 97.6%; Score 571; DB 1; Length 330;
 Best Local Similarity 97.3%; Pred. No. 31e-50;
 Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db 114 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 173
 QY 61 PREEQYNSTYRVVSVLTVLHQDLNCKEYCKVSNKGLPSSIEKTISKAK 110
 Db 174 PREEQYNSTYRVVSVLTVLHQDLNCKEYCKVSNKGLPAPTEKTISKAK 223
 RESULT 2
 ID GC4_HUMAN STANDARD; PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-4 chain C region.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=83157104; PubMed=6299662;
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 1:11-18(1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE=70207560; PubMed=4192699;
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 RL Biochem. J. 117:33-47(1970).
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DR EMBL; K01316; AAB59394.1; ALT_INIT.
 DR PIR; A02150; G4H0.
 DR HSSP; P01842; 7FAB.
 DR MIM; 147130; -.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; IG_like; 1.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98
 FT CH1.
 FT HINGE.
 FT DOMAIN 99 110
 FT CH2.
 FT DOMAIN 111 220
 FT CH3.
 FT DOMAIN 221 327
 FT INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 14 14
 FT DISULFID 27 83
 FT DISULFID 106 106
 FT INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109
 FT DISULFID 141 201
 FT DISULFID 247 305
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 96.6%; Score 565; DB 1; Length 327;
 Best Local Similarity 96.4%; Pred. No. 1.2e-49;
 Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 DB 111 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 170

QY 61 PREEQFNSTYRVSVLTVLHQDLNGKEYCKVKNSKGLPSSIEKTIISKAK 110
 DB 171 PREEQFNSTYRVSVLTVLHQDLNGKEYCKVKNSKGLPSSIEKTIISKAK 220

RESULT 3
 GC3_HUMAN
 ID GC3_HUMAN STANDARD; PRT; 290 AA.
 AC P01860;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
 GN IGHC3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (DISEASE PROTEIN WIS).
 RX MEDLINE=81021548; PubMed=6774747;
 RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
 RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
 RT gamma 3 heavy-chain disease protein Wis.";
 RL Biochemistry 19:4304-4308(1980).
 RN [2]
 RP REVISIONS TO 12-97 OF PROTEIN WIS.
 RX MEDLINE=77118561; PubMed=402363;
 RA Michaelisen T.E., Frangione B., Franklin E.C.;
 RT "Primary structure of the 'hinge' region of human IgG3. Probable
 RT quadruplication of a 15-amino acid residue basic unit.";
 RL J. Biol. Chem. 252:883-889(1977).

RN [3]
 RP REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC).
 RX MEDLINE=77021516; PubMed=823945;
 RA Wolfstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
 RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
 RT Structure of the FC fragment of immunoglobulin G3.";
 RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
 RN [4]
 RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
 RX MEDLINE=82247835; PubMed=6808505;
 RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
 RA Franklin E.C., Hood L., Buxbaum J.N.;
 RT "Gamma Heavy chain disease in man: cDNA sequence supports partial
 RT gene deletion model.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
 CC -1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
 CC INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
 CC NORMALLY PRESENT IN THE HINGE REGION.
 CC -1- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
 CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
 CC REF.2.
 CC -1- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
 CC AND ALL OF THE CH1 REGION.
 CC -1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
 CC OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
 CC GAMMA-3 HEAVY CHAINS.
 CC -1- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
 CC OR ANOTHER GAMMA CHAIN SUBCLASS.
 CC -1- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
 CC TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
 CC IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
 CC SEGMENT (12-28).
 CC -----

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EMBL; J00231; AAA52805.1; ALT_SEQ.
 PIR; A02149; G3HUM1.
 HSSP; P01857; 1FC1.
 MIM; 147120; -.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00410; IG_like; 1.
 DR SMART; SM00407; IGc1; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.
 FT DOMAIN 12 73
 FT HINGE.
 FT DOMAIN 74 183
 FT CH2.
 FT DOMAIN 184 289
 FT CH3.
 FT REPEAT 29 43
 FT REPEAT 44 58
 FT REPEAT 59 73
 FT MOD_RES 1 1
 FT CARBOHYD 6 6
 FT PYRROLIDONE CARBOXYLIC ACID.
 FT N-LINKED (GLCNAC...).
 FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 7 7
 FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 24 24
 FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 27 27
 FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 33 33
 FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 39 39
 FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 42 42
 FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 48 48
 FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 54 54
 FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 57 57
 FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 63 63
 FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 69 69
 FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 72 72
 FT INTERCHAIN (WITH HEAVY CHAIN DIMER).

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FT CARBOHYD 140 N-LINKED (GLCNAC. . .).
FT MOD_RES 290 REMOVED POST-TRANSLATIONALLY.
FT VARIANT 126 OV -> EB (IN ZUC).
FT VARIANT 134 /FTID=VAR_003890.
FT VARIANT 134 P -> L (IN OMM).
FT VARIANT 139 /FTID=VAR_003891.
FT VARIANT 139 F -> Y (IN OMM).
FT VARIANT 182 /FTID=VAR_003892.
FT VARIANT 182 T -> A (IN OMM).
FT VARIANT 227 /FTID=VAR_003893.
FT VARIANT 227 S -> N (IN OMM).
FT VARIANT 227 /FTID=VAR_003894.
FT VARIANT 227 MISSING (IN ZUC).
FT VARIANT 279 /FTID=VAR_003895.
FT VARIANT 279 F -> Y (IN OMM).
FT VARIANT 279 /FTID=VAR_003896.
FT SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;

Query Match 91.1%; Score 533; DB 1; Length 290;
Best Local Similarity 89.1%; Pred. No. 1.8e-46;
Matches 98; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 APELLGSPVFLPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTK 60
DB 74 APELLGSPVFLPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTK 133
QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYCKVKYSGKGLPSSIEKTKISKAK 110
DB 134 PREEQNSTYRVVSVLTVLHQDWLNGKEYCKVKYSGKGLPSSIEKTKISKAK 183

RESULT 4
GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
RT heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
RT evolution of a gene family.";
RL Cell 29:671-679(1982).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT genes.";
RL EMBO J. 1:403-407(1982).
RN [4]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
```

```
RT "The primary structure of a human IgG2 heavy chain: genetic,
RT evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
RN [5]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
RT domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
RN [6]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
RT immunoglobulin gamma chains.";
RL Mol. Immunol. 16:923-925(1979).
RN [7]
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RL Submitted (MAR-1980) to the PIR data bank.
RN [8]
RP SEQUENCE OF 1-121 (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
RT immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
RN [9]
RP DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RN [10]
RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
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CC -----
DR EMBL; J00230; AAB59393.1; -.
DR PIR; A02148; G2H0.
DR HSSP; P01857; 1FC1.
DR MIM; 147110; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 1 98
FT HINGE.
FT DOMAIN 99 110
FT CH2.
FT DOMAIN 111 219
FT CH3.
FT DOMAIN 220 326
FT INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 14 14
FT DISULFID 27 83
FT DISULFID 102 102
FT DISULFID 103 103
FT DISULFID 106 106
FT DISULFID 109 109
FT DISULFID 140 200
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FT DISULFID 246 304
 FT SITE 156 156 AT OR NEAR THE COMPLEMENT-BINDING SITE.
 FT MOD_RES 326 326 REMOVED POST-TRANSLATIONALLY (PROBABLY).
 FT VARIANT 60 60 S -> A (IN MYELOMA PROTEINS TIL & ZIE).
 FT CONFLICT 109 109 /FTIG-VAR_003889.
 FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;

Query Match 90.4%; Score 529; DB 1; Length 326;

Best Local Similarity 91.5%; Pred. No. 5.1e-46;

Matches 97; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 5 LGGPSVFLPPPKDFTLMSRTPVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 64
 Db 114 VAGPSVFLPPPKDFTLMSRTPVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 173

QY 65 QYASTYRVVSVLTVLHODWLNKEYCKYKSNKGLPSISIEKTSKAK 110

Db 174 QFNSTYRVVSVLTVLHODWLNKEYCKYKSNKGLPAPIEKTSKTK 219

RESULT 5

GCB_RAT ID GCB_RAT STANDARD; PRT; 333 AA.

AC P20761;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig gamma-2B chain C region.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89232738; PubMed=3149946;

RA Brueggemann M.;

RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";

RL Gene 74:473-482(1988).

DR PIR; PS0018; PS0018.

DR HSSP; P01842; 7FAB.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003597; Ig_C1.

DR InterPro; IPR003600; Ig_Like.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00410; Ig_Like; 1.

DR SMART; SM00407; IGcl; 2.

DR PROSITE; PS00290; IG_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region.

FT NON_TER 1 1

FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 80

FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 147 207

FT DISULFID 253 311

SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match

Best Local Similarity 76.1%; Score 445; DB 1; Length 333;

Matches 79; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

QY 2 PELLGGPSVFLPPPKDFTLMSRTPVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTP 61
 Db 118 PELLGGPSVFLPPPKDFTLMSRTPVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTP 177

QY 62 REEQYNSTYRVVSVLTVLHODWLNKEYCKYKSNKGLPSISIEKTSKAK 110

Db 178 REEQYNSTYRVVSVLTVLHODWLNKEYCKYKSNKGLPSISIEKTSKPK 226

RESULT 6
 GC_RABIT ID GC_RABIT STANDARD; PRT; 323 AA.
 AC P01870;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma chain C region.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84030930; PubMed=6313520;
 RA Bernstein K.E.; Alexander C.B.; Mage R.G.;
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
 RT F-1 haplotype.";
 RL Biochem. J. 151:337-349(1975).
 RN [3]
 RP SEQUENCE OF 88-266 FROM N.A.
 RX MEDLINE=83299917; PubMed=6193512;
 RA Martens C.L.; Moore K.W.; Steinmetz M.; Hood L.; Knight K.L.;
 RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
 RT heavy chain and identification of two genomic C gamma genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
 RN [4]
 RP SEQUENCE OF 132-161.
 RX MEDLINE=70110015; PubMed=5461106;
 RA Fruchter R.G.; Jackson S.A.; Mole L.E.; Porter R.R.;
 RT "Sequence studies of the Fd section of the heavy chain of rabbit
 RT immunoglobulin G.";
 RL Biochem. J. 116:249-259(1970).
 RN [5]
 RP SEQUENCE OF 129-131 AND 155-322.
 RA Hill R.L.; Lebovitz H.E.; Fellows R.E. Jr.; Delaney R.;
 RL (In) Killander J. (eds.);
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
 RL Stockholm (1967).
 CC -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
 CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
 CC MARKERS AND REF.5 THE E15 MARKER.
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 CC -----
 CC EMBL; M16426; AAA31289.1; -.
 DR PIR; A02161; GHRB.
 DR HSSP; P01857; 1FC1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_C1.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT VARIANT 104 104 T -> M (IN D11 MARKER).
 FT VARIANT 185 185 T -> A (IN E15 MARKER).
 FT CONFLICT 48 48 N -> E (IN REF. 2).

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FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E9A118D579A8B CRC64;

Query Match 74.4%; Score 435; DB 1; Length 323;
Best Local Similarity 72.5%; Pred. No. 1.4e-36;
Matches 79; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 2 PELLGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKP 61
DB 108 PELLGSPVFIFFPKPKDTLMISRTPEVTCVVVDVSDDEPEVQFTWYINNEQVRTARPL 167

QY 62 REEYQNSTYRVSVLTVLHODWLNKGYCKVSKNKLPSSEIKTISKAK 110
DB 168 REQQFNSTIRVSLPLTHODWLRGKFKCKVHNKALPAPIETISKAR 216

RESULT 7
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cystine joining heavy and light chains.;"
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.;"
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.;"
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2

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RT antibodies.;"
RN Biochemistry 13:4804-4811(1974).
RL [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.;"
RL Biochemistry 10:26-31(1971).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; GZGP.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; ig; 3
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 73.8%; Score 432; DB 1; Length 329;
Best Local Similarity 73.4%; Pred. No. 2.9e-36;
Matches 80; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 2 PELLGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKP 61
DB 113 PENLGSPVFIFFPKPKDTLMISRTPEVTCVVVDVSDDEPEVQFTWFDNKPVGNAETKP 172

QY 62 REEYQNSTYRVSVLTVLHODWLNKGYCKVSKNKLPSSEIKTISKAK 110
DB 173 RVEQYNTTFRVESVLPFIQHDWLRGKFKCKVHNKALPAPIETISKTK 221

RESULT 8
GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.;"
RL EMBO J. 3:2041-2046(1984).
CC -----
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DR EMBL: J00451; -: NOT_ANNOTATED_CDS.
DR PIR: B02156; G3MSC.
DR HSSP: P01857; 1FC1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00410; IG_1.
DR SMART: SM00407; IG_2.
DR SMART: SM00410; IG_1.
DR SMART: SM00407; IG_1.
DR PROSITE: PS00290; IG_MHC; 1.
DR Transmembrane; Alternative splicing.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 71.6%; Score 419; DB 1; Length 329;
Best Local Similarity 70.1%; Pred. No. 5.9e-35;
Matches 75; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 4 LLGSPSVFLPPPKDMLTMSRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKPRE 63
DB 116 ILGSPSVFIIPPKDMLTMSRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKPRE 175
QY 64 EOYNSTRVYVSVLTVLHQLDNLNGKEYCKVSKNKGLPSSIEKTSKAK 110
DB 176 AQYNSTRVYVSVLTVLHQLDNLNGKEYCKVSKNKGLPSSIEKTSKAK 222

RESULT 9
GC3M_MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041483; PubMed=6314258;
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
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CC or send an email to license@isb-sib.ch).
DR EMBL: J00451; AAB59655.1; -.
DR EMBL: V01526; CAA24767.1; AUT_SEQ.
DR PIR: A02155; G3MSC.
DR HSSP: P01857; 1FC1.

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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00410; IG_1.
DR SMART: SM00407; IG_2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 71.6%; Score 419; DB 1; Length 398;
Best Local Similarity 70.1%; Pred. No. 7.3e-35;
Matches 75; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 4 LLGSPSVFLPPPKDMLTMSRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKPRE 63
DB 116 ILGSPSVFIIPPKDMLTMSRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKPRE 175
QY 64 EOYNSTRVYVSVLTVLHQLDNLNGKEYCKVSKNKGLPSSIEKTSKAK 110
DB 176 AQYNSTRVYVSVLTVLHQLDNLNGKEYCKVSKNKGLPSSIEKTSKAK 222

RESULT 10
GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RC MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT IgG2a and IgG2b alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain Fc regions of Ig1a and Ig1b allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
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CC or send an email to license@isb-sib.ch).

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DR EMBL: J00479; -: NOT_ANNOTATED_CDS.
DR FIR: A02153; G2MSAB.
DR HSP: P01857; 1FCL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; ig; 3.
DR SMART: SM00410; Ig_like; 1.
DR SMART: SM00407; IGcl; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CB1306 CRC64;

Query Match 69.2%; Score 405; DB 1; Length 335;
Best Local Similarity 66.4%; Pred. No. 1.5e-33;
Matches 73; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 APELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 119 ADPLGGPSVFLFPKIKDVLMSLSPMVTCTVVVDVSEDDPDVQISWFEVNVVHTAQTK 178
QY 61 PREEQYNSTRVSVLTVLHODWLGKVKCKVSNKGLPSSIEKTIKAK 110
Db 179 THREDYNSTRVSVLPTQHQDWSGKEFKCKVNNRPLSPIEKTIKPR 228

RESULT 11
GCAM_MOUSE STANDARD; PRT; 330 AA.
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-2A chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Sikorav J.-L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RL Balb/c gamma 2a heavy chain messenger RNA.";
RN Nucleic Acids Res. 8:3143-3155(1980).
RP [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
and evolution of heavy chain genes: further evidence for intervening
sequence-mediated domain transfer.";
RL Nucleic Acids Res. 9:1365-1381(1981).
RP [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81223894; PubMed=6787604;
RA Olio R., Auffray C., Mochamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
suggests that exons can be exchanged between genes in a multigenic
family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RP [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
immunoglobulin:amino-acid sequence of the Fc fragment. Implications
for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).
RP [5]
RP DISULFIDE BONDS.

RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462(1972).
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CC -----
DR EMBL: V00798; CAA24178.1; -.
DR FIR: A02152; G2MSA.
DR HSP: P01842; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; ig; 3.
DR SMART: SM00410; Ig_like; 1.
DR SMART: SM00407; IGcl; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 68.5%; Score 401; DB 1; Length 330;
Best Local Similarity 66.4%; Pred. No. 3.8e-33;
Matches 73; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 1 APELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 114 APNLLGSPVFLFPKIKDVLMSLSPITCTVVVDVSEDDPDVQISWFEVNVVHTAQTK 173
QY 61 PREEQYNSTRVSVLTVLHODWLGKVKCKVSNKGLPSSIEKTIKAK 110
Db 174 THREDYNSTRVSVLPTQHQDWSGKEFKCKVNNKDLPAPIERTISKPK 223

RESULT 12
GCAM_MOUSE STANDARD; PRT; 399 AA.
AC P01865;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
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CC      IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC      SEGMENT OF MU CHAINS.
CC      -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
CC      IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
CC      THE A ALLELE.
CC
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CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL: J00471; AAB59661.1; ALT_INIT.
CC      PIR: A02154; G2MSAM.
CC      HSP: P01857; 1FC1.
CC      MGI: 96443; Igh-1.
CC      InterPro: IPR003006; Igh-MHC.
CC      InterPro: IPR003597; Ig-cl.
CC      InterPro: IPR003600; Ig_Like.
CC      Pfam: PF00047; Ig; 3.
CC      SMART: SM00410; IG_Like; 1.
CC      SMART: SM00407; IGC1; 2.
CC      PROSITE: PS00290; IG_MHC; 1.
CC      Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW      Transmembrane; Alternative splicing.
FT      NON_TER 1 1
FT      DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT      DISULFID 27 82
FT      DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID 144 204
FT      DISULFID 250 308
FT      TRANSMEM 346 363
FT      DOMAIN 364 399
FT      CARBOHYD 180 180 N-LINKED (GLCNAC. -) (POTENTIAL).
FT      SEQUENCE 399 AA; 44020 MW; 4C38130BFAED3FF0 CRC64;
SQ
Query Match 68.5%; Score 401; DB 1; Length 399;
Best Local Similarity 66.4%; Pred. No. 4.7e-33;
Matches 73; Conservative 17; Mismatches 20; Indels 0; Gaps 0;
QY 1 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVGVGVHNAKTK 60
DB 114 APNLLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVGVGVHNAKTK 173
QY 61 PREQYNSTYRVVSVLTVLDHQLWLNKEYCKVSKNGLPSSIEKTSKAK 110
DB 174 THREDYNSTLRVVSALPIQHQDWMGSEKFKCKVNNKDLPAPIERTISKPK 223
QY 61 PREQYNSTYRVVSVLTVLDHQLWLNKEYCKVSKNGLPSSIEKTSKAK 110
DB 174 THREDYNSTLRVVSALPIQHQDWMGSEKFKCKVNNKDLPAPIERTISKPK 223
RESULT 13
GCC_RAT ID GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RT region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).

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CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL: X07189; CAA30169.1; -.
CC      PIR: S00847; S00847.
CC      HSP: P01857; 1FC1.
CC      InterPro: IPR003006; Ig_MHC.
CC      InterPro: IPR003597; Ig-cl.
CC      InterPro: IPR003600; Ig_Like.
CC      Pfam: PF00047; Ig; 3.
CC      SMART: SM00410; IG_Like; 1.
CC      SMART: SM00407; IGC1; 2.
CC      PROSITE: PS00290; IG_MHC; 1.
CC      Immunoglobulin domain; Immunoglobulin C region.
KW      NON_TER 1 1
FT      DOMAIN 1 97 CH1.
FT      DOMAIN 98 113 HINGE.
FT      DOMAIN 114 222 CH2.
FT      DOMAIN 223 329 CH3.
FT      DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT      DISULFID 27 82
FT      DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT      DISULFID 143 203
FT      DISULFID 249 307
FT      SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;
SQ
Query Match 68.4%; Score 400; DB 1; Length 329;
Best Local Similarity 67.9%; Pred. No. 4.8e-33;
Matches 72; Conservative 17; Mismatches 17; Indels 0; Gaps 0;
QY 5 LGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVGVGVHNAKTKPRE 64
DB 117 LGRPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVGVGVHNAKTKPRE 110
QY 65 QYNSTYRVVSVLTVLDHQLWLNKEYCKVSKNGLPSSIEKTSKAK 110
DB 177 QLNGTRVSVTLHIQHQDWMGSEKFKCKVNNKDLPSPIKTSKPR 222
RESULT 14
GCC_MOUSE ID GCC_MOUSE STANDARD; PRT; 336 AA.
AC P01866;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2B chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (A ALLELE).
RX MEDLINE=80120716; PubMed=6766534;
RA Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
RT "Complete nucleotide sequence of immunoglobulin gamma2b chain gene
RT cloned from newborn mouse DNA.";
RL Nature 283:786-789(1980).
RN [2]
RP SEQUENCE FROM N.A. (MPC 11).
RX MEDLINE=80081501; PubMed=117548;
RA Tucker P.W., Marcu K.B., Slightner J.L., Blattner F.R.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT gamma 2b heavy chain messenger RNA.";
RL Science 206:1299-1303(1979).

```

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[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=80081502; PubMed=117549;
RA Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
RT "Sequence of the cloned gene for the constant region of murine gamma
RL 2b immunoglobulin heavy chain.";
RT Sequence 206:1303-1306(1979).
RN [4]
RP SEQUENCE FROM N.A. (B ALLELE).
RX MEDLINE=82173203; PubMed=6803173;
RA Ollio R., Rougeon F.;
RT "Mouse immunoglobulin allotypes: post-duplication divergence of gamma
RL 2a and gamma 2b chain genes.";
RL Nature 296:761-763(1982).
RN [5]
RP CARBOHYDRATE-LINKAGE SITE THR-105.
RX MEDLINE=94216359; PubMed=7512967;
RA Kim H., Yamauchi Y., Masuda K., Matsunaga C., Yamamoto K.,
RA Irimura T., Takahashi N., Kato K., Arata Y.;
RT "O-glycosylation in hinge region of mouse immunoglobulin G2b.";
RL J. Biol. Chem. 269:12345-12350(1994).
CC CC -I- PWM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS
CC MODIFIED WITH 2 SULFIC ACID RESIDUES.
CC -I- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA
CC CHAINS.
CC -I- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.
CC PIR: A02157; G2MS11.
DR HSSP: P01857; 1FC1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-Cl.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00410; IG_Like; 1.
DR SMART: SM00407; IG1; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 150 210
FT DISULFID 256 314
FT CARBOHYD 105 105
FT MOD_RES 336 336
FT VARIANT 163 163
FT VARIANT 194 194
FT VARIANT 300 300
FT VARIANT 301 301
FT CONFLICT 25 25
FT CONFLICT 36 36
FT CONFLICT 239 239
FT CONFLICT 336 AA; 36658 MW; 7D879662607C356E CRC64;
SQ SEQUENCE

O-LINKED (GALNAC...).
REMOVED POST-TRANSLATIONALLY (PROBABLE).
Q -> R (IN B ALLELE).
T -> A (IN B ALLELE).
N -> D (IN B ALLELE).
M -> I (IN B ALLELE).
L -> S (IN REF. 2 AND 3).
S -> P (IN REF. 2 AND 3).
I -> T (IN REF. 2 AND 3).

Query Match 68.4%; Score 400; DB 1; Length 336;
Best Local Similarity 66.4%; Pred. No. 4.9e-33;
Matches 73; Conservative 16; Mismatches 21; Indels 0; Gaps

QY 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db ||| ||||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
120 APNLEGGPSVFIFPPNKIKDLVMSLTPTKVTCCVVDVSEDDPDVQISFVNVEVHTAQTK 179

QY 61 PREEOXNSRYRVSVLTVLHQDWLNGKEKCKVSKNKGFLPSIEKTSKAK 110
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
180 THREDYNSIRYVSVLTPIQHQDWSGKEFKCKVNNKNDLPSPERTISKIK 229

RESULT 15
GCBM_MOUSE
ID GCBM_MOUSE STANDARD; PRT; 405 AA.

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Matches 73; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPKPKDQTLMSRTPVTCVVVDYSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db 120 APNLEGGPSVFIFPPNIRKIDVLMISLTPKVCYVVDVSEDDPDQISWFFVNNVEVHTAQTK 179

QY 61 PREEQNSTYRVVSVLTVLIHQDLNGKEYCKVSNKGLPSSIEKTISKAK 110
 Db 180 THREDYNSTIRVVSTLPTIQHQDWMMSGKEFKCKVNNKDLPSPIERTISKIK 229

Search completed: June 21, 2002, 09:00:25
 Job time: 1449 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 08:37:54 ; Search time 102.05 Seconds
(without alignments)
103.575 Million cell updates/sec

Title: US-09-674-857-8
Perfect score: 585
Sequence: 1 APELLGGPSVFLPPPKD.....CKVSNKGLPSSIEKTISKAK 110
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571	97.6	234	2 PT0207	Ig gamma chain C r
2	571	97.6	255	4 S31866	Ig gamma-1 chain C
3	571	97.6	330	1 GHU	Ig gamma-1 chain C
4	571	97.6	374	2 S69339	Ig heavy chain V r
5	565	96.6	327	1 G4HU	Ig gamma-4 chain C
6	553	94.5	377	2 A60764	Ig gamma-3 chain C
7	553	94.5	377	2 A23511	Ig gamma-3 chain C
8	533	91.1	289	1 G3HUW1	Ig gamma-3 heavy C
9	529	90.4	326	1 G2HU	Ig gamma-2 chain C
10	458	78.3	328	2 I47160	Ig gamma-2 chain C
11	458	78.3	328	2 I47159	Ig gamma-2a chain
12	453	77.4	277	2 I47162	Ig gamma-4 chain c
13	447	76.4	470	2 S22080	Ig heavy chain pre
14	445	76.1	333	2 PS0018	Ig gamma-2b chain
15	435	74.4	323	1 GHRB	Ig gamma chain C r
16	435	74.4	328	2 I47161	Ig gamma 3 chain c
17	435	74.4	328	2 I47158	Ig gamma 1 chain C
18	432	73.8	329	1 G2GP	Ig gamma-2 chain C
19	428	73.2	308	2 C30554	Ig heavy chain C r
20	428	73.2	472	2 S31459	Ig gamma-1 chain -
21	419	71.6	329	1 G3MSC	Ig gamma-3 chain C
22	419	71.6	398	1 G3MSM	Ig gamma-3 chain C
23	410	70.1	327	2 S06611	Ig gamma-2 chain C
24	405	69.2	335	1 G2MSAB	Ig gamma-2a chain
25	401	68.5	330	1 G2MSA	Ig gamma-2a chain
26	401	68.5	399	1 G2MSAM	Ig gamma-2a chain
27	401	68.5	469	2 S37483	Ig gamma-2a chain
28	400	68.4	329	2 S00847	Ig gamma-2c chain
29	400	68.4	405	1 G2MSBM	Ig gamma-2b chain

30	400	68.4	474	1 G2MS11	Ig gamma-2b chain
31	396.5	67.8	324	1 GIMS	Ig gamma-1 chain C
32	396.5	67.8	393	1 GIMS	Ig gamma-1 chain C
33	396.5	67.8	444	2 PC4436	monoclonal antibod
34	391	66.8	446	2 S40295	Ig gamma-2a chain
35	386	66.0	475	2 S01321	Ig gamma-2b chain
36	380	65.0	326	2 PS0017	Ig gamma-1 chain C
37	339	57.9	322	2 PS0019	Ig gamma-2a chain
38	309	52.8	112	2 B30503	Ig gamma-2a chain
39	276	47.2	88	2 A30503	Ig gamma-2b chain
40	249	42.6	180	2 I46732	Ig gamma heavy cha
41	167.5	28.6	426	2 I36948	Ig epsilon-chain -
42	166.5	28.5	428	1 EHHU	Ig epsilon chain C
43	162	27.7	152	2 S14236	Ig gamma-1 chain C
44	157	26.8	549	2 S04845	Ig heavy chain pre
45	153	26.2	429	1 EHRT	Ig epsilon chain C

ALIGNMENTS

RESULT 1

PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 97.6%; Score 571; DB 2; Length 234;
Best Local Similarity 97.3%; Pred. No. 1.5e-49;
Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	APELLGGPSVFLPPPKD	TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK	60
Db	25	APELLGGPSVFLPPPKD	TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK	84
QY	61	PREEQNSTYRVVSVLT	VLHQLDNLGKEYKCKVSNKGLPSSIEKTISKAK	110
Db	85	PREEQNSTYRVVSVLT	VLHQLDNLGKEYKCKVSNKGLPSSIEKTISKAK	134

RESULT 2

S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filpula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FIL>
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 97.6%; Score 571; DB 4; Length 255;

Best Local Similarity 97.3%; Pred. No. 1.6e-49; Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Db 39 APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK 98

QY 61 PREEQVNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKGLPSSIEKTSKAK 110

Db 99 PREEQVNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKTISKAK 148

RESULT 3

GHHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999

C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers,

A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A:Reference number: S33887; MUID:83001943

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113-235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A:Reference number: A90563; MUID:71064024

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-197,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,

A:Note: this sequence has the Gln(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A:Reference number: A90564; MUID:71064025

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'O',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,

A:Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

igen Primaerstruktur.

A:Reference number: A91668; MUID:77070269

A:Contents: myeloma protein Nie

A:Accession: B91668

A:Molecule type: protein

A:Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27

A:Note: this sequence has the Gln(17) and Gln(1) markers

R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983

A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1

A:Reference number: A91723; MUID:83289131

A:Contents: myeloma protein KOL; disulfide bonds

A:Accession: A91723

A:Molecule type: protein

A:Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <

A:Note: this sequence has the Gln(3) and Gln(non-1) markers

R:Galli, W.E.; Edelman, G.M.

Biochemistry 9, 3188-3196, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul

A:Reference number: A90565; MUID:71064027

A:Contents: annotation; disulfide bonds

R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976

A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunog

enbromide cleavage products, and the disulfide bridges.

A:Reference number: A91667; MUID:77070267

A:Contents: annotation; disulfide bonds

C:Genetics:

A:Gene: GDB:IGHG1

A:Cross-references: GDB:120085; OMIM:147100

A:Map position: 14q32.33-14q32.33

A:introns: 99/1: 114/1; 224/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:137-206/Domain: immunoglobulin homology <IM2>

F:243-310/Domain: immunoglobulin homology <IM3>

F:27-83,144-204,250-308/Disulfide bonds: #status experimental

F:103/Disulfide bonds: interchain (to light chain) #status experimental

F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental

F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 97.6%; Score 571; DB 1; Length 330;

Best Local Similarity 97.3%; Pred. No. 2.2e-49;

Matches 107; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

Db 114 APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK 173

QY 61 PREEQVNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKGLPSSIEKTSKAK 110

Db 174 PREEQVNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKTISKAK 223

RESULT 4

S69339

Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000

C:Accession: S69339; S72664

R:Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 229, 54-60, 1995

A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A:Reference number: S69339; MUID:95262687

A:Accession: S69339

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-374 <KHA>

A:Cross-references: EMBL:X81695

R:Khamlichi, A.A.

submitted to the EMBL Data Library, September 1994

A:Reference number: S72664

A:Accession: S72664

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-140,'C',142-374 <KH2>

A:Cross-references: EMBL:X81695

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 con
A;Reference number: A60764; MUID:90007613
A;Accession: A60764
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 94.5%; Score 553; DB 2: Length 377;
Best Local Similarity 93.6%; Pred. No. 1.6e-47;
Matches 103; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNATK 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 161 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNATK 220

QY 61 PREEQYNSTRVSVLTVLHDWLNGLNGEYCKVSKNKGLPSSIEKTISKAK 110
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 221 PREEQYNSTRVSVLTVLHDWLNGLNGEYCKVSKNKGLPAPIEKTISKTK 270

RESULT 7
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:
A;Reference number: A23511; MUID:86148507
A;Accession: A23511
A:Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:l19339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 94.5%; Score 553; DB 2: Length 377;
Best Local Similarity 93.6%; Pred. No. 1.6e-47;
Matches 103; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNATK 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 161 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNATK 220

QY 61 PREEQYNSTRVSVLTVLHDWLNGLNGEYCKVSKNKGLPSSIEKTISKAK 110
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 221 PREEQYNSTRVSVLTVLHDWLNGLNGEYCKVSKNKGLPAPIEKTISKTK 270

RESULT 8
G3HUWI
Ig gamma-3 heavy chain disease proteins - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C;Accession: A90442; A92219; A90198; A93915; A02149
R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 hea


```
Db 174 QNSTRVVSVLVVHQDWLNGKCKVSNKGLPAPIEKTSKTK 219
[::::::::::::::::::::::::::::::::::::::::::::::::::]
RESULT 10
I47160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845
A:Accession: I47160
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C:Genetics:
A:Gene: IgG2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 458; DB 2; Length 328;
Best Local Similarity 78.8%; Pred. No. 4.2e-38;
Matches 82; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

QY 7 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66
[::::::::::::::::::::::::::::::::::::::::::::::::::]
Db 116 GPSVFIFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQF 175
[::::::::::::::::::::::::::::::::::::::::::::::::::]

QY 67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
[::::::::::::::::::::::::::::::::::::::::::::::::::]
Db 176 NSTYRVVSVLPIQHQLWNGKEFKCKVNNKDLPAITRIISKAK 219
[::::::::::::::::::::::::::::::::::::::::::::::::::]

RESULT 11
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C:Genetics:
A:Gene: IgG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 458; DB 2; Length 328;
Best Local Similarity 78.8%; Pred. No. 4.2e-38;
Matches 82; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

QY 7 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66
[::::::::::::::::::::::::::::::::::::::::::::::::::]
Db 116 GPSVFIFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQF 175
[::::::::::::::::::::::::::::::::::::::::::::::::::]

QY 67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
[::::::::::::::::::::::::::::::::::::::::::::::::::]
Db 176 NSTYRVVSVLPIQHQLWNGKEFKCKVNNKDLPAITRIISKAK 219
[::::::::::::::::::::::::::::::::::::::::::::::::::]

RESULT 12
I47162
Ig gamma 4 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47162
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845
A:Accession: I47162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C:Genetics:
A:Gene: IgG4
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 453; DB 2; Length 277;
Best Local Similarity 77.9%; Pred. No. 1.1e-37;
Matches 81; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 7 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66
[::::::::::::::::::::::::::::::::::::::::::::::::::]
Db 65 GPSAFIFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQF 124
[::::::::::::::::::::::::::::::::::::::::::::::::::]

QY 67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
[::::::::::::::::::::::::::::::::::::::::::::::::::]
Db 125 NSTYRVVSVLPIQHQLWNGKEFKCKVNNKDLPAITRIISKAK 168
[::::::::::::::::::::::::::::::::::::::::::::::::::]

RESULT 13
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S22080; S06610; A31303
R:Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22080
A:Accession: S22080
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-470 <SAN>
A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and 9
A:Reference number: S06610; MUID:90097956
A:Accession: S06610
A:Molecule type: DNA
A:Residues: 142-470 <SYM>
A:Cross-references: EMBL:X16701
A:Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: Ig CH gamma-1
A:Introns: 98/1; 111/1; 221/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IMM>
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.4%; Score 447; DB 2; Length 470;
Best Local Similarity 74.3%; Pred. No. 8e-37;
Matches 81; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 2 PELGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
[::::::::::::::::::::::::::::::::::::::::::::::::::]
Db 253 PELPGPSVFIFFPKPKDTLTISGTEVTCVVVDVGHDDPEVDFSWFVDVENVATATKP 312
[::::::::::::::::::::::::::::::::::::::::::::::::::]
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Db 174 QNSTRVVSVLVVHQDWLNGKCKVSNKGLPAPIEKTSKTK 219
[::::::::::::::::::::::::::::::::::::::::::::::::::]
RESULT 10
I47160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47162
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845
A:Accession: I47162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C:Genetics:
A:Gene: IgG4
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 453; DB 2; Length 277;
Best Local Similarity 77.9%; Pred. No. 1.1e-37;
Matches 81; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 7 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66
[::::::::::::::::::::::::::::::::::::::::::::::::::]
Db 65 GPSAFIFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQF 124
[::::::::::::::::::::::::::::::::::::::::::::::::::]

QY 67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
[::::::::::::::::::::::::::::::::::::::::::::::::::]
Db 125 NSTYRVVSVLPIQHQLWNGKEFKCKVNNKDLPAITRIISKAK 168
[::::::::::::::::::::::::::::::::::::::::::::::::::]

RESULT 13
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S22080; S06610; A31303
R:Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22080
A:Accession: S22080
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-470 <SAN>
A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and 9
A:Reference number: S06610; MUID:90097956
A:Accession: S06610
A:Molecule type: DNA
A:Residues: 142-470 <SYM>
A:Cross-references: EMBL:X16701
A:Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: Ig CH gamma-1
A:Introns: 98/1; 111/1; 221/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IMM>
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.4%; Score 447; DB 2; Length 470;
Best Local Similarity 74.3%; Pred. No. 8e-37;
Matches 81; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 2 PELGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
[::::::::::::::::::::::::::::::::::::::::::::::::::]
Db 253 PELPGPSVFIFFPKPKDTLTISGTEVTCVVVDVGHDDPEVDFSWFVDVENVATATKP 312
[::::::::::::::::::::::::::::::::::::::::::::::::::]
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QY 62 REEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTISKAK 110
|||||:||||| | : |||| | |||: |||: | : |||: |
Db 313 REEQFNSTYRVSVSALRIQHODWTGGKFKCKVHNEGLPAPIVRTISRTK 361
|||||:||||| | : |||| | |||: |||: | : |||: |

RESULT 14
PS0018
Ig gamma-2b chain C region - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Jul-1999
C;Accession: PS0018; B25941
R;Brueggemann, M.
Gene 74, 473-482, 1988
A;Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.
A;Reference number: PS0017; MUID:89232738
A;Accession: PS0018
A;Molecule type: DNA
A;Residues: 1-333 <BRU>
R;Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A;Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody
A;Reference number: A25941; MUID:86287397
A;Accession: B25941
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 227-333 <BR2>
C;Genetics:
A;Introns: 96/1; 117/1; 227/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-82/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 445; DB 2; Length 333;
Best Local Similarity 72.5%; Pred. No. 8.4e-37;
Matches 79; Conservative 18; Mismatches 12; Indels 0; Gaps 0;
QY 2 PELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
|||||:||||| | : |||| | |||: |||: | : |||: |
Db 118 PELLGGPSVFIFPPKPKDILLISQNAKVTCCVVVDVSEEDPDVQFSWVNVEVHTAQTP 177
|||||:||||| | : |||| | |||: |||: | : |||: |

QY 62 REEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTISKAK 110
|||||:||||| | : |||| | |||: |||: | : |||: |
Db 178 REEQYNSTFRVSALPIQHODWMSGKFKCKVNNKALPSPIEKTISKPK 226
|||||:||||| | : |||| | |||: |||: | : |||: |

RESULT 15
GHRB
Ig gamma chain C region - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 16-Jul-1999
C;Accession: A91749; A90290; A93928; A90245; A94416; A02161
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot
A;Reference number: A91749; MUID:84030930
A;Accession: A91749
A;Molecule type: mRNA
A;Residues: 1-323 <BER>
A;Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R;Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob
A;Reference number: A90290; MUID:76135469
A;Accession: A90290
A;Molecule type: protein
A;Residues: 1-47, E', 49-71, 'PV', 72-128 <PRA>
R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A;Title: Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma heavy chain
A;Reference number: A93928; MUID:83299917
A;Accession: A93928

A;Molecule type: mRNA
A;Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A;Cross-references: GB:M16426; NID:gl65111; PIDN:AAA31289.1; PID:gl65112
A;Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic ma
R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobul
A;Reference number: A90245; MUID:70110015
A;Accession: A90245
A;Molecule type: protein
A;Residues: 132-143, 'E', 145-161 <FRU>
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wikse
A;Reference number: A94416
A;Accession: A94416
A;Molecule type: protein
A;Residues: 129-131; 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, '
A;Note: this has the e15 allotypic marker, 185-Ala
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (h
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-82/Domain: immunoglobulin homology <IM1>
F;130-199/Domain: immunoglobulin homology <IM2>
F;236-303/Domain: immunoglobulin homology <IM3>
F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 74.4%; Score 435; DB 1; Length 323;
Best Local Similarity 72.5%; Pred. No. 8.1e-36;
Matches 79; Conservative 13; Mismatches 17; Indels 0; Gaps 0;
QY 2 PELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
|||||:||||| | : |||| | |||: |||: | : |||: |
Db 108 PELLGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSDDDPEVQFTWYINNEQVTRAPPL 167
|||||:||||| | : |||| | |||: |||: | : |||: |

QY 62 REEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTISKAK 110
|||||:||||| | : |||| | |||: |||: | : |||: |
Db 168 REEQFNSTIRVSVTLPIHODWLRGKFKCKVNNKALPAPIERTISKAR 216
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Search completed: June 21, 2002, 08:37:55
Job time: 429 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:32:15 ; Search time 77.71 Seconds
(without alignments)
34.575 Million cell updates/sec

Title: US-09-674-857-7
Perfect score: 583
Sequence: 1 APELGGSVFLFPKPKDT.....CKVSNKGLPSSIEKTIKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	583	100.0	110	3	US-08-444-644-44
2	583	100.0	110	4	US-08-232-246A-44
3	583	100.0	327	2	US-08-761-277A-47
4	583	100.0	382	1	US-08-470-299-7
5	583	100.0	443	5	PCT-US96-13152-4
6	583	100.0	467	1	US-08-704-744-81
7	583	100.0	467	2	US-07-916-098A-45
8	583	100.0	467	4	US-08-523-89A-8
9	579	99.3	109	2	US-08-070-116A-4
10	576	98.8	382	1	US-08-470-299-10
11	576	98.8	467	4	US-08-523-89A-10
12	576	98.8	467	4	US-08-523-89A-12
13	570	97.8	326	3	US-08-808-720-3
14	570	97.8	328	3	US-08-808-720-1
15	570	97.8	331	3	US-08-808-720-5
16	570	97.8	331	3	US-08-808-720-7
17	556	95.4	468	4	US-09-485-737B-67
18	556	95.4	711	4	US-09-485-737B-90
19	551	94.5	110	3	US-08-444-644-21
20	551	94.5	110	4	US-08-232-246A-21
21	551	94.5	116	2	US-08-232-539D-55
22	551	94.5	212	1	US-08-430-633-4
23	551	94.5	212	2	US-08-620-694A-4
24	551	94.5	212	2	US-08-936-85A-4
25	551	94.5	212	3	US-09-022-255-4
26	551	94.5	212	3	US-09-022-696-4
27	551	94.5	212	3	US-09-022-253-4

28	551	94.5	212	3	US-09-022-260-4	Sequence 4, Appli
29	551	94.5	212	4	US-09-022-259-4	Sequence 4, Appli
30	551	94.5	212	4	US-09-022-257-4	Sequence 4, Appli
31	551	94.5	232	2	US-08-595-043A-50	Sequence 50, Appli
32	551	94.5	235	4	US-09-131-247-6	Sequence 6, Appli
33	551	94.5	254	2	US-08-284-391B-33	Sequence 33, Appli
34	551	94.5	254	4	US-09-218-950-33	Sequence 33, Appli
35	551	94.5	316	4	US-09-178-869-4	Sequence 4, Appli
36	551	94.5	331	4	US-09-178-869-2	Sequence 2, Appli
37	551	94.5	347	1	US-07-940-861-43	Sequence 43, Appli
38	551	94.5	347	1	US-08-459-512-43	Sequence 43, Appli
39	551	94.5	347	2	US-08-459-657-43	Sequence 43, Appli
40	551	94.5	347	2	US-08-460-132-43	Sequence 43, Appli
41	551	94.5	347	4	US-08-466-465-8	Sequence 8, Appli
42	551	94.5	347	5	PCT-US92-02050-43	Sequence 43, Appli
43	551	94.5	360	4	US-09-180-100-11	Sequence 11, Appli
44	551	94.5	371	1	US-08-236-311-7	Sequence 7, Appli
45	551	94.5	371	3	US-08-457-918-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-444-644-44
; Sequence 44, Application US/08444644
; Patent No. 601555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

APPLICANT: Murphy, Kay E.
APPLICANT: Chapman, Conrad G.
APPLICANT: Clinkensbeard, Helen E.
APPLICANT: Young, Peter R.
APPLICANT: Shatzman, Allan R.
TITLE OF INVENTION: No. 5783181el Compounds
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,299
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P31005C3
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-470-299-7

Query Match 100.0%; Score 583; DB 1; Length 382;
Best Local Similarity 100.0%; Pred. No. 7.3e-63;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVHNATK 60
|||||
Db 166 APEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVHNATK 225
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QY 61 PREEQFNSTYRVSVTLVTLHQDLNKGCKYCKVSNKGLPSSIEKTISKAK 110
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Db 226 PREEQFNSTYRVSVTLVTLHQDLNKGCKYCKVSNKGLPSSIEKTISKAK 275
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RESULT 5
PCT-US96-13152-4
Sequence 4, Application PC/TUS9613152
GENERAL INFORMATION:
APPLICANT: Martin, Ulrich, et al.
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
ADDRESSEE: Attn: Norman D. Hanson
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/13152
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 443
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-13152-4

Query Match 100.0%; Score 583; DB 5; Length 443;
Best Local Similarity 100.0%; Pred. No. 8.9e-63;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVHNATK 60
|||||
Db 227 APEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVHNATK 286
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QY 61 PREEQFNSTYRVSVTLVTLHQDLNKGCKYCKVSNKGLPSSIEKTISKAK 110
|||||
Db 287 PREEQFNSTYRVSVTLVTLHQDLNKGCKYCKVSNKGLPSSIEKTISKAK 336
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RESULT 6
US-08-704-744-81
Sequence 81, Application US/08704744
Patent No. 5705154
GENERAL INFORMATION:
APPLICANT: Dallee, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.3
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,744
FILING DATE: 06-SEPT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208886
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: PCT/US/95/02400
FILING DATE: 08-MAR-1995
ATTORNEY/AGENT INFORMATION:

US-08-704-744-81

Db 251 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDSOEDPEVQFNWYVDGVEVHNAKTK 310

/ APPLICANT: Newman, Roland A.
 / APPLICANT: Reff, Mitchell E.
 / TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
 / TITLE OF INVENTION: Therapy
 / NUMBER OF SEQUENCES: 59
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 / STREET: 699 Prince Street
 / CITY: Alexandria
 / STATE: VA
 / COUNTRY: USA
 / ZIP: 22314-3187

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/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/
/ NAME: Teskin, Robin L.
/
/ REGISTRATION NUMBER: 35,030
/ REFERENCE/DOCKET NUMBER: 012712-165
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-836-6620
/ TELEFAX: 703-836-2021
/
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 467 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-523-894-8

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Query Match      100.0%; Score 583; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.6e-63;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 PREEQFNSTYRVSVTLVHQDLNGKEYCKVSNKGLPSSIEKTISKAK 110
Db 311 PREEQFNSTYRVSVTLVHQDLNGKEYCKVSNKGLPSSIEKTISKAK 360

RESULT 9

US-08-070-116A-4
; Sequence 4, Application US/08070116A
; Patent No. 5885573
; GENERAL INFORMATION:
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Bluestone, Jeffrey A.
; TITLE OF INVENTION: Methods and Materials For Modulation
; TITLE OF INVENTION: of the Immuno-suppressive Activity and
; TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,116A
; FILING DATE: 01-JUN-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-070-116A-4

Query Match 99.3%; Score 579; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4e-63;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PEFLLGSPSVFLPPPKDITLMSRTPEVTCVVVDVSDPEVFQFNWYDGVGVHNAKTKP 61
Db 1 PEFLLGSPSVFLPPPKDITLMSRTPEVTCVVVDVSDPEVFQFNWYDGVGVHNAKTKP 60
QY 62 REEQFNSTYRVSVTLVHQDLNGKEYCKVSNKGLPSSIEKTISKAK 110
Db 61 REEQFNSTYRVSVTLVHQDLNGKEYCKVSNKGLPSSIEKTISKAK 109

RESULT 10

US-08-470-299-10
; Sequence 10, Application US/08470299
; Patent No. 5783181
; GENERAL INFORMATION:
; APPLICANT: Browne, Michael J.
; APPLICANT: Murphy, Kay E.
; APPLICANT: Chapman, Conrad G.
; APPLICANT: Clinkbeard, Helen E.
; APPLICANT: Young, Peter R.
; APPLICANT: Shatzman, Allan R.

; TITLE OF INVENTION: No. 5783181el Compounds
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,299
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P31005C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-470-299-10

Query Match 98.8%; Score 576; DB 1; Length 382;
Best Local Similarity 99.1%; Pred. No. 5.2e-62;
Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLPPPKDITLMSRTPEVTCVVVDVSDPEVFQFNWYDGVGVHNAKTK 60
Db 166 APEFEGGPSVFLPPPKDITLMSRTPEVTCVVVDVSDPEVFQFNWYDGVGVHNAKTK 225
QY 61 PREEQFNSTYRVSVTLVHQDLNGKEYCKVSNKGLPSSIEKTISKAK 110
Db 226 PREEQFNSTYRVSVTLVHQDLNGKEYCKVSNKGLPSSIEKTISKAK 275

RESULT 11

US-08-523-894-10
; Sequence 10, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995

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; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-523-894-10

Query Match          98.8%; Score 576; DB 4; Length 467;
Best Local Similarity 99.1%; Pred. No. 6.8e-62;
Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 251 APEFEGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 310

QY 61 PREEQFNSTYRVVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 311 PREEQFNSTYRVVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 360

RESULT 12
US-08-523-894-12
; Sequence 12, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-523-894-12
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Query Match          98.8%; Score 576; DB 4; Length 467;
Best Local Similarity 99.1%; Pred. No. 6.8e-62;
Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 251 APEFEGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 310

QY 61 PREEQFNSTYRVVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 311 PREEQFNSTYRVVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 360

RESULT 13
US-08-808-720-3
; Sequence 3, Application US/08808720
; Patent No. 6100387
; GENERAL INFORMATION:
; APPLICANT: Herrmann, Steve
; APPLICANT: Swanberg, Stephen
; TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
; TITLE OF INVENTION: CHEMOKINE DOMAINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,720
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne
; REGISTRATION NUMBER: P-41,323
; REFERENCE/DOCKET NUMBER: G15291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 498-8284
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 326 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-808-720-3

Query Match          97.8%; Score 570; DB 3; Length 326;
Best Local Similarity 98.2%; Pred. No. 2.2e-61;
Matches 108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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Db 110 APEFEGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 169

QY 61 PREEQFNSTYRVVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 170 PREEQFNSTYRVVSVLTVHLQDWLNGKEYCKVSNKGLPSSIEKTIKAK 219

RESULT 14
US-08-808-720-1
; Sequence 1, Application US/08808720
; Patent No. 6100387
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; GENERAL INFORMATION:
; APPLICANT: Herrmann, Steve
; APPLICANT: Swanberg, Stephen
; TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
; TITLE OF INVENTION: CHEMOKINE DOMAINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/808,720
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne
; REGISTRATION NUMBER: P-41,323
; REFERENCE/DOCKET NUMBER: G15291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-808-720-1

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Query Match          97.8%; Score 570; DB 3; Length 328;
Best Local Similarity 98.2%; Pred. No. 2.3e-61;
Matches 108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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Db 112 APEFGAPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 171

QY 61 PREEQFNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
    ||||| 1 |||||
Db 172 PREEQFNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 221

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RESULT 15
US-08-808-720-5
; Sequence 5, Application US/08808720
; Patent No. 6100387
; GENERAL INFORMATION:
; APPLICANT: Herrmann, Steve
; APPLICANT: Swanberg, Stephen
; TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
; TITLE OF INVENTION: CHEMOKINE DOMAINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,720
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne
; REGISTRATION NUMBER: P-41,323
; REFERENCE/DOCKET NUMBER: G15291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-808-720-5

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Query Match          97.8%; Score 570; DB 3; Length 331;
Best Local Similarity 98.2%; Pred. No. 2.3e-61;
Matches 108; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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Db 115 APEFGAPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 174

QY 61 PREEQFNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
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Db 175 PREEQFNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 224

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Job time: 90 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:36:08 ; Search time 224.82 Seconds
(without alignments)
54.346 Million cell updates/sec

Title: US-09-674-857-7
Perfect score: 583
Sequence: 1 APEFLGSPVFLFPKPKDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	583	100.0	218	AA191717	Amino acid sequenc
3	583	100.0	218	AA191717	Human IgG4. Homo
4	583	100.0	218	AA191717	Human IgG4 FC regi
5	583	100.0	327	AA191717	Immunoglobulin C-g
6	583	100.0	329	AA191717	Amino acid sequenc
7	583	100.0	329	AA191717	Human IgG1 C-gamma
8	583	100.0	382	AA191717	IL4.Y124D/IgG4 pro
9	583	100.0	396	AA191717	Leptin 1-167/IgG4
10	583	100.0	432	AA191717	Human IFN-beta and
11	583	100.0	433	AA191717	Interferon alpha-i

12	583	100.0	443	18	AA191717	Humanised anti-L-s
13	583	100.0	444	20	AA191717	Human IgG4 chain C
14	583	100.0	463	18	AA191717	2A2 Human IgG4 exp
15	583	100.0	463	18	AA191717	Murine anti-porcine
16	583	100.0	464	18	AA191717	3F4 Human IgG4 exp
17	583	100.0	464	18	AA191717	Murine anti-porcine
18	583	100.0	467	16	AA191717	Anti-human IL-4 hu
19	583	100.0	467	18	AA191717	Human gamma-4 heav
20	583	100.0	468	13	AA191717	pre-5A8 humanised
21	583	100.0	564	21	AA191717	Human ACAM4/IgG4-F
22	583	100.0	598	21	AA191717	Human ACAM6/IgG4-F
23	583	100.0	751	21	AA191717	Human secreted K10
24	583	100.0	784	21	AA191717	Human secreted K10
25	579	99.3	109	16	AA191717	OKT3 monoclonal an
26	577	99.0	447	18	AA191717	TF8-5G9 CDR-grafte
27	576	98.8	382	17	AA191717	IL4.Y124D/IgG4 PE
28	576	98.8	396	18	AA191717	Leptin 1-167/IgG4
29	576	98.8	467	18	AA191717	Human gamma-4PE he
30	576	98.8	467	18	AA191717	Human gamma-4E hea
31	573	98.3	464	12	AA191717	CD4-specific CDR-g
32	570	97.8	326	19	AA191717	Human chemokine SD
33	570	97.8	328	19	AA191717	Human chemokine SD
34	570	97.8	331	19	AA191717	Human chemokine MI
35	570	97.8	331	19	AA191717	Human chemokine MI
36	570	97.8	374	18	AA191717	CTLA4-IgG4 fusion
37	570	97.8	374	18	AA191717	CTLA4-modified IgG
38	570	97.8	422	20	AA191717	P-selectin ligand
39	570	97.8	533	20	AA191717	P-selectin ligand
40	570	97.8	646	20	AA191717	P-selectin ligand
41	566	97.1	462	22	AA191717	Humanised 323/A3 (
42	566	96.1	462	22	AA191717	Humanised 323/A3 (
43	556	95.4	468	20	AA191717	D9D10 heavy chain
44	556	95.4	711	20	AA191717	MoTAblII fusion pro
45	552	94.7	462	18	AA191717	2A2 (Chimeric) hum

ALIGNMENTS

RESULT 1

AA191717
ID AAR41717 standard; Protein; 110 AA.
AC AAR41717;
XX
XX 20-OCT-1993 (first entry)
XX Undefined ORF2 encoded by plasmid pAH4808.
XX Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625;
KW heavy; light; chain; variable; constant; region; anti-human; pAH4807;
KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
KW endothelial cell; conjugate; neuropharmacological; gamma-3; gamma-4;
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
KW Parkinsons disease; Alzheimers disease; SP2/0 cell.
XX Synthetic.
XX
XX WO9310819-A.
XX
XX 10-JUN-1993.
XX
XX 24-NOV-1992; 92WO-US10206.
XX
XX 26-NOV-1991; 91US-0800458.
XX (ALKE-) ALKERMES INC.
XX
XX Friden PM;
XX
XX WPI; 1993-196742/24.
XX
XX N-PSDB; AAQ43848.

PT Antibody conjugates specific for transferrin receptor - used
 PT for diagnosis and treatment of cancer, AIDS and neurological
 XX disorders

PS Disclosure; Fig 19U; 151pp; English.

XX The sequences given in AAR41715-18 are encoded by the expression vector
 CC PAH4808. This vector represents the cloning of the human gamma
 CC isotype, gamma-4, with the variable region of the murine monoclonal
 CC antibody 128.1. This plasmid encodes a chimeric monoclonal antibody
 CC in which the heavy chain (VH) is derived from a murine source and the
 CC sequences encoding CH1, CH2 and CH3 are derived from a human source.
 CC This vector, in combination with the chimeric light chain vector,
 CC pK4611 (see also AAQ43845), was transfected into Sp2/0 cells and clones
 CC were isolated. 128.1 is an anti-human transferrin receptor antibody
 CC which binds to the transferrin receptor on brain capillary endothelial
 CC cells. This antibody may be used in a conjugate in which it is linked
 CC to a neuropharmaceutical or diagnostic agent. The conjugate may be
 CC used to treat or prevent neurological disorders eg. brain tumours,
 CC AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may
 CC also be used for diagnostic methods.

XX Sequence 110 AA;

Query Match 100.0%; Score 583; DB 14; Length 110;
 Best Local Similarity 100.0%; Pred. No. 4.5e-53;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEFLGSPVFLFPKPKDLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVVHNATK 60
 Db 1 apeflgspvflfpkpkdltmsrtpevtcvvvdvsqedpevqfnwvydgvvhnatk 60

QY 61 PREQFNSTYRVSVLTVLHODMLNGKEYCKVSNKGLPSSIEKTISKAK 110
 Db 61 preeqfnstyrsvsvltvlhqdwlngkeyckvsnkglpssiektiskak 110

RESULT 2

AAB07478
 ID AAB07478 standard; protein; 218 AA.

XX AAB07478;

XX 20-OCT-2000 (first entry)

XX Amino acid sequence of native IgG Fc region humIgG4.

XX IgG antibody; light chain; Fc region; effector function; cancer;
 KW allergy; asthma; LFA-1-mediated disorder; tumour; cancer.

XX Homo sapiens.

XX WO200042072-A2.

XX 20-JUL-2000.

XX 14-JAN-2000; 2000WO-US00973.

XX 15-JAN-1999; 99US-0116023.

XX (GETH) GENENTECH INC.

XX Presta LG;

XX WPI; 2000-476035/41.

XX New Fc region-containing polypeptides that have altered effector
 PT function due to one or more amino acid modifications in the Fc region,
 PT useful in the treatment of cancer and allergic conditions such as
 PT asthma -

XX Disclosure; Fig 22A; 132pp; English.

XX

CC AAB07474-78 represent native IgG Fc regions. The proteins are used to
 CC produce Fc region-containing polypeptides that have altered effector
 CC function as a consequence of one or more amino acid modifications in
 CC the Fc region. The variant polypeptides are useful for treating
 CC cancer, allergic conditions such as asthma (with an anti-IgE antibody),
 CC and LFA-1-mediated disorders. Where the polypeptide binds the HER2
 CC receptor, the disorder preferably is HER2-expressing cancer, e.g. a
 CC benign or malignant tumour characterized by overexpression of the
 CC HER2 receptor. Such cancers include breast cancer, squamous cell
 CC cancer, small-cell lung cancer, non-small cell lung cancer,
 CC gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical
 CC cancer, ovarian cancer, bladder cancer, hepatoma, colon cancer,
 CC colorectal cancer, endometrial carcinoma, salivary gland carcinoma,
 CC kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid
 CC cancer, hepatic carcinoma and various types of head and neck cancer.

XX Sequence 218 AA;

Query Match 100.0%; Score 583; DB 21; Length 218;
 Best Local Similarity 100.0%; Pred. No. 1e-52;
 Matches 110; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 APEFLGSPVFLFPKPKDLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVVHNATK 60
 Db 2 apeflgspvflfpkpkdltmsrtpevtcvvvdvsqedpevqfnwvydgvvhnatk 61

QY 61 PREQFNSTYRVSVLTVLHODMLNGKEYCKVSNKGLPSSIEKTISKAK 110
 Db 62 preeqfnstyrsvsvltvlhqdwlngkeyckvsnkglpssiektiskak 111

RESULT 3

AAB67205
 ID AAB67205 standard; protein; 218 AA.

XX AAB67205;

XX 10-APR-2001 (first entry)

XX Human IgG4.

XX Fusion protein; immunoglobulin; multidimerization domain; ligand.

XX Homo sapiens.

XX WO200102440-A1.

XX 11-JAN-2001.

XX 30-JUN-2000; 2000WO-US18185.

XX 02-JUL-1999; 99US-0142088.

XX (GETH) GENENTECH INC.

XX Dennis MS, Lazarus RA;

XX WPI; 2001-123106/13.

XX Novel fusion polypeptides comprising a peptide ligand domain which
 PT functions to target hybrid molecule to target cell, and immunoglobulin
 PT constant region multimerization domain -

XX Disclosure; Fig 2; 69pp; English.

XX The present invention relates to a fusion protein, comprising a
 CC peptide ligand and an immunoglobulin (Ig) constant region
 CC multimerization domain (IB). The hybrid molecules comprising
 CC the peptide ligands and their functional derivatives can be used
 CC in the same applications as, a peptide ligand can be used. For
 CC example the peptide ligand can bind ErbB2. The peptide ligand

CC may kind to and inhibit the activity associated with a particular
 XX target molecule.

SQ Sequence 218 AA;

Query Match 100.0%; Score 583; DB 22; Length 218;
 Best Local Similarity 100.0%; Pred. No. 1e-52;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEFLGSPSVFLPPKPKDTLMSRTPEVTCVVVDVSDQEDPEVFQFNWYDGVGVHNAKTK 60
 |||||
 Db 2 apeflgspsvflppkpkdtlmsrtpevtcvcvvdvsqdepevfqfnwvdgvvhnaktk 61
 |||||

QY 61 PREQFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKSAK 110
 |||||
 Db 62 preeqfnstyrvvsvltvlhqdwlngkeyckvsnkglpssiektiskak 111
 |||||

RESULT 4

AAW37346 standard; Protein; 218 AA.
 XX
 AC AAW37346;
 XX
 DT 10-APR-2001 (first entry)
 XX
 DE Human IgG4 Fc region amino acid sequence.
 XX
 KW Human; erB2; HER2; cancer; nervous system disease; stroke; ischaemia;
 KW metabolic disorder; nutritional deficiency; Alzheimer's disease;
 KW Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea;
 KW Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.
 XX
 OS Homo sapiens.
 XX
 PN WO200101748-A2.
 XX
 PD 11-JAN-2001.
 XX
 PF 30-JUN-2000; 2000WO-US18283.
 XX
 PR 02-JUL-1999; 99US-0142232.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Dennis MS;
 XX
 DR WPI; 2001-123048/13.
 XX
 PT Non-naturally occurring peptide ligands which compete for binding human
 PT erB2 gene products, useful for treating e.g. Alzheimer's disease,
 PT multiple sclerosis and diabetic neuropathy -
 XX
 PS Disclosure; Figure 2A; 116pp; English.
 XX
 CC This invention relates to non-naturally occurring peptide ligands which
 CC bind to the human erB2 gene product ErbB2 (also known as HER2). Peptides
 CC represented in AAB76430 - AAB76420 and AAB76432 - AAB76509 are examples
 CC of the ErbB2 binding ligands of the invention. Sequences
 CC AAB76421 - AAB76431 represent antibody Fc amino acid sequences used in
 CC the isolation of the peptides of the invention. The peptides compete for
 CC binding ErbB2 with naturally occurring ligands, and may be used to treat
 CC disorders characterized by over expression of HER2/ErbB2 such as cancers,
 CC diseases of the nervous system, musculature and epithelia, e.g. nervous
 CC system damage resulting from trauma, surgery, strokes, ischaemia,
 CC infection, metabolic disorders, nutritional deficiency or toxic agents.
 CC In particular the synthetic peptide ligands may be used to treat
 CC Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis,
 CC Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease
 CC and neuropathy associated with diabetes.

XX Sequence 218 AA;

Query Match 100.0%; Score 583; DB 22; Length 218;
 Best Local Similarity 100.0%; Pred. No. 1e-52;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEFLGSPSVFLPPKPKDTLMSRTPEVTCVVVDVSDQEDPEVFQFNWYDGVGVHNAKTK 60
 |||||
 Db 2 apeflgspsvflppkpkdtlmsrtpevtcvcvvdvsqdepevfqfnwvdgvvhnaktk 61
 |||||

QY 61 PREQFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKSAK 110
 |||||
 Db 62 preeqfnstyrvvsvltvlhqdwlngkeyckvsnkglpssiektiskak 111
 |||||

RESULT 5

AAW37346 standard; Protein; 327 AA.
 XX
 AC AAW37346;
 XX
 DT 11-MAY-1998 (first entry)
 XX
 DE Immunoglobulin C-gamma-4 region.
 XX
 KW Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;
 KW gene amplification; immunotherapy; therapy; immunoglobulin;
 KW C-gamma-4; constant region.
 XX
 OS Homo sapiens.
 XX
 PN WO9741244-A1.
 XX
 PD 06-NOV-1997.
 XX
 PF 25-APR-1997; 97WO-US07039.
 XX
 PR 06-DEC-1996; 96US-0761277.
 XX
 PD 01-MAY-1996; 96US-0644664.
 XX
 PA (GENI-) GENITOPE CORP.
 XX
 PI Denney DW;
 XX
 DR WPI; 1997-549743/50.
 XX
 DR N-PSDB; AAT97189.
 XX
 PT Multivalent vaccine to treat B cell lymphoma or leukaemia -
 PT comprises at least 2 different recombinant variable regions of
 PT immunoglobulin molecules derived from B cell lymphoma cells
 XX
 PS Example 10; Page 126-127; 177pp; English.
 XX
 CC The protein comprises an immunoglobulin (Ig) C-gamma-4 region.
 CC This invention provides a method for the production of tumour-
 CC specific Ig derived from a B-cell lymphoma patient. In the novel
 CC method, expression plasmids containing the patient's VH region(s)
 CC joined to either a C-gamma-3 (see AAT97188) or C-gamma-4 (see AAT97189)
 CC sequence and expression plasmids containing the patient's VL
 CC region(s) joined to either a C-kappa (see AAT97190) or C-lambda-2
 CC (see AAT97191) sequence are cotransfected along with a selectable and
 CC amplifiable marker into a cell line (e.g. BW5147.G.1.4), and
 CC transfected cells are then subjected to selection and amplification.
 CC The method permits the production of a multivalent vaccine which
 CC reflects the degree of somatic variation found within the patient's
 CC tumour. These novel multivalent vaccines provide superior vaccines
 CC for the treatment of B-cell lymphoma.

SQ Sequence 327 AA;

Query Match 100.0%; Score 583; DB 18; Length 327;
 Best Local Similarity 100.0%; Pred. No. 1.7e-52;

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEFLGSPSVLEFPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
 Db 111 afeiflgpsvlfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwvydgvvhnatk 170

QY 61 PREQFNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
 Db 171 preeqfnstyrsvsvltvlhqdwlngkeyckvsnkgplpsiektiskak 220

RESULT 6
 AAW70801
 ID AAW70801 standard; protein; 329 AA.
 AC AAW70801;
 XX
 DT 03-FEB-1999 (first entry)
 DE Amino acid sequence of C-gamma-4.
 KW gp130; cytokine antagonist; interleukin; gamma-interferon;
 KW granulocyte macrophage colony-stimulating factor; J peptide;
 KW transforming growth factor-beta.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Protein 2..329
 FT /note= "C-gamma-4"
 XX
 PN US5844099-A.
 XX
 PD 01-DEC-1998.
 XX
 PF 27-NOV-1995; 95US-0563105.
 XX
 PR 27-NOV-1995; 95US-0563105.
 PR 20-OCT-1993; 93US-0140222.
 XX
 PA (REGE-) REGENERON PHARM INC.
 XX
 PI Economides A, Stahl N, Yancopoulos GD;
 DR WPI; 1999-044669/04.
 XX
 CC Cytokine antagonists - comprising extracellular domains of
 PT specificity-determining and signal-transducing components of
 PT cytokine receptor
 XX
 PS Example 4; Fig 12; 46pp; English.
 XX
 CC The present sequence represents the amino acid sequence of
 CC C-gamma-4. The protein is used in the course of the invention.
 CC The specification describes cytokine antagonists comprising only the
 CC extracellular domain of the specificity-determining component of
 CC the cytokine receptor and the extracellular domain of a
 CC signal-transducing component of the cytokine receptor. The cytokine
 CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
 CC granulocyte macrophage colony-stimulating factor (GM-CSF),
 CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
 CC antagonist is capable of binding the cytokine to form a nonfunctional
 CC complex. The compounds have therapeutic activity as cytokine antagonists
 CC and can also be used in assays for identifying novel agonists and
 CC antagonists of cytokines.
 XX
 SQ Sequence 329 AA;

Query Match 100.0%; Score 583; DB 20; Length 329;
 Best Local Similarity 100.0%; Pred. No. 1.7e-52;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEFLGSPSVLEFPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNATK 60
 Db 113 afeiflgpsvlfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwvydgvvhnatk 172

QY 61 PREQFNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110
 Db 173 preeqfnstyrsvsvltvlhqdwlngkeyckvsnkgplpsiektiskak 222

RESULT 7
 AAY92190
 ID AAY92190 standard; protein; 329 AA.
 AC AAY92190;
 XX
 DT 01-AUG-2000 (first entry)
 DE Human IgG1 C-gamma-4 domain.
 KW gp130-C-gamma-1; cytokine; antagonist; CNTF; receptor; fusion protein;
 KW cytotatic; immunomodulator; osteopathic.
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..2
 FT /note= "Ser-Gly bridge"
 FT Protein 3..329
 FT /label= C-gamma-4
 XX
 PN WO200018932-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 22-SEP-1999; 99WO-US22045.
 XX
 PR 25-SEP-1998; 98US-0101858.
 PR 19-MAY-1999; 99US-0313942.
 XX
 PA (REGE-) REGENERON PHARM INC.
 XX
 PI Stahl N, Yancopoulos GD;
 XX
 DR WPI; 2000-293165/25.
 XX
 CC Isolated nucleic acid molecule for treating cytokine-related diseases
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine
 PT to form a nonfunctional complex
 XX
 PS Example 4; Fig 12; 152pp; English.
 XX
 CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor,
 CC (SR-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (ciliary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specificity determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the

CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.
 XX
 SQ Sequence 329 AA;

Query Match 100.0%; Score 583; DB 21; Length 329;
 Best Local Similarity 100.0%; Pred. No. 1.7e-52;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVVHNATK 60
 |||||
 Db 113 apegfpgpsvflppkpkdtlmisrtpetvcvvdvsqgedpevqfnwvgvevhnakt 172
 |||||
 QY 61 PREQFNSTYRVVSVLTVLHQDLNGKEYKCKVSNKGLPSSIEKTSKAK 110
 |||||
 Db 173 preeqfnstyrvvsvltvlhqdlngkeykckvsnkglpssiektiskak 222

RESULT 8
 AAR90921
 ID AAR90921 standard; Protein; 382 AA.
 XX
 AC AAR90921;
 XX
 DT 09-MAY-1996 (first entry)
 XX
 DE IL4.Y124D/IgG4 protein fusion.
 XX
 KW Interleukin-4; interleukin-13; antagonist; IL-4; IL-13;
 KW immunoglobulin; IgG; constant domain; allergy; autoimmune disease;
 KW chronic infection; IL4.Y124D/IgG4; fusion protein; therapy.
 XX
 OS Synthetic.
 XX
 PN WO9604388-A1.
 XX
 PD 15-FEB-1996.
 XX
 PF 28-JUL-1995; 95WO-EP03036.
 XX
 PR 06-JUN-1995; 95US-0468297.
 PR 29-JUL-1994; 94GB-0013379.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Browne MJ, Chapman CG, Clinkenbeard HE, Murphy KE;
 PI Shatzman AR, Young PR;
 XX
 DR WPI; 1996-129404/13.
 DR N-PSDB; AAT12659.
 XX
 PT New soluble protein antagonists of interleukin-4 and interleukin-13
 PT - comprise IL-4 mutant fused to Ig constant domain, useful in
 PT treating e.g. allergy, autoimmune disease or chronic infection
 XX
 PS Claim 8; Page 27; 35pp; English.

CC A fusion protein (AAR90921) consists of a human interleukin-4 (IL-4)
 CC mutant, IL-4.Y124D, in which tyrosine at position 124 is replaced
 CC by aspartic acid, fused to the hinge-CH2-CH3 region of human IgG4.
 CC It is the product of a gene fusion (AAT12659) constructed in
 CC vector pDB952. The fusion protein can be expressed in host cells,
 CC e.g. HeLa, and used as a soluble IL-4 and/or IL-13 antagonist
 CC to treat conditions caused by undesirable effects of these
 CC interleukins.

Sequence 382 AA;

Query Match 100.0%; Score 583; DB 18; Length 396;
 Best Local Similarity 100.0%; Pred. No. 2.1e-52;

Query Match 100.0%; Score 583; DB 17; Length 382;
 Best Local Similarity 100.0%; Pred. No. 2e-52;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYDGVVHNATK 60
 |||||
 Db 166 apegfpgpsvflppkpkdtlmisrtpetvcvvdvsqgedpevqfnwvgvevhnakt 225
 |||||
 QY 61 PREQFNSTYRVVSVLTVLHQDLNGKEYKCKVSNKGLPSSIEKTSKAK 110
 |||||
 Db 226 preeqfnstyrvvsvltvlhqdlngkeykckvsnkglpssiektiskak 275

RESULT 9
 AAW10534
 ID AAW10534 standard; Protein; 396 AA.
 XX
 AC AAW10534;
 XX
 DT 26-SEP-1997 (first entry)
 XX
 DE Leptin 1-167/IgG4 hinge-CH2-CH3 fusion protein.
 XX
 KW Leptin; ob; obese; immunoglobulin G4; IgG4; hinge-CH2-CH3; fusion;
 KW chimeric; prolonged clearance rate; treatment; prophylaxis;
 KW obesity; atherosclerosis; hypertension; type II diabetes; cosmetic;
 KW body appearance; weight reduction.
 XX
 OS Homo sapiens.
 OS Synthetic.

PH Key Location/Qualifiers
 FT Protein 1..167
 FT /note= "human leptin residues 1-167"
 FT Protein 168-396
 FT /note= "human IgG4 hinge-CH3-CH4 region"
 XX
 PN WO9700319-A2.

XX
 PD 03-JAN-1997.
 XX
 PF 11-JUN-1996; 96WO-GB01388.
 XX
 PR 13-JUN-1995; 95GB-0011935.
 XX
 XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Browne MJ, Chapman CG, Clinkenbeard HE, Robinson JH;
 PI WPI; 1997-077526/07.
 DR N-PSDB; AAT60717.
 XX

PT Chimeric leptin having prolonged clearance rate - useful for
 PT treatment, or prophylaxis of obesity or associated conditions, e.g.
 PT atherosclerosis, hypertension and type II diabetes
 XX
 PS Claim 9; Pages 11-12; 24pp; English.

CC The present sequence is the leptin 1-167/IgG4 hinge-CH2-CH3
 CC fusion protein, which comprises residues 1-167 of human leptin
 CC linked to the hinge-CH2-CH3 region of the human immunoglobulin G4
 CC (IgG4) protein. The chimeric leptin, which has good
 CC pharmacological activity, combined with a prolonged clearance rate,
 CC can be used in the treatment or prophylaxis of obesity or
 CC associated conditions, e.g. atherosclerosis, hypertension and Type
 CC II diabetes. It can also be used in cosmetic treatments for the
 CC improvement of body appearance, e.g. weight reduction treatment.

Sequence 396 AA;

SQ Sequence 433 AA;

Query Match 100.0%; Score 583; DB 18; Length 433;
 Best Local Similarity 100.0%; Pred. No. 2.4e-52;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNKTK 60
 |||
 Db 217 apeflggpsvflfpkpkdtlmisrtpevtcvvdvsgdpevqfnwvydgvvhnaktk 276
 |||

QY 61 PREEFNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAK 110
 |||
 Db 277 preefnstyrsvvltvlhqdlngkeyckvsnkglpssiektiskak 326
 |||

RESULT 12
 AAW13564
 ID AAW13564 standard; Protein; 443 AA.
 XX
 AC AAW13564;
 XX
 DT 03-JUN-1997 (first entry)
 XX
 DE Humanised anti-L-selectin antibody HuDreg 55 heavy chain.
 XX
 KW L-selectin; humanised antibody; HuDreg 55; acute organ damage;
 KW organ failure; poly-trauma; haemorrhagic-traumatic shock.
 XX
 OS Chimeric Mus sp.;
 OS Chimeric Homo sapiens.
 XX
 PN WO9706822-A1.
 XX
 PD 27-FEB-1997.
 XX
 PF 14-AUG-1996; 96WO-US13152.
 XX
 PR 27-DEC-1995; 95US-0578953.
 PR 17-AUG-1995; 95EP-0112895.
 PR 19-SEP-1995; 95EP-0114696.
 XX
 PA (BOE) BOEHRINGER MANNHEIM GMBH.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX
 PI Co M, Haselbeck A, Martin U, Schumacher G;
 XX
 DR WPI; 1997-165036/15.
 DR N-PSDB; AAT61281.
 XX
 PT Using anti-selectin antibody to prevent acute organ damage and
 PT multiple organ failure - during extracorporeal circulation or
 PT following polytrauma, e. g. haemorrhagic-traumatic shock
 XX
 PS Disclosure; Page 34-36; 52pp; English.
 XX
 CC Humanised anti-L-selectin antibody HuDreg 55 comprises 2 heavy
 CC chains each having the sequence given in AAW13564 and 2 light chains
 CC each having the sequence given in AAW13563. These are encoded by the
 CC cDNA clones given in AAT61281 and AAT61280. HuDreg 55 can be used to
 CC prevent multiple organ failure associated with polytrauma and for
 CC the prevention of acute organ damage associated with extracorporeal
 CC blood circulation. The antibody inhibits interaction between the
 CC carbohydrate-recognising domain of the selectin and the
 CC corresponding cell surface receptor.
 XX
 SQ Sequence 443 AA;

Query Match 100.0%; Score 583; DB 18; Length 443;
 Best Local Similarity 100.0%; Pred. No. 2.4e-52;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNKTK 60
 |||
 Db 227 apeflggpsvflfpkpkdtlmisrtpevtcvvdvsgdpevqfnwvydgvvhnaktk 286
 |||

QY 61 PREEFNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAK 110
 |||
 Db 287 preefnstyrsvvltvlhqdlngkeyckvsnkglpssiektiskak 336
 |||

RESULT 13
 AAY31672
 ID AAY31672 standard; Protein; 444 AA.
 XX
 AC AAY31672;
 XX
 DT 09-NOV-1999 (first entry)
 XX
 DE Human IgG4 chain C.
 XX
 KW IgG4; C-gamma-4; antibody; fusion protein; circulating half-life;
 KW human; drug delivery.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..117
 FT /note= "the identity of these residues is not
 FT specified"
 XX
 PN WO9943713-A1.
 XX
 PD 02-SEP-1999.
 XX
 PF 24-FEB-1999; 99WO-US03966.
 XX
 PR 25-FEB-1998; 98US-0075887.
 XX
 PA (LEXI-) LEXIGEN PHARM CORP.
 XX
 PI Gillies SD, Lan Y, Lo K, Wesolowski J;
 XX WPI; 1999-527594/44.
 XX
 PT New antibody-based fusion proteins, used for the delivery of e.g. a
 PT cytokine, ligand-binding protein or protein toxin to target cells in
 PT vivo
 XX
 PS Disclosure; Page 35-36; 41pp; English.
 XX
 CC The present sequence represents the constant region of human IgG
 CC isotype 4 (IgG4, C-gamma-4). C-gamma-1 (see AAY31669) and C-gamma-3
 CC (see AAY31671) bind Fc receptors with high affinity, whereas C-gamma-4
 CC has 10-fold lower binding affinity and C-gamma-2 (see AAY31670) does
 CC not bind to Fc receptor gamma-1. The invention provides methods
 CC for the genetic construction and expression of antibody-based
 CC fusion proteins with enhanced circulating half-lives. The
 CC fusion proteins lack the ability to bind to immunoglobulin Fc
 CC receptors, either as a consequence of the antibody isotype used
 CC for protein construction, i.e. a C-gamma-2 constant region (Fc)
 CC or a C-gamma-4 Fc receptor, or through directed mutagenesis of
 CC antibody isotypes that normally bind Fc receptors, i.e. C-gamma-1
 CC or C-gamma-3. The methods can be used to increase the
 CC circulating half-life of a non-immunoglobulin (Ig) protein such as
 CC a cytokine, e.g. tumour necrosis factor (TNF), an interleukin or a
 CC lymphokine such as a lymphotoxin or a colony stimulating factor, a
 CC ligand-binding protein, e.g. CD4, CTLA-4, TNF receptor or an
 CC interleukin receptor, or a protein toxin (claimed). The fusion
 CC proteins are used to deliver selectively the second non-Ig protein
 CC to a target cell in vivo so that the second non-Ig protein can
 CC exert a localised biological effect.
 XX
 SQ Sequence 444 AA;

Query Match 100.0%; Score 583; DB 20; Length 444;
 Best Local Similarity 100.0%; Pred. No. 2.4e-52;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAKTK 60
 |||||
 Db 228 apeflggpsvflppkpkdtlmisrtpevtcvvvdvsqdepevqfnwyvdgvevhnatk 287
 |||||

QY 61 PREEQFNSTYRVVSVLTVLHQDLNGKEYCKVSKNGLPSSIEKTIKAK 110
 |||||
 Db 288 preeqfnstyrvvsvltvlhqdlngkeyckvsknkglpssiektiskak 337
 |||||

RESULT 14
 AAW14935
 ID AAW14935 standard; Protein; 463 AA.
 AC AAW14935;
 XX
 DT 16-JUN-1997 (first entry)
 DE 2A2 Human IgG4 expression plasmid insert product (heavy chain).
 XX
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX
 OS Mus sp.
 XX
 PN W09711971-A1.
 XX
 PD 03-APR-1997.
 XX
 PF 27-SEP-1996; 96WO-US15575.
 XX
 PR 26-SEP-1996; 96US-0004489.
 PR 28-SEP-1995; 95US-0004489.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 XX
 DR WPI; 1997-212855/19.
 DR N-PSDB; AAT62933.
 XX
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 XX
 PS Disclosure; Page 48-50; 105pp; English.
 XX
 CC Heavy chain (AAW14935) and light chain (AAW14936) sequences
 CC correspond to murine anti-porcine soluble vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody 2A2 (see also AAW14931-32). They
 CC are encoded by a 2A2 human IgG4 expression plasmid insert (see
 CC also AAT62933). A chimeric antibody specific for porcine VCAM can be
 CC produced in transfected host cells. It is useful for diagnosing
 CC human rejection of porcine xenotransplants and for improving
 CC xenotransplantation of porcine cells, tissues and organs into human
 CC recipients.
 XX
 SQ Sequence 463 AA;

Query Match 100.0%; Score 583; DB 18; Length 463;
 Best Local Similarity 100.0%; Pred. No. 2.6e-52;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAKTK 60
 |||||
 Db 247 apeflggpsvflppkpkdtlmisrtpevtcvvvdvsqdepevqfnwyvdgvevhnatk 306
 |||||

QY 61 PREEQFNSTYRVVSVLTVLHQDLNGKEYCKVSKNGLPSSIEKTIKAK 110
 |||||
 Db 307 preeqfnstyrvvsvltvlhqdlngkeyckvsknkglpssiektiskak 356
 |||||

RESULT 15
 AAW14932
 ID AAW14932 standard; Protein; 463 AA.
 XX
 AC AAW14932;
 DT 16-JUN-1997 (first entry)
 DE Murine anti-porcine VCAM 2A2 heavy chain.
 XX
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX
 OS Mus sp.
 XX
 FH Key
 FT Region
 FT /label= CDR1
 FT Region
 FT /label= CDR2
 FT /label= CDR3
 FT Region
 FT 118..125
 FT /label= CDR3
 PN W09711971-A1.
 XX
 PD 03-APR-1997.
 XX
 PF 27-SEP-1996; 96WO-US15575.
 XX
 PR 26-SEP-1996; 96US-0004489.
 PR 28-SEP-1995; 95US-0004489.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 XX
 DR WPI; 1997-212855/19.
 DR N-PSDB; AAT62930.
 XX
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 XX
 PS Disclosure; Page 40-42; 105pp; English.
 XX
 CC Heavy chain (AAW14932) and light chain (AAW14931) sequences are
 CC provided for the murine anti-porcine soluble vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody (MAb) 2A2. Hybridoma 2A2 was
 CC produced by standard techniques using recombinant, soluble porcine
 CC VCAM as immunogen. Chimeric antibodies can be produced by cloning
 CC MAb 2A2 and 3F4 (see also AAW14937-38) variable regions into
 CC expression plasmid pAPEX-3p modified to contain the human gamma4
 CC constant region in place of the human gamma1 CI region. Sequences
 CC are provided for 2A2 (chimeric) human G2/G4 cDNA (AAW14933), a 2A2
 CC human G2/G4 expression plasmid insert product (AAW14934), a 2A2
 CC human IgG4 expression plasmid insert product (AAW14935), and 2A2
 CC chimeric antibodies are specific for porcine VCAM. They are useful
 CC for diagnosing human rejection of porcine xenotransplants and for
 CC improving xenotransplantation of porcine cells, tissues and organs
 CC into human recipients.
 XX
 SQ Sequence 463 AA;

Query Match 100.0%; Score 583; DB 18; Length 463;
 Query Match 100.0%; Score 583; DB 18; Length 463;

Best Local Similarity 100.0%; Pred. No. 2.6e-52;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	APEFLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTK	60
Db	247	apeflggpsvflfppkpkdtlmisrtpevtcvtvdvsqdepevfqfnwydgvevhnack	306
QY	61	PREEQFNSTYRVVSVLTVLTQDHLNGKEYKCKVSNKGLPSSIEKTIKAK	110
Db	307	preeqfnstyrvvsvltvltqdwlngkeykckvsnkglpssiektiskak	356

Search completed: June 21, 2002, 08:36:08
 Job time: 322 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:59:32 ; Search time 176.89 Seconds
(without alignments)
107.578 Million cell updates/sec

Title: US-09-674-857-7
Perfect score: 583
Sequence: 1 APEFLGGPSVFLFPKPKDT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: sp.archaea.*
 - 2: sp.bacteria.*
 - 3: sp.fungi.*
 - 4: sp.human.*
 - 5: sp.invertebrate.*
 - 6: sp.mammal.*
 - 7: sp.mhc.*
 - 8: sp.organelle.*
 - 9: sp.phage.*
 - 10: sp.plant.*
 - 11: sp.rodent.*
 - 12: sp.virus.*
 - 13: sp.vertebrate.*
 - 14: sp.unclassified.*
 - 15: sp.rviro.*
 - 16: sp.bacteriap.*
 - 17: sp.archheap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	551	94.5	701	4 Q96PQ8	Q96PQ8 homo sapien
2	472	81.0	337	6 Q95M34	Q95M34 equus caball
3	405	69.5	437	11 Q9R1A4	Q9R1A4 mus musculus
4	405	69.5	463	11 Q99LC4	Q99LC4 mus musculus
5	403	69.1	473	11 Q9D8L4	Q9D8L4 mus musculus
6	398	68.3	473	11 Q91Z05	Q91Z05 mus musculus
7	390	66.9	468	11 Q99L31	Q99L31 mus musculus
8	390	66.9	473	11 Q99L25	Q99L25 mus musculus
9	138	23.7	375	4 Q9BSZ1	Q9BSZ1 homo sapien
10	138	23.7	597	4 Q9QB8	Q9QB8 homo sapien
11	138	23.7	597	4 Q9BU10	Q9BU10 homo sapien
12	138	23.7	597	4 Q9GBB9	Q9GBB9 homo sapien
13	138	23.7	613	4 Q96EY0	Q96EY0 homo sapien
14	138	23.7	614	4 Q96GA6	Q96GA6 homo sapien
15	138	23.7	618	4 Q96AA6	Q96AA6 homo sapien
16	120.5	20.7	130	11 Q9D8W4	Q9D8W4 mus musculus

17	120.5	20.7	233	11 Q91V32	Q91V32 m adult mal
18	120.5	20.7	384	4 Q9UP60	Q9UP60 homo sapien
19	120.5	20.7	416	4 Q9NP66	Q9NP66 homo sapien
20	120.5	20.7	494	4 Q96K68	Q96K68 homo sapien
21	120.5	20.7	496	4 Q96KX8	Q96KX8 homo sapien
22	120.5	20.7	496	4 Q96DK0	Q96DK0 homo sapien
23	118.5	20.3	684	13 Q90544	Q90544 ginglymosto
24	116.5	20.0	500	4 Q9BRV0	Q9BRV0 homo sapien
25	114.5	19.6	233	4 Q96169	Q96169 homo sapien
26	114.5	19.6	235	11 Q99M11	Q99M11 mus musculus
27	114.5	19.6	236	4 Q96E61	Q96E61 homo sapien
28	112.5	19.3	486	11 Q91Z07	Q91Z07 mus musculus
29	112.5	19.3	487	11 Q99KA4	Q99KA4 mus musculus
30	111.5	19.1	479	11 Q99M22	Q99M22 mus musculus
31	111.5	19.1	484	11 Q99LA6	Q99LA6 mus musculus
32	110.5	19.0	479	11 Q91WP5	Q91WP5 mus musculus
33	110.5	19.0	481	11 Q91WT3	Q91WT3 mus musculus
34	110.5	19.0	481	11 Q91WT1	Q91WT1 mus musculus
35	110.5	19.0	482	11 Q91X92	Q91X92 mus musculus
36	110.5	19.0	488	11 Q91WR1	Q91WR1 mus musculus
37	109.5	18.8	426	11 Q9DCD9	Q9DCD9 mus musculus
38	109.5	18.8	480	11 Q91XE1	Q91XE1 mus musculus
39	100	17.2	211	11 Q91XL0	Q91XL0 mus musculus
40	99	17.0	233	11 Q91WS9	Q91WS9 mus musculus
41	99	17.0	234	11 Q91WF8	Q91WF8 mus musculus
42	99	17.0	235	11 Q91W12	Q91W12 mus musculus
43	99	17.0	238	11 Q99M37	Q99M37 mus musculus
44	99	17.0	1215	5 Q9V787	Q9V787 drosophila
45	97	16.6	214	11 Q9R1A5	Q9R1A5 mus musculus

ALIGNMENTS

RESULT 1

Q96PQ8 PRELIMINARY; PRT; 701 AA.
ID Q96PQ8;
AC Q96PQ8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL; AF272774; AAK58686.1; -.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 94.5%; Score 551; DB 4; Length 701;
Best Local Similarity 93.6%; Pred. No. 3.4e-52;
Matches 103; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSDPEVFQFNWYDGVGVHNAKTK 60

Db 485 APEFLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSDPEVFQFNWYDGVGVHNAKTK 544

QY 61 PREEQNSTYRVSVTLVHODWLNKGYCKVSNKGLPSSIEKTISKAK 110

Db 545 PREEQNSTYRVSVTLVHODWLNKGYCKVSNKGLPSSIEKTISKAK 594

RESULT 2

Q95M34 PRELIMINARY; PRT; 337 AA.
ID Q95M34


```
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Ozawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Willing L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FB8 CRC64;

Query Match 69.1%; Score 403; DB 11; Length 473;
Best Local Similarity 65.5%; Pred. No. 4.3e-36;
Matches 72; Conservative 19; Mismatches 19; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLPPPKKDTLMSRTPETCVVVDVDSQEDPEVQFNWYDGVGVHNAKTK 60
Db 257 APDLLGGPSVFIFPPPKIKDVLMSLTPKVTVCVVVDVSEDDPDVQISWFVNNVEVHTAQTK 316
QY 61 PREEQFNSTYRVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKSKAK 110
Db 317 THREDYNSTLRVVSALPIQHQMWSGKFKCKVNNKALPSPIEKTIKSKPR 366

RESULT 6
Q91205 PRELIMINARY; PRT; 473 AA.
ID Q91205;
AC Q91205;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE HYPOTHETICAL 51.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Ozawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Willing L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FB8 CRC64;

Query Match 66.9%; Score 390; DB 11; Length 468;
Best Local Similarity 64.5%; Pred. No. 1.1e-34;
Matches 71; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLPPPKKDTLMSRTPETCVVVDVDSQEDPEVQFNWYDGVGVHNAKTK 60
Db 252 APNLLGGPSVFIFPPPKIKDVLMSLSPMVTVCVVVDVSEDDPDVQISWFVNNVEVHTAQTK 311
QY 61 PREEQFNSTYRVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKSKAK 110
Db 312 THREDYNSTLRVVSALPIQHQMWSGKFKCKVNNKALPAPERTISKPK 361

RESULT 8
Q99L25 PRELIMINARY; PRT; 473 AA.
ID Q99L25;
AC Q99L25;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
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01-DEC-2001 (TREMBLrel. 19, Created)
DT
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE
DE HYPOTHETICAL 67.8 KDA PROTEIN.
OS
OS Homo sapiens (Human).
OC
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX
OX NCBI_TaxID=9606;
RN
RN [1]
RP
RP SEQUENCE FROM N.A.
RC
RC TISSUE=Lymph, AND LYMPHOMA;
RA
RA Strausberg R.

Query Match	23.7%	Score 138;	DB 4;	Length 618;		
Best Local Similarity	28.7%;	Pred. No. 9.7e-07;				
Matches	29;	Conservative	25; Mismatches	45; Indels	2; Gaps	2;
QY	10	VFLPPRPKDTLMTSRPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQENST	69			
dDb	368	VFAIPPS-FASIFLTKTSLTCLVTDLTTVD-SVTISWTQRGEAVKTHNISHPNAT	425			
QY	70	YRVYSVLTVLHQDWLNCKEYKCKVKSNKGLPSSIEKTIISKAK	110			
dDb	426	FSVAGEASICEDWNNSGRFTCTVTHDLPSPLKQTISRPK	466			

Search completed: June 21, 2002, 08:59:32
Job time: 1631 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	583	100.0	327	1	GC4_HUMAN	P01861	homo sapien
2	551	94.5	330	1	GC1_HUMAN	P01857	homo sapien
3	528	90.6	290	1	GC3_HUMAN	P01860	homo sapien
4	528	90.6	326	1	GC2_HUMAN	P01859	homo sapien
5	443	76.0	323	1	GC_RABIT	P01870	oryctolagus
6	443	76.0	333	1	GCB_RAT	P20761	rattus norv
7	437	75.0	329	1	GC2_CAVPO	P01862	cavia porcea
8	416	71.4	329	1	GC3_MOUSE	P22436	mus musculus
9	416	71.4	398	1	GC3M_MOUSE	P03987	mus musculus
10	407	69.8	329	1	GCC_RAT	P20762	rattus norv
11	405	69.5	324	1	GCI_MOUSE	P01868	mus musculus
12	405	69.5	393	1	GC1M_MOUSE	P01869	mus musculus
13	403	69.1	335	1	GCAB_MOUSE	P01864	mus musculus
14	399	68.4	330	1	GCAAB_MOUSE	P01863	mus musculus
15	399	68.4	399	1	GCAM_MOUSE	P01865	mus musculus
16	398	68.3	336	1	GCB_MOUSE	P01866	mus musculus
17	398	68.3	405	1	GCBM_MOUSE	P01867	mus musculus
18	389	66.7	326	1	GCI_RAT	P20759	rattus norv
19	343	58.8	322	1	GCA_RAT	P20760	rattus norv
20	166.5	28.6	428	1	EPC_HUMAN	P01854	homo sapien
21	151	25.9	429	1	EPC_RAT	P01855	rattus norv
22	151	25.9	457	1	MUC_SUNMU	P20768	suncus muri
23	140	24.0	421	1	EPC_MOUSE	P06336	mus musculus
24	138.5	23.8	299	1	ALC_RABIT	P01879	oryctolagus
25	138	23.7	454	1	MUC_HUMAN	P01871	homo sapien
26	136	23.3	391	1	MUCB_HUMAN	P04220	homo sapien
27	134	23.0	106	1	KAC_CANIS	P01834	homo sapien
28	129.5	22.2	454	1	MUC_MESAU	P06337	mesocricetu
29	129	22.1	455	1	MUC_MOUSE	P01872	mus musculus
30	129	22.1	476	1	MUCM_MOUSE	P01873	mus musculus
31	125	21.4	103	1	LAC_CHICK	P20763	gallus gall
32	125	21.4	450	1	MUC_CANFA	P01874	canis famila
33	125	21.4	458	1	MUC_RABIT	P03988	oryctolagus

FT DISULFID 141 201
 FT DISULFID 247 305
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 100.0%; Score 583; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 5.8e-52;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEFLGSPVFLPPPKDPTLMISRTPEVTCVVVDYSQEDPEVQFNWYVDGVVHNKATK 60
 |||
 DB 111 APEFLGSPVFLPPPKDPTLMISRTPEVTCVVVDYSQEDPEVQFNWYVDGVVHNKATK 170
 |||

QY 61 PREEQFNSTYRVSVLTVLHQDLNGLKCKYKCKVSNKGLPSSIEKTIKSKAK 110
 |||
 DB 171 PREEQFNSTYRVSVLTVLHQDLNGLKCKYKCKVSNKGLPSSIEKTIKSKAK 220
 |||

RESULT 2
 GCI_HUMAN STANDARD; PRT; 330 AA.
 ID GCI_HUMAN
 AC P01857;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-1 chain C region.
 GN IGHG1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RX SEQUENCE FROM N.A.
 RX MEDLINE=82274238; PubMed=6287432;
 RA Ellison J.W., Berson B.J., Hood L.E.;
 RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
 RL Nucleic Acids Res. 10:4071-4079 (1982).
 RN [2]
 RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
 RP MEDLINE=71064024; PubMed=5489771;
 RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
 RA Waxdal M.J., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
 RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
 RL Biochemistry 9:3161-3170 (1970).
 RN [3]
 RP SEQUENCE OF 136-329 (EU).
 RP MEDLINE=71064025; PubMed=5530842;
 RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
 RA Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
 RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
 RL Biochemistry 9:3171-3181 (1970).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN NIE).
 RP MEDLINE=77070269; PubMed=826475;
 RA Ponstingl H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a
 RT monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The
 RT chymotryptic peptides of the H-chain, alignment of the tryptic
 RT peptides and discussion of the complete structure.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).
 RN [5]
 RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
 RP MEDLINE=63289131; PubMed=6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747 (1983).
 RN [6]
 RP DISULFIDE BONDS.
 RP MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196 (1970).
 RN [7]
 RP DISULFIDE BONDS.
 RP MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein NIE). I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540 (1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RP MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370 (1981).
 CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
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 CC -----
 CC EMBL; J00228; AAC82527.1; ALT_INIT.
 DR PIR; A02146; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR MIM; 147100;
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003600; Ig_Like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; Ig_Like; 1.
 DR SMART; SM00407; IGCL; 2.
 DR PROSITE; PS00290; IG_MHC; 2.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT VARIANT 241 241
 FT STRAND 123 126
 FT


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FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164
FT STRAND 165 166
FT STRAND 175 178
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FT STRAND 202 206
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 240
FT TURN 241 242
FT STRAND 245 256
FT STRAND 260 266
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
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FT TURN 316 317
FT STRAND 320 324
FT SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 94.5%; Score 551; DB 1; Length 330;
Best Local Similarity 93.6%; Pred. No. 1e-48;
Matches 103; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 APEFLGGPSVFLPPPKDTLMISRPETCVVVDVVSQEDPEVQFNWYVDGVGVHNAKTK 60
Db 114 APELLGGPSVFLPPPKDTLMISRPETCVVVDVVSQEDPEVQFNWYVDGVGVHNAKTK 173

QY 61 PREEQNSYRYVSVTLVHQLWLNCKEYKCKVSNKGLPSSIEKTIKSKAK 110
Db 174 PREEQNSYRYVSVTLVHQLWLNCKEYKCKVSNKALPAPIEKTIKSKAK 223

RESULT 3
GC3_HUMAN STANDARD; PRT; 290 AA.
AC P01860;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN IGHG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (DISEASE PROTEIN WIS).
RX MEDLINE=81021548; PubMed=6774747;
RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
RL Biochemistry 19:4304-4308(1980).
RN [2]
RP REVISIONS TO 12-97 OF PROTEIN WIS.
RX MEDLINE=77118561; PubMed=402363;
RA Michaelson T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable
quadruplication of a 15-amino acid residue basic unit.";
RL J. Biol. Chem. 252:883-889(1977).
```

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RN [3]
RP REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC).
RX MEDLINE=77021516; PubMed=823945;
RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
Structure of the Fc fragment of immunoglobulin G3.";
RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN [4]
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX MEDLINE=82247835; PubMed=6808505;
RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
RT "Gamma Heavy chain disease in man: cDNA sequence supports partial
gene deletion model.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC -!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.
CC -!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
REF.2.
CC -!- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
AND ALL OF THE CH1 REGION.
CC -!- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
GAMMA-3 HEAVY CHAINS.
CC -!- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
OR ANOTHER GAMMA CHAIN SUBCLASS.
CC -!- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
SEGMENT (12-28).
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00231; AAA52805.1; ALT_SEQ.
DR PIR; A02149; G3HUI.
DR HSP; P01857; 1FC1.
DR MIM; 147120; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.
FT DOMAIN 12 73
FT HINGE.
FT DOMAIN 74 183
FT CH2.
FT DOMAIN 184 289
FT CH3.
FT REPEAT 29 43
FT REPEAT 44 58
FT REPEAT 59 73
FT MOD_RES 1 1
FT CARBOHYD 6 6
FT PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 7 7
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 24 24
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 27 27
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 33 33
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 39 39
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 42 42
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 48 48
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 54 54
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 57 57
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 63 63
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 69 69
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 72 72
FT INTERCHAIN (WITH HEAVY CHAIN DIMER).
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FT CARBOHYD 140 N-LINKED (GLNAC...).
FT MOD_RES 250 REMOVED POST-TRANSLATIONALLY.
FT VARIANT 126 QV -> EB (IN ZUC).
FT VARIANT 134 /FTid=VAR_003890.
FT VARIANT 139 P -> L (IN OMM).
FT VARIANT 139 /FTid=VAR_003891.
FT VARIANT 182 F -> Y (IN OMM).
FT VARIANT 182 /FTid=VAR_003892.
FT VARIANT 227 T -> A (IN OMM).
FT VARIANT 227 /FTid=VAR_003893.
FT VARIANT 227 S -> N (IN OMM).
FT VARIANT 227 /FTid=VAR_003894.
FT VARIANT 279 MISSING (IN ZUC).
FT VARIANT 279 /FTid=VAR_003895.
FT VARIANT 279 F -> Y (IN OMM).
FT VARIANT 279 /FTid=VAR_003896.
SQ SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;

Query Match 90.6%; Score 528; DB 1; Length 290;
Best Local Similarity 89.18; Pred. No. 1.9e-46;
Matches 98; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEFGGSPVLFPPKPKDTLMISRTPEVTCVVVDVSDPEVFQNNYVDGVEVHNAKTK 60
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 74 APELGGSPVLFPPKPKDTLMISRTPEVTCVVVDVSDPEVFQNNYVDGVEVHNAKTK 133
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 PREQFNSTFRVSVTLVTHQDNLNGKEYCKVSKNGLPSSIEKTSKAK 110
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 134 PREQFNSTFRVSVTLVTHQDNLNGKEYCKVSKNGLPSSIEKTSKAK 183
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RESULT 4
ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
   heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata S., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
   evolution of a gene family.";
RL Cell 29:671-679(1982).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
   heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
   genes.";
RL EMBO J. 1:403-407(1982).
RN [4]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;

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```

RT "The primary structure of a human IgG2 heavy chain: genetic,
   evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
RN [5]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
   domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
RN [6]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
   immunoglobulins gamma chains.";
RL Mol. Immunol. 16:923-925(1979).
RN [7]
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RL Submitted (MAR-1980) to the PIR data bank.
RN [8]
RP SEQUENCE OF 1-121 (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
   immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
RN [9]
RP DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RN [10]
RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
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DR EMBL; J00230; AAB59393.1; -
DR PIR; A02148; G2HU.
DR HSP; P01857; 1FC1.
DR MIN; 147110; -
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 102 102
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200

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FT DISULFID 246 304
FT SITE 156 156
FT MOD_RES 326 326
FT VARIANT 60 60
FT CONFLICT 109 109
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;

Query Match
Best Local Similarity 90.6%; Score 528; DB 1; Length 326;
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 5 LGSPSVFLPPPKDGLMISRTPEVTCVVVDVSDPEVQFNWYDGVVHNAKTPREE 64
Db 114 VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSDPEVQFNWYDGVVHNAKTPREE 173
QY 65 QFNSTYRVSVLTVLHODWLNKKEYCKVSNKGLPSSIEKTIKSKAK 110
Db 174 QFNSTYRVSVLTVLHODWLNKKEYCKVSNKGLPAPIEKTIKSKTK 219

RESULT 5
GC_RABIT STANDARD; PRT; 323 AA.
ID GC_RABIT
AC P01870
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-1 haplotype.";
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299517; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT immunoglobulin G.";
RL Biochem. J. 116:249-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E., Jr., Delaney R.;
RL (In) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC -!- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC MARKERS AND REF.5 THE E15 MARKER.
CC -----
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CC -----
CC EMBL; M16426; AAA31289.1; -.
DR PIR; A02161; GHRB.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match
Best Local Similarity 76.0%; Score 443; DB 1; Length 323;
Matches 81; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 2 PEFLLGGPSVFLPPPKDGLMISRTPEVTCVVVDVSDPEVQFNWYDGVVHNAKTPK 61
Db 108 PELLGGPSVFLPPPKDGLMISRTPEVTCVVVDVSDPEVQFNWYDGVVHNAKTPK 167
QY 62 REQFNSTYRVSVLTVLHODWLNKKEYCKVSNKGLPSSIEKTIKSKAK 110
Db 168 REQFNSTYRVSVLTVLHODWLNKKEYCKVSNKGLPAPIEKTIKSKAK 216

RESULT 6
GCB_RAT STANDARD; PRT; 333 AA.
ID GCB_RAT
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Bruesgammann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; ig; 3.

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DR SMART; SM00410; IG-like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 76.0%; Score 443; DB 1; Length 333;
Best Local Similarity 71.8%; Pred. No. 9.4e-38;
Matches 78; Conservative 19; Mismatches 12; Indels 0; Gaps 0;

QY 2 PEFLLGSPVFLFPKPKDILMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKP 61
DB 118 PELLGSPVFIFFPKPKDKILLISQNAKVTCTVVVDVSEEDPQVQSFVNVVHTAQTP 177

QY 62 REEQFNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAK 110
DB 178 REEQYNSTFRWSALPIQHODWMSGKEFKCKVNNKALPSPIEKTSKPK 226

RESULT 7
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN 1;
RS SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN 12;
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971)..
RN 13;
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN 14;
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN 15;
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
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RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN 16;
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003597; IG_Cl.
DR InterPro; IPR003600; IG_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG-like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 75.0%; Score 437; DB 1; Length 329;
Best Local Similarity 74.3%; Pred. No. 3.8e-37;
Matches 81; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 2 PEFLLGSPVFLFPKPKDILMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKP 61
DB 113 PENLLGSPVFIFFPKPKDILMISLTPVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKP 172

QY 62 REEQFNSTYRVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAK 110
DB 173 RVEQYNTFRVSVLPIQHODWLNKGEYKCKVNNKALPAPIEKTSKTK 221

RESULT 8
GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; ig; 3.
DR SMART: SM00410; IG-like; 1.
DR SMART: SM00407; IGcl; 2.
DR SMART: SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT FT NON_TER 1 1
FT FT DOMAIN 1 97
FT FT DOMAIN 98 113
FT FT DOMAIN 114 223
FT FT DOMAIN 224 327
FT FT TRANSMEM 346 362
FT FT DOMAIN 363 398
FT FT CONFLICT 333 333
FT FT CONFLICT 342 342
FT FT CONFLICT 388 388
FT FT CONFLICT 398 388
SQ SEQUENCE 398 AA; CF7F264B50A41B95 CRC64;

Query Match 71.4%; Score 416; DB 1; Length 398;
Best Local Similarity 69.8%; Pred. No. 6 3e-35;
Matches 74; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 5 LGGSPVFLFPKPKDTLMISTPEVTCCVVVDVSQEDPEVFQFNWVGVEVHNAKTKPREE 64
Db 117 LGGSPVFIFPPKKDALMISLTLPKVTCCVVVDSEDDPDVHVSFWFDNKVHTAWTQPREA 176
QY 65 QFNSTYRVSVLTVLHDWLNGKEYCKVKSNGLPSSIEKTITSAK 110
Db 177 QYNSTFRVWSALPIQHODMRGKEFKCKVNKNKALPAPIERTISRPK 222

RESULT 10
GCC_RAT STANDARD; PRT; 329 AA.
ID AC P20762;
DC 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Rueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RL region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:337-319(1988).
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CC -----
DR EMBL; X07189; CAA30169.1; -.
DR PIR; S00847; S00847.
DR HSSP; P01857; lfc1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig_like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00410; IG-like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.

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KW Immunoglobulin domain; Immunoglobulin C region.

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FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

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Query Match 69.8%; Score 407; DB 1; Length 329;
 Best Local Similarity 68.9%; Pred. No. 4.2e-34;
 Matches 73; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 5 LGSPVFLPPKDTLMISTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE 64

Db 117 LGSPVFIFFPKDKILMITLPKVTCTVVDVSEEDPVQFSFVFNVRVFTAQTPHEE 176

QY 65 QFNSTYRVSVLTVLHODWLNKGEYCKVSNKGLPSSIEKTSKAK 110

Db 177 QLNGTFRVSTLHQHDMWSGKEFKCKVNNKDLPSPIEKTSKPR 222

RESULT 11

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ID GC1_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salser W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=78242288; PubMed=98524;
RA Adegugbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
murine myeloma gammal chain.";
RL J. Biol. Chem. 253:6068-6075(1978).
RN [5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=78008889; PubMed=5073237;

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RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
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CC -----
CC EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR EMBL; V00793; CAA24175.1; -
DR EMBL; V00795; CAA24176.1; -
DR PIR; A02159; GIMS.
DR HSSP; P01842; 7FAB.
DR GlycoSuiteDB; P01868; -
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
FT NON_TER 1 97
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT FTIG-CAR_000055.
FT DISULFID 244 302 REMOVED POST-TRANSLATIONALLY.
FT MOD_RES 324 324 N -> D (IN REF. 3).
FT CONFLICT 276 276 N -> D (IN REF. 3).
FT CONFLICT 278 278 N -> D (IN REF. 3).
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;

Query Match 69.5%; Score 405; DB 1; Length 324;
Best Local Similarity 69.6%; Pred. No. 6.6e-34;
Matches 71; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 9 SVFLPPPKDKTLMISTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 68
Db 116 SVFIFFPKDKVLTITLPKVTCTVVDVSKDDPEVQFSFVFNVRVFTAQTPHEE 175

QY 69 TFRVSVLTVLHODWLNKGEYCKVSNKGLPSSIEKTSKAK 110
Db 176 TFRSVSELPIMHODWLNKGEYCKVSNKGLPSSIEKTSKAK 217

RESULT 12
GC1_MOUSE
ID GC1_MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

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DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00410; Ig_like; 1.
DR SMART: SM00407; Ig_c1; 2.
DR PROSITE: PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15
FT DISULFID 27 82
FT DISULFID 107 107
FT DISULFID 110 110
FT DISULFID 112 112
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 68.4%; Score 399; DB 1; Length 330;
Best Local Similarity 65.5%; Pred.No.2.7e-33;
Matches 72; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 1 APEFLGGSVFLFPKPKDTLMISTPEVTCVVDVSDPEVQFNWTVDGVGVHNAKTK 60
Db || |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
114 APNLGGSVFIFPKIKDLVILSLPVTCTVVDVSDPDQVQISWFEVNVVHTAQ 173

QY 61 PREEFNFTYRVSVLTVLHODWLNKRYCKVSKNGLPSSIEKTIKAK 110
Db |::|||::|||::|||:||||:||||:||||:||||:||||:||||:
174 THREYNSTLRVVSALPIQHODWMSGKFEKCKVNNKDLPAPIERTISKPK 223

RESULT 15
GCAM_MOUSE STANDARD; PRT; 399 AA.
ID GCAM_MOUSE
AC P01865;
DT 21-JUL-1986 (Rel. 01, Created)
DI 01-AUG-1991 (Rel. 19, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SQ SEQUENCE FROM N.A.
MEDLINE=82222190; PubMed=6283537;
Yamawaki-kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.",
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC SEGMENT OF MU CHAINS.
CC -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
CC IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
CC THE A ALLELE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL: J00471; AAB59661.1; ALT_INIT.
CC PIR: A02154; G2MSAM.
CC HSP: P01857; 1FCL.
CC MGD: MGI:96443; Igh-1.

```


DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00410; Ig_Like; 1.
 DR SMART: SM00407; Ig_C1; 2.
 DR PROSITE: PS00290; Ig_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Transmembrane; Alternative splicing.
 FT NON_TER 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT TRANSMEM 346 363
 FT DOMAIN 364 399
 FT CARBOHYD 180 180 N-LINKED (GLCNAC...).(POTENTIAL).
 SQ SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;

Query Match 68.4%; Score 399; DB 1; Length 399;
 Best Local Similarity 65.5%; Pred. No. 3 4e-33;
 Matches 72; Conservative 18; Mismatches 20; Indels 0; Gaps 0;
 QY 1 APEFLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSQEDPEVQFNMYVDGVEVHNATK 60
 || |||||:|||| || |||| | |||||:||||:||||:||||:|:
 Db 114 APNLGGPSVFIPPPKIKDVLMSLSPIVTCVVVDVSEDDPDQVISMVNNVEVHTAQ 173
 QY 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
 | :||| |||| | :|||:||||:||||:| ||: ||||| |
 Db 174 THREDYNSTLRVVSALPIQHDMMSCGKFKCKVNNKDLPAPIERTISKPK 223

Search completed: June 21, 2002, 09:00:25
 Job time: 1449 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:37:53 ; Search time 102.05 Seconds

(without alignments)
103.575 Million cell updates/sec

Title: US-09-674-857-4

Perfect score: 586

Sequence: 1 APELLGGPSVFLPPKPKDT.....CKVSNKALPAPIEKTISKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	586	100.0	234	2 PT0207	Ig gamma chain C r
2	586	100.0	255	4 S31866	Ig gamma-1 chain C
3	586	100.0	330	1 GHU	Ig gamma-1 chain C
4	586	100.0	374	2 S69339	Ig heavy chain V r
5	568	96.9	377	2 A60764	Ig gamma-3 chain C
6	568	96.9	377	2 A23511	Ig gamma-3 chain C
7	551	94.0	327	1 G4HU	Ig gamma-4 chain C
8	548	93.5	289	1 G3HUI	Ig gamma-3 heavy c
9	534	91.1	326	1 G2HU	Ig gamma-2 chain C
10	468	79.9	328	2 I47160	Ig gamma 2b chain
11	468	79.9	328	2 I47159	Ig gamma 2a chain
12	463	79.0	277	2 I47162	Ig gamma 4 chain c
13	454	77.5	333	2 PS0018	Ig gamma-2b chain
14	452	77.1	470	2 S22080	Ig heavy chain pre
15	450	76.8	329	1 GHRB	Ig gamma chain C r
16	447	76.3	323	1 G2GP	Ig gamma-2 chain C
17	445	75.9	328	2 I47161	Ig gamma 3 chain c
18	445	75.9	328	2 I47158	Ig heavy chain C r
19	443	75.6	308	2 C30554	Ig gamma-1 chain -
20	443	75.6	472	2 S31459	Ig gamma-3 chain C
21	434	74.1	329	1 G3NSC	Ig gamma-3 chain C
22	434	74.1	398	1 G3MSM	Ig gamma-2a chain
23	414	70.6	335	1 G2MSAB	Ig gamma-1 chain C
24	411.5	70.2	324	1 G1MS	Ig gamma-1 chain C
25	411.5	70.2	393	1 G1MSM	Ig gamma-1 chain C
26	411.5	70.2	444	2 PC4436	monoclonal antibod
27	411	70.1	330	1 G2NSA	Ig gamma-2a chain
28	411	70.1	399	1 G2MSAM	Ig gamma-2a chain
29	411	70.1	469	2 S37483	Ig gamma-2a chain

30	404	68.9	329	2 S00847	Ig gamma-2c chain
31	404	68.9	405	1 G2MSBM	Ig gamma-2b chain
32	404	68.9	474	1 G2MS11	Ig gamma-2 chain C
33	402	68.6	327	2 S06611	Ig gamma-2a chain
34	401	68.4	446	2 S40295	Ig gamma-2b chain
35	396	67.6	475	2 S01321	Ig gamma-1 chain C
36	389	66.4	326	2 PS0017	Ig gamma-2a chain
37	354	60.4	322	2 PS0019	Ig gamma-2a chain
38	319	54.4	112	2 B30503	Ig gamma-2b chain
39	275	46.9	88	2 A30503	Ig gamma heavy cha
40	264	45.1	180	2 I46732	Ig gamma-1 chain C
41	177	30.2	152	2 S14236	Ig epsilon-chain -
42	165.5	28.2	426	2 I36948	Ig epsilon chain C
43	164.5	28.1	428	1 EHHU	Ig heavy chain pre
44	161	27.5	549	2 S04845	Ig epsilon chain C
45	160	27.3	429	1 EHRT	Ig epsilon chain C

ALIGNMENTS

RESULT 1

PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C>Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 586; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 9.3e-52;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

DB 25 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 84

QY 61 PREEOYNSTYRVVSVLTVLDLNGKEYCKVSNKALPAPIEKTISKAK 110

DB 85 PREEOYNSTYRVVSVLTVLDLNGKEYCKVSNKALPAPIEKTISKAK 134

RESULT 2

S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
C>Date: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filpula, D.
A:Description: Screening method for protein-protein interactions of cloned gene products submitted to the EMBL Data Library, February 1993
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FIL>
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 100.0%; Score 586; DB 4; Length 255;

Best Local Similarity 100.0%; Pred. No. le-51;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|||||
Db 39 APELLGGPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 98
|||||

QY 61 PREEQNSTYRVSVLTVLHODWLNKGYCKVSKNKPAPLEKTIKAK 110
|||||
Db 99 PREEQNSTYRVSVLTVLHODWLNKGYCKVSKNKPAPLEKTIKAK 148
|||||

RESULT 3
GHU

Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
A:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: EMBL:Z17370
A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:Cross-references: EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A:Reference number: A90563; MUID:71064024
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96,'R',98-135 <GUN>
A:Note: this sequence has the G1m(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
A:Reference number: A90564; MUID:71064025
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primaerstruktur
A:Reference number: A91668; MUID:77070269
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A:Note: this sequence has the G1m(17) and G1m(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983

A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <
A:Note: this sequence has the G1m(3) and G1m(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul
A:Reference number: A90565; MUID:71064027
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Role of antibody structure. The primary structure of monoclonal IgG1 immunog
enbromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (h
ain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-204,250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 586; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.4e-51;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|||||
Db 114 APELLGGPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 173
|||||

QY 61 PREEQNSTYRVSVLTVLHODWLNKGYCKVSKNKPAPLEKTIKAK 110
|||||
Db 174 PREEQNSTYRVSVLTVLHODWLNKGYCKVSKNKPAPLEKTIKAK 223
|||||

RESULT 4
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
A:Accession: S69339; S72664
R:Khamlichi, A.A.; Aucouturier, P.; Freud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140,'C',142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Matches	106;	Conservative	2;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	APELGGPSVFLPPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK	60						
Db	161	APELGGPSVFLPPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK	220						
QY	61	PREEQNSTYRVVSVLTFLHODWLNGKEYCKVSNKALPAPIETISKAK	110						
Db	221	PREEQNSTYRVVSVLTFLHODWLNGKEYCKVSNKALPAPIETISKAK	270						
RESULT	7								
G4HU		Ig gamma-4 chain C region - human							
C:Species:		Homo sapiens (man)							
C:Date:		02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999							
C:Accession:		A90933; A90249; A02150							
R:Ellison, J.;		Buxbaum, J.; Hood, L.							
DNA 1, 11-18, 1981									
A:Title:		Nucleotide sequence of a human immunoglobulin C-gamma4 gene.							
A:Reference number:		A90933; MUID:83157104							
A:Accession:		A90933							
A:Molecule type:		DNA							
A:Residues:		1-327 <ELL>							
A:Note:		The sequence was determined from the germline gene							
R:Pink, J.R.L.;		Buttery, S.H.; De Vries, G.M.; Milstein, C.							
Biochem. J. 117, 33-47, 1970									
A:Title:		Human immunoglobulin subclasses. Partial amino acid sequence of the constant							
A:Reference number:		A90249; MUID:70207560							
A:Accession:		A90249							
A:Molecule type:		protein							
A:Residues:		1-30; 81-326 <PIN>							
C:Genetics:									
A:Gene:		GDB:IGHG4							
A:Cross-references:		GDB:119340; OMIM:147130							
A:Map position:		14q32.33-14q32.33							
A:Introns:		99/1; 111/1; 221/1							
C:Complex:		An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into									
C:Superfamily:		immunoglobulin C region; immunoglobulin homology							
C:Keywords:		duplication; glycoprotein; heterotetramer; immunoglobulin							
F:20-85/Domain:		immunoglobulin homology <IMI>							
F:99-110/Region:		hinge							
F:134-203/Domain:		immunoglobulin homology <IM2>							
F:240-307/Domain:		immunoglobulin homology <IM3>							
F:14/Disulfide bonds:		interchain (to light chain) #status experimental							
F:27-83,141-201,247-305/Disulfide bonds:		#status predicted							
F:106,109/Disulfide bonds:		interchain (to heavy chain) #status experimental							
F:177/Binding site:		carbohydrate (Asn) (covalent) #status predicted							
Query Match		94.0%; Score 551; DB 1; Length 327;							
Best Local Similarity		93.6%; Pred. No. 4.8e-48;							
Matches	103;	Conservative	3;	Mismatches	4;	Indels	0;	Gaps	0;
QY	1	APELGGPSVFLPPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK	60						
Db	111	APELGGPSVFLPPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK	170						
QY	61	PREEQNSTYRVVSVLTFLHODWLNGKEYCKVSNKALPAPIETISKAK	110						
Db	171	PREEQNSTYRVVSVLTFLHODWLNGKEYCKVSNKALPAPIETISKAK	220						
RESULT	8								
G3HUW1		Ig gamma-3 heavy chain disease proteins - human							
C:Species:		Homo sapiens (man)							
C:Date:		31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999							
C:Accession:		A90442; A92219; A90198; A93919; A02149							
R:Frangione, B.;		Rosenwasser, E.; Preilli, F.; Franklin, E.C.							
Biochemistry 19, 4304-4308, 1980									
A:Title:		Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 hea							

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Query Match      91.1%; Score 534; DB 1; Length 326;
Best Local Similarity 92.5%; Pred. No. 2.5e-46;
Matches 98; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 5 LGGSPVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREE 64
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 114 VAGSPVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVDFNWYVDGVEVHNKATKPREE 173

QY 65 QYNSTRYRVSVLVTLHQDWLNGEYKCKVSNKALPAPIEKTISKAK 110

```


RESULT 14

S22080

Ig heavy chain precursor (B/WT.4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

A:Accession: S22080; S06610; A31303
R:Sanders, P.G.

submitted to the EMBL Data Library, November 1991

A:Reference number: S22080

A:Accession: S22080

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-470 <SAS>

A:CROSS-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440

R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.

Mol. Immunol. 26, 841-850, 1989

A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2

A:Reference number: S06610; MUID:90097956

A:Accession: S06610

A:Molecule type: DNA

A:Residues: 142-470 <SYM>

A:CROSS-references: EMBL:X16701

A:Note: the sequence was determined from the germline gene

C:Genetics:

A:Gene: Ig CH gamma-1

A:Introns: 98/1; 111/1; 221/1

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein

F:161-225/Domain: immunoglobulin homology <IMM>

F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 77.1%; Score 452; DB 2; Length 470;

Matches 82; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 2 PELLGGPSVFLPPPKDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61

DB 253 PELLGGPSVFIFFPKPKDTLTISGTPEVTCVVVDVGHDDPEVKSFWFDDVENVATTATKP 312

QY 62 REEQNSTYRVSVLTVLHODWLNKGEKCKVSNKALPAPIETISKAK 110

DB 313 REEQNSTYRVSVLTVLHODWLNKGEKCKVSNKALPAPIETISKAK 361

RESULT 15

GHRB

Ig gamma chain C region - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 16-Jul-1999

C:Accession: A91749; A90290; A93928; A90245; A94416; A02161

R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.

Immunogenetics 18, 387-397, 1983

A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplotype

A:Reference number: A91749; MUID:84030930

A:Accession: A91749

A:Molecule type: mRNA

A:Residues: 1-323 <BER>

A:Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr

R:Pratt, D.M.; Mole, L.E.

Biochem. J. 151, 337-349, 1975

A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin

A:Reference number: A90290; MUID:76135469

A:Accession: A90290

A:Molecule type: protein

R:Residues: 1-47, 'E', '49-71, 'PV', '72-128 <PRA>

R:Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982

A:Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain

A:Reference number: A93928; MUID:83299917

A:Accession: A93928

A:Molecule type: mRNA

A:Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>

A:CROSS-references: GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:g165112

A:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.

Biochem. J. 116, 249-259, 1970

A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin

A:Reference number: A90245; MUID:70110015

A:Accession: A90245

A:Molecule type: protein

A:Residues: 132-143, 'E', 145-161 <FRU>

R:Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.

in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almquist and Wikse

A:Reference number: A94416

A:Accession: A94416

A:Molecule type: protein

A:Residues: 129-131; 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'A'

A:Note: this has the e15 allotypic marker, 185-Ala

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:130-199/Domain: immunoglobulin homology <IM1>

F:20-82/Domain: immunoglobulin homology <IM2>

F:236-303/Domain: immunoglobulin homology <IM3>

F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 76.8%; Score 450; DB 1; Length 323;

Matches 82; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 2 PELLGGPSVFLPPPKDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61

DB 108 PELLGGPSVFIFFPKPKDTLTISGTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 167

QY 62 REEQNSTYRVSVLTVLHODWLNKGEKCKVSNKALPAPIETISKAK 110

DB 168 REEQNSTYRVSVLTVLHODWLNKGEKCKVSNKALPAPIETISKAK 216

Search completed: June 21, 2002, 08:37:53

Job time: 47 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 08:32:14 ; Search time 77.71 Seconds
(without alignments)
34.575 Million cell updates/sec

Title: US-09-674-857-4
Perfect score: 586
Sequence: 1 APELLGSPVFLPPKPKDT.....CKVSNKALPAPIKTSKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA: *
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep: *
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	586	100.0	110	3 US-08-444-644-21	Sequence 21, Appl
2	586	100.0	110	4 US-08-232-246A-21	Sequence 21, Appl
3	586	100.0	116	2 US-08-232-539D-55	Sequence 55, Appl
4	586	100.0	212	1 US-08-430-633-4	Sequence 4, Appl
5	586	100.0	212	2 US-08-620-694A-4	Sequence 4, Appl
6	586	100.0	212	2 US-08-936-854-4	Sequence 4, Appl
7	586	100.0	212	3 US-09-022-255-4	Sequence 4, Appl
8	586	100.0	212	3 US-09-022-696-4	Sequence 4, Appl
9	586	100.0	212	3 US-09-022-253-4	Sequence 4, Appl
10	586	100.0	212	3 US-09-022-260-4	Sequence 4, Appl
11	586	100.0	212	4 US-09-022-259-4	Sequence 4, Appl
12	586	100.0	212	4 US-09-022-257-4	Sequence 4, Appl
13	586	100.0	232	2 US-08-595-043A-50	Sequence 50, Appl
14	586	100.0	235	4 US-09-131-247-6	Sequence 6, Appl
15	586	100.0	254	2 US-08-284-391B-33	Sequence 33, Appl
16	586	100.0	254	4 US-09-218-950-33	Sequence 33, Appl
17	586	100.0	316	4 US-09-178-869-4	Sequence 4, Appl
18	586	100.0	331	4 US-09-178-869-2	Sequence 2, Appl
19	586	100.0	347	1 US-07-940-861-43	Sequence 43, Appl
20	586	100.0	347	1 US-08-459-512-43	Sequence 43, Appl
21	586	100.0	347	2 US-08-459-657-43	Sequence 43, Appl
22	586	100.0	347	2 US-08-460-132-43	Sequence 43, Appl
23	586	100.0	347	4 US-08-466-465-8	Sequence 8, Appl
24	586	100.0	347	5 PCT-US92-02050-43	Sequence 43, Appl
25	586	100.0	360	4 US-09-180-100-11	Sequence 11, Appl
26	586	100.0	371	1 US-08-236-311-7	Sequence 7, Appl
27	586	100.0	371	3 US-08-457-918-7	Sequence 7, Appl

28	586	100.0	376	4 US-09-180-100-22	Sequence 22, Appl
29	586	100.0	387	1 US-08-470-299-4	Sequence 4, Appl
30	586	100.0	388	4 US-09-131-247-16	Sequence 16, Appl
31	586	100.0	389	4 US-09-131-247-14	Sequence 14, Appl
32	586	100.0	396	2 US-08-784-512-3	Sequence 3, Appl
33	586	100.0	396	4 US-09-176-228-3	Sequence 3, Appl
34	586	100.0	424	4 US-09-333-593A-8	Sequence 8, Appl
35	586	100.0	424	5 PCT-US95-03866-12	Sequence 12, Appl
36	586	100.0	424	5 PCT-US95-03866-14	Sequence 14, Appl
37	586	100.0	437	5 PCT-US96-10043-11	Sequence 11, Appl
38	586	100.0	442	5 PCT-US96-10043-9	Sequence 9, Appl
39	586	100.0	446	3 US-08-397-411-7	Sequence 7, Appl
40	586	100.0	449	1 US-08-458-516-13	Sequence 13, Appl
41	586	100.0	449	3 US-08-897-236-23	Sequence 23, Appl
42	586	100.0	449	4 US-09-679-397-2	Sequence 2, Appl
43	586	100.0	451	2 US-08-887-352B-16	Sequence 16, Appl
44	586	100.0	451	4 US-08-887-352B-18	Sequence 18, Appl
45	586	100.0	451	2 US-08-887-352B-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-444-644-21
; Sequence 21, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear


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;
; GENERAL INFORMATION:
; APPLICANT: ALDERSON, MARK
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: COHEN, JEFFREY
; APPLICANT: COMEAU, MICHAEL
; APPLICANT: FARRAH, THERESA
; APPLICANT: SPRIGGS, MELANIE
; TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF2 Proteins
; TITLE OF INVENTION: That Bind MHC Class II Beta Chains
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,633
; FILING DATE: 28-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/235,397
; FILING DATE: 04/28/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2612
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: IgG1 FC
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; US-08-430-633-4
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; Query Match 100.0%; Score 586; DB 1; Length 212;
; Best Local Similarity 100.0%; Pred. No. 2.5e-62;
; Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 APELLGSPSVFLPPPKDFTLMSRTPVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
; |
; Db 14 APELLGSPSVFLPPPKDFTLMSRTPVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
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; QY 61 PREEQNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAK 110
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; Db 74 PREEQNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAK 123
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; RESULT 5
; US-08-620-694A-4
; Sequence 4, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: IMMUNEX CORPORATION
```

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;
;
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: IgG1 FC
;
; US-08-620-694A-4
;
; Query Match 100.0%; Score 586; DB 2; Length 212;
; Best Local Similarity 100.0%; Pred. No. 2.5e-62;
; Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 APELLGSPSVFLPPPKDFTLMSRTPVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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; Db 14 APELLGSPSVFLPPPKDFTLMSRTPVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
; |
; QY 61 PREEQNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAK 110
; |
; Db 74 PREEQNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAK 123
; |
;
; RESULT 6
; US-08-936-854-4
; Sequence 4, Application US/08936854
; Patent No. 5925734
; GENERAL INFORMATION:
; APPLICANT: ALDERSON, MARK
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: COHEN, JEFFREY
; APPLICANT: COMEAU, MICHAEL
; APPLICANT: FARRAH, THERESA
; APPLICANT: SPRIGGS, MELANIE
; TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF2 Proteins
; TITLE OF INVENTION: That Bind MHC Class II Beta Chains
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: IMMUNEX CORPORATION
```

STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936.854
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430.633
FILING DATE: 28-APR-1995
APPLICATION NUMBER: 08/235.397
FILING DATE: 04/28/94
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORGANISM: Human
IMMEDIATE SOURCE:
CLONE: IgG1 Fc
US-08-936-854-4

Query Match 100.0%; Score 586; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 2.5e-62;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 14 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
Db 74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123

RESULT 7
US-09-022-255-4
Sequence 4, Application US/09022255
Patent No. 6072033
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022.255
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620.694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538.765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410.535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Human
IMMEDIATE SOURCE:
CLONE: IgG1 Fc
US-09-022-255-4

Query Match 100.0%; Score 586; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 2.5e-62;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 14 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
Db 74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123

RESULT 8
US-09-022-696-4
Sequence 4, Application US/09022696
Patent No. 6072037
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022.696
FILING DATE:
CLASSIFICATION:

[illegible]

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: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,695
: REFERENCE/DOCKET NUMBER: 2617-B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 212 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: ORIGINAL SOURCE:
: ORGANISM: Human
: IMMEDIATE SOURCE:
: CLONE: IgG1 FC
: US-09-022-260-4

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	Query Match	100.0%;	Score 586;	DB 3;	Length 212;
	Best Local Similarity	100.0%;	Pred. No. 2.5e-62;		
	Matches 110;	Conservative 0;	Mismatches 0;	Indels	
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Db	14	APELLGGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVH			
QY	61	PREEOYNSTVRVYSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTTSKAK			110
Db	74	PREEQYNSTVRVYSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTTSKAK			123

RESULT 11
US-09-2259-4
; Sequence 4, Application US/09022259-4
; Patent No. 6191104
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6191104
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating
; SOFTWARE: Microsoft Word for #
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/0022
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,695
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/411
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-
; TELECOMMUNICATION INFORMATION:

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: TELEPHONE: (206)587-0430
: TELEFAX: (206)
:
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 212 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: ORIGINAL SOURCE:
: ORGANISM: Human
: IMMEDIATE SOURCE:
: CLONE: IgG1 FC
US-09-022-259-4

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Query Match	100.0%;	Score 586;	DB 4;	Length 212;
Best Local Similarity	100.0%;	Pred. No. 2.5e-62;		
Matches 110;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFANFYVDGVEVHNA	60	
Db	14	APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFANFYVDGVEVHNA	73	
QY	61	PREQYNSTRYVSVLVFLHQQDWLNGEYKCKVSNKALPAPIEKTISKAK	110	
Db	74	PREQYNSTRYVSVLVFLHQQDWLNGEYKCKVSNKALPAPIEKTISKAK	123	

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RESULT 12
US-09-022-257-4
; Sequence 4, Application US/09022257
; Patent No. 6197525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)597-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids

```



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; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: 19G1 Fc
US-09-022-257-4

Query Match          100.0%; Score 586; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 2.5e-62;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 APELLGGPSVFLFPPPKDILMISRTPEVTICVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
      |||||
Db    14 APELLGGPSVFLFPPPKDILMISRTPEVTICVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
      |||||

QY   61 PREEQYNSTYRVSVLTAVLHQDWLNGKEYCKVSNKALPAPIETISKAK 110
      |||||
Db    74 PREEQYNSTYRVSVLTAVLHQDWLNGKEYCKVSNKALPAPIETISKAK 123
      |||||

RESULT 13
US-08-595-043A-50
; Sequence 50, Application US/08595043A
; Patent No. 5935824
; GENERAL INFORMATION:
; APPLICANT: SGARLATO, GREGORY D.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,043A
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: SGAR-00371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-595-043A-50

Query Match          100.0%; Score 586; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.8e-62;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 APELLGGPSVFLFPPPKDILMISRTPEVTICVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
      |||||
Db    16 APELLGGPSVFLFPPPKDILMISRTPEVTICVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75
      |||||

QY   61 PREEQYNSTYRVSVLTAVLHQDWLNGKEYCKVSNKALPAPIETISKAK 110
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; APPLICATION NUMBER: 08/195,395
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: 07/847,566
; FILING DATE: 06-MAR-1992
; APPLICATION NUMBER: 07/665,961
; FILING DATE: 07-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Elbing, Karen L
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/247001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:

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; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-284-391B-33

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Query Match      100.0%; Score 586; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 3.2e-62;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 16 APELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75

Qy 61 PREEQYNSTYRVSVLTIVLHODWLNKGYKCKVSNKALPAPIETISKAK 110
Db 76 PREEQYNSTYRVSVLTIVLHODWLNKGYKCKVSNKALPAPIETISKAK 125

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Search completed: June 21, 2002, 08:32:15
Job time: 89 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:37:52 ; Search time 102.05 Seconds
(without alignments)
102.633 Million cell updates/sec

Title: US-09-674-857-2
Perfect score: 580
Sequence: 1 APPVAGSFVFLPPKPKDTL.....CKVSNKGLPSSIEKTSKTK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	98.6	326	1 G2HU	Ig gamma-2 chain C
2	536	92.4	327	1 G4HU	Ig gamma-4 chain C
3	529	91.2	377	2 A60764	Ig gamma-3 chain C
4	529	91.2	377	2 A23511	Ig gamma-3 chain C
5	526	90.7	234	2 PT0207	Ig gamma chain C r
6	524	90.3	255	4 S31866	Ig gamma-1 chain C
7	524	90.3	330	1 GHU	Ig gamma-1 chain C
8	524	90.3	374	2 S69339	Ig heavy chain V r
9	516	89.0	289	1 G3HUW1	Ig gamma-3 heavy c
10	457	78.8	328	2 I47160	Ig gamma 2b chain
11	457	78.8	328	2 I47159	Ig gamma 2a chain
12	452	77.9	277	2 I47162	Ig gamma 4 chain c
13	441	76.0	328	2 I47161	Ig gamma 3 chain c
14	441	76.0	328	2 I47158	Ig gamma 1 chain c
15	429	74.0	470	2 S22080	Ig heavy chain pre
16	425	73.3	308	2 C30554	Ig heavy chain C r
17	425	73.3	329	1 G2GP	Ig gamma-2 chain C
18	425	73.3	472	2 S31459	Ig gamma-1 chain -
19	423	72.9	333	2 PS0018	Ig gamma-2b chain
20	418	72.1	337	1 GHRB	Ig gamma chain C r
21	414	71.4	327	2 S06611	Ig gamma-2 chain C
22	410.5	70.8	329	1 G3MSC	Ig gamma-3 chain C
23	410.5	70.8	398	1 G3MSM	Ig gamma-3 chain C
24	410	70.7	324	1 GLMS	Ig gamma-1 chain C
25	410	70.7	393	1 GLMSM	Ig gamma-1 chain C
26	410	70.7	444	2 PC4436	monoclonal antibod
27	400	69.0	329	2 S00847	Ig gamma-2c chain
28	384	66.2	326	2 PS0017	Ig gamma-1 chain C
29	383	66.0	335	1 G2MSAB	Ig gamma-2a chain

30	383	66.0	405	1 G2MSBM	Ig gamma-2b chain
31	383	66.0	474	1 G2MS11	Ig gamma-2b chain
32	378	65.2	330	1 G2MSA	Ig gamma-2a chain
33	378	65.2	399	1 G2MSAM	Ig gamma-2a chain
34	378	65.2	469	2 S37483	Ig gamma-2a chain
35	369	63.6	475	2 S01321	Ig gamma-2b chain
36	368	63.4	446	2 S40295	Ig gamma-2a chain
37	342	59.0	322	2 PS0019	Ig gamma-2a chain
38	310	53.4	112	2 B30503	Ig gamma-2a chain
39	277	47.8	88	2 A30503	Ig gamma-2b chain
40	254	43.8	180	2 I46732	Ig gamma heavy cha
41	173.5	29.9	426	2 I36948	Ig epsilon-chain -
42	172.5	29.7	428	1 EHHU	Ig epsilon chain C
43	172	29.7	152	2 S14236	Ig gamma-1 chain C
44	156	26.9	549	2 S04845	Ig heavy chain pre
45	152	26.2	457	2 S03961	Ig mu chain C regi

ALIGNMENTS

RESULT 1
G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain
A:Reference number: A93906; MUID:82197621
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; PID:G6066056
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, an
A:Reference number: A92809; MUID:81007873
A:Contents: myeloma protein Til
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of
A:Reference number: A90752; MUID:80001357
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24,'E',26-57,'EV',60-85;132-171,'222',175,'B',177-193,'D',195-196,'Q',1
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobuli
A:Reference number: A93132; MUID:80114419
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation: Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amid
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500
A:Contents: annotation; myeloma protein Sa, disulfide bonds

Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 63
: |||||
Db 165 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTPREE 224
QY 64 QFNSTRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109
: |||||
Db 225 QYNSTRVSVLTVHODWLNKGEYKCKVSNKALPAPIEKTIKTK 270

RESULT 5

PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <HR>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 526; DB 2; Length 234;
Best Local Similarity 86.8%; Pred. No. 3 5e-46;
Matches 99; Conservative 5; Mismatches 4; Indels 6; Gaps 1;

QY 2 PPVA-----GPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 55
|||
Db 21 PPCAAPPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 80
QY 56 AKTKPREQFNSTRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109
: |||||
Db 81 AKTKPREQFNSTRVSVLTVVHODWLNKGEYKCKVSNKALPAPIEKTIKTK 134

RESULT 6

S31866
Ig gamma-1 chain C region - synthetic
C:Species: Synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filpula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products.
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FIL>
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 90.3%; Score 524; DB 4; Length 255;
Best Local Similarity 86.0%; Pred. No. 6.1e-46;
Matches 98; Conservative 6; Mismatches 4; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 55
|||
Db 35 PPCAPPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 94
QY 56 AKTKPREQFNSTRVSVLTVVHODWLNKGEYKCKVSNKGLPSSIEKTIKTK 109
: |||||
Db 95 AKTKPREQFNSTRVSVLTVVHODWLNKGEYKCKVSNKALPAPIEKTIKTK 148

RESULT 7

GHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C:Accession: A93433; S33887; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: EMBL:Z17370
A:Note: This sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) marker
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A:Reference number: S33887; MUID:83001943
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:Cross-references: EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A:Reference number: A90563; MUID:71064024
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96, 'R', '98-135 <CUN>
A:Note: This sequence has the Gln(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A:Reference number: A90564; MUID:71064025
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2
A:Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni
igen Primaerstruktur.
A:Reference number: A91668; MUID:77070269
A:Contents: myeloma protein Nle
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E'
A:Note: this sequence has the Gln(17) and Gln(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'N', 242-266, 'D', 268-271, 'D', 273-330 <
A:Note: this sequence has the Gln(3) and Gln(non-1) markers
R:Galli, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul

|||||
Db 138 QFNSTRVSVLTVLQKNWLDGKCKVSNKALPAPIEKTISKTK 183
RESULT 10
I47160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845
A:Accession: I47160
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C:Genetics:
A:Gene: IgG2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>
Query Match 78.8%; Score 457; DB 2; Length 328;
Best Local Similarity 78.8%; Pred. No. 5.7e-39; Mismatches 9; Indels 0; Gaps 0;
Matches 82; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 6 GPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQF 65
|||||
Db 116 GPSVFIFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQF 175
QY 66 NSTFRVSVLTVVHQDLNGKEYCKVKSNKGLPSPSIEKTIISKTK 109
|||||
Db 176 NSTYRVSVLPIQHODWLNKGEKFKCKVNNKDLAPAPITRIISKAK 219
RESULT 11
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C:Genetics:
A:Gene: IgG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>
Query Match 78.8%; Score 457; DB 2; Length 328;
Best Local Similarity 78.8%; Pred. No. 5.7e-39; Mismatches 9; Indels 0; Gaps 0;
Matches 82; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 6 GPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQF 65
|||||
Db 116 GPSVFIFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQF 175
QY 66 NSTFRVSVLTVVHQDLNGKEYCKVKSNKGLPSPSIEKTIISKTK 109
|||||
Db 176 NSTYRVSVLPIQHODWLNKGEKFKCKVNNKDLAPAPITRIISKAK 219
RESULT 12
I47158
Ig gamma 1 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47158

I47162
Ig gamma 4 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47162
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845
A:Accession: I47162
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C:Genetics:
A:Gene: IgG4
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>
Query Match 77.9%; Score 452; DB 2; Length 277;
Best Local Similarity 77.9%; Pred. No. 1.5e-38; Mismatches 81; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
Matches 81; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
QY 6 GPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQF 65
|||||
Db 65 GPSAFIFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQF 124
QY 66 NSTFRVSVLTVVHQDLNGKEYCKVKSNKGLPSPSIEKTIISKTK 109
|||||
Db 125 NSTYRVSVLPIQHODWLNKGEKFKCKVNNKDLAPAPITRIISKAK 168
RESULT 13
I47161
Ig gamma 3 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47161
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845
A:Accession: I47161
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128
C:Genetics:
A:Gene: IgG3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>
Query Match 76.0%; Score 441; DB 2; Length 328;
Best Local Similarity 77.9%; Pred. No. 2.4e-37; Mismatches 12; Mismatches 11; Indels 0; Gaps 0;
Matches 81; Conservative 12; Mismatches 11; Indels 0; Gaps 0;
QY 4 VAGSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
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Db 114 VAGSVFIFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 173
QY 64 QFNSTRVSVLTVVHQDLNGKEYCKVKSNKGLPSPSIEKTIISKTK 107
|||||
Db 174 QFNSTRVSVLPIQHODWLNKGEKFKCKVNNKDLAPAPITRIISKTK 217
RESULT 14
I47158
Ig gamma 1 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47158

R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A:Reference number: I47158; MUID:95015845
A:Accession: I47158
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
C:Genetics:
A:Gene: IgG1
A:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Search completed: June 21, 2002, 08:37:53
Job time: 427 sec

Query Match 76.0%; Score 441; DB 2; Length 328;
Best Local Similarity 77.9%; Pred. No. 2.4e-37;
Matches 81; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 4 VAGPSVLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVGVHNAKTRPREE 63
Db 114 VAGPSVFIFPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVGVHNAKTRPREE 173

QY 64 QFNSTFRVSVLTIVVHODWLNKGEYCKVSKNGLPSSIEKTISK 107

Db 174 QFNSTFRVSVLTIVVHODWLNKGEYCKVSKNGLPSSIEKTISK 217

RESULT 15

S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S22080; S06610; A31303
R:Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22080
A:Accession: S22080
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-470 <SAN>
A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma
A:Reference number: S06610; MUID:90097956
A:Accession: S06610
A:Molecule type: DNA
A:Residues: 142-470 <SYM>
A:Cross-references: EMBL:X16701
A>Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: Ig CH gamma-1
A:Introns: 98/1; 111/1; 221/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IMM>
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 74.0%; Score 429; DB 2; Length 470;
Best Local Similarity 71.8%; Pred. No. 6.3e-36;
Matches 79; Conservative 13; Mismatches 16; Indels 2; Gaps 1;

QY 2 PP--VAGPSVLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVGVHNAKTK 59

Db 252 PPELPGGVSFIFPPPKDITLTISGTPETCVVVDVSHEDPEVFQFNWYDGVGVHNAKTK 311

QY 60 PREEQFNSTFRVSVLTIVVHODWLNKGEYCKVSKNGLPSSIEKTISKTK 109

Db 312 PREEQFNSTFRVSVLTIVVHODWLNKGEYCKVSKNGLPSSIEKTISKTK 361

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:30:46 ; Search time 77.71 Seconds
(without alignments)
34.261 Million cell updates/sec

Title: US-09-674-857-1
Perfect score: 581
Sequence: 1 APPVAGSVFLFPKPKDTL.....CKVSKGLPSSIEKTSKAK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
SUMMARIES							
1	554	95.4	109	3	US-08-444-644-30	Sequence 30, Appl	
2	554	95.4	109	4	US-08-232-246A-30	Sequence 30, Appl	
3	554	95.4	432	3	US-08-477-460B-2	Sequence 2, Appl	
4	554	95.4	432	3	US-08-379-516-2	Sequence 2, Appl	
5	554	95.4	432	4	US-09-329-916-2	Sequence 2, Appl	
6	554	95.4	432	4	US-08-485-372A-2	Sequence 2, Appl	
7	554	95.4	432	4	US-09-409-006A-2	Sequence 2, Appl	
8	554	95.4	432	5	PCT-US93-07422-2	Sequence 2, Appl	
9	554	95.4	530	3	US-08-477-460B-4	Sequence 4, Appl	
10	554	95.4	530	3	US-08-379-516-4	Sequence 4, Appl	
11	554	95.4	530	4	US-09-329-916-4	Sequence 4, Appl	
12	554	95.4	530	4	US-08-485-372A-4	Sequence 4, Appl	
13	554	95.4	530	4	US-09-409-006A-4	Sequence 4, Appl	
14	554	95.4	530	5	PCT-US93-07422-4	Sequence 4, Appl	
15	551	94.8	450	2	US-08-788-800-12	Sequence 12, Appl	
16	551	94.8	469	2	US-07-934-373C-23	Sequence 23, Appl	
17	551	94.8	469	3	US-08-437-642B-23	Sequence 23, Appl	
18	551	94.8	552	5	PCT-US93-07832-23	Sequence 23, Appl	
19	548	94.3	468	4	US-09-485-737B-67	Sequence 67, Appl	
20	548	94.3	711	4	US-09-485-737B-90	Sequence 90, Appl	
21	544	93.6	326	2	US-08-656-586-9	Sequence 9, Appl	
22	543	93.5	116	2	US-08-232-539D-55	Sequence 55, Appl	
23	543	93.5	212	1	US-08-430-633-4	Sequence 4, Appl	
24	543	93.5	212	1	US-08-620-694A-4	Sequence 4, Appl	
25	543	93.5	212	2	US-08-936-854-4	Sequence 4, Appl	
26	543	93.5	212	3	US-09-022-255-4	Sequence 4, Appl	
27	543	93.5	212	3	US-09-022-696-4	Sequence 4, Appl	

28	543	93.5	212	3	US-09-022-253-4	Sequence 4, Appl
29	543	93.5	212	3	US-09-022-260-4	Sequence 4, Appl
30	543	93.5	212	4	US-09-022-259-4	Sequence 4, Appl
31	543	93.5	212	4	US-09-022-257-4	Sequence 4, Appl
32	543	93.5	232	2	US-08-595-043A-50	Sequence 50, Appl
33	543	93.5	235	4	US-09-131-247-6	Sequence 6, Appl
34	543	93.5	254	2	US-08-284-391B-33	Sequence 33, Appl
35	543	93.5	254	4	US-09-218-950-33	Sequence 33, Appl
36	543	93.5	331	4	US-09-178-869-2	Sequence 2, Appl
37	543	93.5	347	1	US-07-940-861-43	Sequence 43, Appl
38	543	93.5	347	1	US-08-459-512-43	Sequence 43, Appl
39	543	93.5	347	2	US-08-459-657-43	Sequence 43, Appl
40	543	93.5	347	2	US-08-460-132-43	Sequence 43, Appl
41	543	93.5	347	4	US-08-466-465-8	Sequence 8, Appl
42	543	93.5	347	5	PCT-US92-02050-43	Sequence 43, Appl
43	543	93.5	360	4	US-09-180-100-11	Sequence 11, Appl
44	543	93.5	371	1	US-08-236-311-7	Sequence 7, Appl
45	543	93.5	371	3	US-08-457-918-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-444-644-30
; Sequence 30, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-444-644-30

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Query Match 95.4%; Score 554; DB 3; Length 109;
Best Local Similarity 93.6%; Pred. No. 9.7e-57;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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RESULT      2
US-08-232-246A-30
; Sequence 30, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Eriden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173

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Query Match          95.4%; Score 554; DB 4; Length 109;
Best Local Similarity 93.6%; Pred. No. 9.7e-57;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
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Db	1	APPVAGSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVFNKYVDGVEVHNAKTKP	60
Qy	61	REQYNASTYRVSVLTVLHQDWLNGKEYCKVSKNGLPSSIEKTIKAK	109
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RESULT      3
US-08-477-460B-2
; Sequence 2, Application US/08477460B
; Patent No. 6034223
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 IMMUNO
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,460B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ UI NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
; US-08-477-460B-2

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Query Match          95.4%; Score 554; DB 3; Length 432;
Best Local Similarity 93.6%; Pred. No. 5.9e-56;
Matches 102: Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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QY	61	REQQNSTYRVVSVLTVLHODWLNGLGEYCKVSNKGLPSSIEKTIISKAK	109
Db	277	REQFNSTPRVSVLVVHODWLNGLGEYCKVSNKGLPAPIETISKTK	325

RESULT

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; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
;
US-09-329-916-2

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Best Local Similarity 93.6%; Pred.No.5.9e-56;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps

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Db 217 APPVAGSVLFFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 276
;
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;

RESULT 6
US-08-485-372A-2
; Sequence 2, Application US/08485372A
; Patent No. 6187748
; GENERAL INFORMATION:
; APPLICANT: Beaudry, Gary A.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,372A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,227
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37690-II-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien

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; CELL TYPE: lymphocyte
US-08-485-372A-2

Query Match	95.4%	Score 554;	DB 4;	Length 432;
Best Local Similarity	93.6%	Pred. NO. 5.9e-56;		
Matches 102; Conservative	5;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1	APPVAGPSVFLFP	PKD	TL	MI	SR	PE	VT	CV	VV	VS	SH	ED	PE	VK	FN	WY	DG	VE	HN	AK	TK	60
Db	217	APPVAGPSVFLFP <th>PKD</th> <th>TL</th> <th>MI</th> <th>SR</th> <th>PE</th> <th>VT</th> <th>CV</th> <th>VV</th> <th>VS</th> <th>SH</th> <th>ED</th> <th>PE</th> <th>VK</th> <th>FN</th> <th>WY</th> <th>DG</th> <th>VE</th> <th>HN</th> <th>AK</th> <th>TK</th> <th>276</th>	PKD	TL	MI	SR	PE	VT	CV	VV	VS	SH	ED	PE	VK	FN	WY	DG	VE	HN	AK	TK	276

Qy	61	REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEK	109
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Db	277	REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKT	325
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RESULT 7
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 ; Sequence 2, Application US/09409006A
 ; Patent No. 6342586
 ; GENERAL INFORMATION:
 ; APPLICANT: Progenics Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
 ; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 422523 COOP III

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1  TITLE: 42233 COOP 01
2  INFORMATION FOR SEQ ID NO: 2:
3  SEQUENCE CHARACTERISTICS:
4  LENGTH: 432 amino acids
5  TYPE: amino acid
6  STRANDEDNESS: unknown
7  TOPOLOGY: unknown
8  MOLECULE TYPE: protein
9  ORIGINAL SOURCE:
10 ORGANISM: homo sapien
11 CELL TYPE: lymphocyte
12 US-09-409-006A-2

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Query Match 95.4%; Score 554; DB 4; Length 432;
Best Local Similarity 93.6%; Pred. No. 5.9e-56;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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 217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276
 |||||

Qy	61	REEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEK	109
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RESULT      8
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; Sequence 2, Application PC/TUS9307422
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07422
; FILING DATE: 19930806

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJMJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
PCT-US93-07422-2

Query Match 95.4%; Score 554; DB 5; Length 432;
Best Local Similarity 93.6%; Pred. No. 5.9e-56;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY	1	217
Db	APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60	APPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276

```

61 REEQNSTYRVVSVLTVLHQDWLNGKEYCKVSKNGLPSSIEKTTISKAK 109
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
277 REEQFNSTRVSVLTVVHQDWLNGKEYCKVSKNGLPAPIEKTISKTK 325

```

RESULT 9
US-08-477-460B-4
; Sequence 4, Application US/08477460B
; Patent No. 6034223
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-379-516-4

Query Match          95.4%; Score 554; DB 3; Length 530;
Best Local Similarity 93.6%; Pred. No. 7.6e-56;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1 APPVAGSVFLFPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      315 APPVAGSVFLFPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 374
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      61 REEQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIISKAK 109
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      375 REEQNSTYRVSVLTVLHQDLNGKEYCKVSNKGLPAPIEKTISKTK 423
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
US-09-329-916-4
; Sequence 4, Application US/09329916
; Patent No. 6177549
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/329,916
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,460
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-09-329-916-4

Query Match          95.4%; Score 554; DB 4; Length 530;

```

```

RESULT 13
US-09-409-006A-4
; Sequence 4, Application US/09409006A
; Patent No. 6342586
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIEY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/409,006A
; FILING DATE: 29-SEP-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
;
US-09-409-006A-4

Query Match          95.4%; Score 554; DB 4; Length 530;
Best Local Similarity 93.6%; Pred. No. 7.6e-56;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy      1 APPVAGPSVLFPKPKDITLMISTPTEVCVVDDVSHPEDPEVKFNWYVDGVGVHNAKTGP 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      315 APPVAGPSVLFPKPKDITLMISTPTEVCVVDDVSHPEDPEVQFNWYVDGVGVHNAKTGP 374

Qy      61 REEQYNSTYRVSVLTVLHQDLWGKEYCKVKSNKGLPSPSIETISKRAK 109
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      375 REEQFNSTFRVSVLTVVHQDLWGKEYCKVKSNKGLPAPIEKTISKTK 423

RESULT 14
PCT-US93-07422-4
; Sequence 4, Application PC/TUS9307422
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIEY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham

```


STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 19930806
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
PCT-US93-07422-4

Query Match 95.4%; Score 554; DB 5; Length 530;
Best Local Similarity 93.6%; Pred. No. 7.6e-56;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
|||||
Db 315 APPVAGPSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 374
|||||
QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109
|||||
Db 375 REEQFNSTFRVSVLTVLHQDWLNGKEYKCKVSNKGLPAPLPIETISKTK 423
|||||

RESULT 15

US-08-788-800-12
Sequence 12, Application US/08788800
Patent No. 5914112
GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
APPLICANT: Thomas, G. Roger
APPLICANT: Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,800
FILING DATE: 22-Jan-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0987r1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7188
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-788-800-12

Query Match 94.8%; Score 551; DB 2; Length 450;
Best Local Similarity 92.7%; Pred. No. 1.4e-55;
Matches 101; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 1 APPVAGPSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
|||||
Db 235 APPVAGPSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGMEVHNAKTKP 294
|||||
QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 109
|||||
Db 295 REEQFNSTFRVSVLTVLHQDWLNGKEYKCKVSNKGLPAPLPIETISKTK 343
|||||

Search completed: June 21, 2002, 08:32:13
Job time: 87 sec

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R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:

A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) and two identical heavy (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83, 140-200, 246-304/Disulfide bonds: #status experimental
F:102, 103, 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.4%; Score 554; DB 1: Length, 326;
Best Local Similarity 93.6%; Pred. No. 7, 2e-48;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
DB 111 APPVAGSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 170
QY 61 REQYNSTYRVSVLTVLHODWLNKGYCKVSKNKGKGLPSSIEKTIISKAK 109
DB 171 REQYNSTYRVSVLTVLHODWLNKGYCKVSKNKGKGLPAPIETISKT 219

RESULT 2

QY 2
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 93.8%; Score 545; DB 2: Length 234;
Best Local Similarity 91.2%; Pred. No. 3, 9e-47;
Matches 104; Conservative 1; Mismatches 3; Indels 6; Gaps 1;

QY 2 PPVA-----GPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 55
DB 21 PPAAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 80
QY 56 AKTKPREQYNSTYRVSVLTVLHODWLNKGYCKVSKNKGKGLPSSIEKTIISKAK 109
DB 81 AKTKPREQYNSTYRVSVLTVLHODWLNKGYCKVSKNKGKGLPAPIETISKAK 134

RESULT 3

QY 3
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866

R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FBL>
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 93.5%; Score 543; DB 4: Length 255;
Best Local Similarity 90.4%; Pred. No. 6, 8e-47;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 55
DB 35 PPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 94

QY 56 AKTKPREQYNSTYRVSVLTVLHODWLNKGYCKVSKNKGKGLPSSIEKTIISKAK 109
DB 95 AKTKPREQYNSTYRVSVLTVLHODWLNKGYCKVSKNKGKGLPAPIETISKAK 148

RESULT 4

QY 4
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C:Accession: A93433; S33887; B90563; A90564; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.
A:Reference number: A93433; MUID:82274238
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: EMBL:Z17370
A:Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) marker
A:Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992

QY 4
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A:Reference number: S33887; MUID:83001943
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113; 235-330 <TAK>
A:Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid se

QY 4
A:Reference number: A90563; MUID:71064024
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-135 <CUN>
A:Note: this sequence has the Gln(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

QY 4
A:Reference number: A90564; MUID:71064025
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein

A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, 'A':Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie), igen Primaerstruktur.
A:Reference number: A91668; MUID:77070269
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A:Note: this sequence has the Gln(17) and Gln(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A:Note: this sequence has the Gln(3) and Gln(non-1) markers
R:Call, W.E.; Edelman, G.W.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 9/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83, 144-204, 250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 93.5%; Score 543; DB 1; Length 330;
Best Local Similarity 90.4%; Pred. No. 9.2e-47;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55

Db 110 PPCPAPELLGGPSVFLPFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 169

QY 56 AKTKPREQYNSTYRVVSVLTVQLHQLDNLGKEYCKVSNKGLPSSIEKTISKAK 109

Db 170 AKTKPREQYNSTYRVVSVLTVQLHQLDNLGKEYCKVSNKALPAPIETISKAK 223

RESULT 5

S69339

Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000

A:Accession: S69339; S72664

R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.

A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A:Reference number: S69339; MUID:95262687

A:Accession: S69339
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamilichi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 93.5%; Score 543; DB 2; Length 374;
Best Local Similarity 90.4%; Pred. No. 1.1e-46;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55

Db 154 PPCPAPELLGGPSVFLPFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 213

QY 56 AKTKPREQYNSTYRVVSVLTVQLHQLDNLGKEYCKVSNKGLPSSIEKTISKAK 109

Db 214 AKTKPREQYNSTYRVVSVLTVQLHQLDNLGKEYCKVSNKALPAPIETISKAK 267

RESULT 6

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999

A:Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 <ELL>

A:Note: the sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constan

A:Reference number: A90249; MUID:70207560

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30; 81-326 <PIN>

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 9/1; 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83, 141-201, 247-305/Disulfide bonds: #status predicted

F:106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.9%; Score 540; DB 1; Length 327;
Best Local Similarity 95.3%; Pred. No. 1.8e-46;
Matches 101; Conservative 3; Mismatches 2; Indels 0; Gaps 0;


```
I47162
Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A;Reference number: I47158; MUID:95015845
A;Accession: I47162
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A;Residues: 1-277 <KAC>
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C;Genetics:
A;Gene: IgG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMX>
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	Query Match	Score	DB 2:	Length	Mismatches	Gaps
QY	6 GPSVFLPPPKDKDILMISRTPEVTVCVVVDVSHEDEPVKNWTVDGVEVNNAKTTPREEQY 65 : : : : : : : : : :	78.0%;	DB 2;	Length 277; Best Local Similarity 77.9%; Pred. No. 7.7e-38;	Indels 0;	Gaps 0;
Dd	65 GPSEAFIFPFPKKDTLMISRTPKVTCCVVVDVDSQENPEVFQSWTYDVGVHTAGTRPRKEGF 124 : : : : : : : : : :					
QY	66 NSTRYRVSVLVNLHODWLNGKEYCKVKSNKGLPSSIEKTISKAK 109 : : : : : : : : : :					
Dd	125 NSTRYRVSVLVPIQHODWLNGREKFCKVNNKDLPAPITRIISRKA 168 : : : : : : : : : :					

```
RESULT 13
I47161
Ig gamma 3 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47161
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A;Reference number: I47158; MUID:95015845
A;Accession: I47161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128
C;Genetics:
A;Gene: IgG3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMX>
```

	Query Match	Score	DB 2:	Length	Mismatches	Gaps
QY	4 VAGPSVELFPKPDKDTLMISRTPEVTTCVVVDVSHPEDPEVKFNWTVDGVEVHNAAKTTPREE 63 : : : : : : : : : :	76.1%;	DB 2;	Length 328; Best Local Similarity 77.1%; Pred. No. 1.2e-36;	Indels 0;	Gaps 0;
Dd	114 VAGPSVFIFFPKPDTLMSIQSTPTETCVVVDVSKAEAVQFSWIYVGVEVHTATRPKEE 173 : : : : : : : : : :					
QY	64 QYNSTRYRVSVLTVLHQDWLNAGEKYCKVSNKGLSPSSIEKTISKIA 108 : : : : : : : : : :					
Dd	174 QFNSTRYRVSVLPIQHODWLNGEKFKCNVNDLPAPITRTTISA 218 : : : : : : : : : :					

```
RESULT 14
I47158
Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
```

R:Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a

A:Reference number: I47158; MUID:95015845

A:Accession: I47158

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-328 <KAC>

C:Genetics:

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 442; DB 2: Length 328;
Best Local Similarity 77.1%; Pred. No. 1.2e-36;
Matches 81; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 63

Db 114 VAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 173

QY 64 QYNSTYRVSVLTVLQDNLNGKEYCKVSNKGLPSSIEKTSKA 108

Db 174 QFNSTYRVSVLTVLQDNLNGKEYCKVSNKGLPSSIEKTSKA 218

RESULT 15

S22080

Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine

N:Alternate names: Ig gamma-1 chain C region (clone 8.10)

C:Species: Bos primigenius taurus (cattle)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S22080; S06610; A31303

R:Sanders, P.G.

submitted to the EMBL Data Library, November 1991

A:Reference number: S22080

A:Accession: S22080

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-470 <SAN>

A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440

R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.

Mol. Immunol. 26, 841-850, 1989

A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma

A:Reference number: S06610; MUID:90097956

A:Accession: S06610

A:Molecule type: DNA

A:Residues: 142-470 <SYM>

A:Cross-references: EMBL:X16701

A>Note: the sequence was determined from the germline gene

C:Genetics:

A:Gene: Ig CH gamma-1

A:Introns: 98/1; 111/1; 221/1

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein

F:161-225/Domain: immunoglobulin homology <IMM>

F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.8%; Score 429; DB 2: Length 470;
Best Local Similarity 71.8%; Pred. No. 3.6e-35;
Matches 79; Conservative 12; Mismatches 17; Indels 2; Gaps 1;

QY 2 PP--VAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59

Db 252 PPPELGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 311

QY 60 PREEQNSTYRVSVLTVLQDNLNGKEYCKVSNKGLPSSIEKTSKAK 109

Db 312 PREEQNSTYRVSVLTVLQDNLNGKEYCKVSNKGLPSSIEKTSKAK 361

Search completed: June 21, 2002, 08:37:52
Job time: 426 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:36:16 ; Search time 48.19 Seconds
(without alignments)
87.579 Million cell updates/sec

Title: US-09-674-857-1

Perfect score: 581
Sequence: 1 APPVAGPSVFLFPKPKDTL.....CKVSNKGLPSSIEKTSKAK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554	95.4	326	1 GC2_HUMAN	P01859 homo sapien
2	543	93.5	330	1 GC1_HUMAN	P01857 homo sapien
3	540	92.9	327	1 GC4_HUMAN	P01861 homo sapien
4	504	86.7	290	1 GC3_HUMAN	P01860 homo sapien
5	420	72.3	333	1 GCB_RAT	P20761 rattus norv
6	417	71.8	329	1 GC2_CAVPO	P01862 cavia porce
7	413	71.1	323	1 GC_RABIT	P01870 oryctolagus
8	410.5	70.7	329	1 GC3_MOUSE	P22436 mus musculu
9	410.5	70.7	398	1 GC3_MOUSE	P03987 mus musculu
10	396	68.2	324	1 GC1_MOUSE	P01868 mus musculu
11	396	68.2	393	1 GC1_MOUSE	P01869 mus musculu
12	392	67.5	329	1 GCC_RAT	P20762 rattus norv
13	382	65.7	335	1 GCAB_MOUSE	P01864 mus musculu
14	382	65.7	336	1 GCB_MOUSE	P01866 mus musculu
15	382	65.7	405	1 GCB_MOUSE	P01867 mus musculu
16	380	65.4	326	1 GCL_RAT	P20759 rattus norv
17	377	64.9	330	1 GCRA_MOUSE	P01863 mus musculu
18	377	64.9	399	1 GCAM_MOUSE	P01865 mus musculu
19	339	58.3	322	1 GCA_RAT	P20760 rattus norv
20	166.5	28.7	428	1 EPC_HUMAN	P01854 homo sapien
21	153	26.3	429	1 EPC_RAT	P01855 rattus norv
22	153	26.3	457	1 MUC_SUNMU	P20768 suncus muri
23	139.5	24.0	299	1 ALC_RABIT	P01879 oryctolagus
24	139	23.9	106	1 KAC_HUMAN	P01834 homo sapien
25	139	23.9	391	1 MUCB_HUMAN	P04220 homo sapien
26	138	23.8	421	1 EPC_MOUSE	P06336 mus musculu
27	138	23.8	454	1 MUC_HUMAN	P01871 homo sapien
28	132	22.7	103	1 LAC_CHICK	P20763 gallus gall
29	132	22.7	454	1 MUC_MESAU	P06337 mesocricetu
30	132	22.7	455	1 MUC_MOUSE	P01872 mus musculu
31	132	22.7	476	1 MUC_MOUSE	P01873 mus musculu
32	127.5	21.9	105	1 LAC1_MOUSE	P01843 mus musculu
33	126.5	21.8	105	1 LAC5_MOUSE	P20765 mus musculu

RESULT 1					ALIGNMENTS				
ID	GC2_HUMAN	STANDARD;	PRT;	326 AA.					
AC	P01859;								
DT	21-JUL-1986 (Rel. 01, Created)								
DT	21-JUL-1986 (Rel. 01, Last sequence update)								
DT	16-OCT-2001 (Rel. 40, Last annotation update)								
DE	Ig gamma-2 chain C region.								
GN	IGHG2.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
[1]									
RN	SEQUENCE OF 2-326 FROM N.A.								
RP	MEDLINE=82197621; PubMed=6804948;								
RX	Ellison J.W., Hood L.E.;								
RA	"Linkage and sequence homology of two human immunoglobulin gamma								
RT	heavy chain constant region genes.";								
RL	Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).								
[2]									
RN	SEQUENCE OF 88-115 FROM N.A.								
RP	TISSUE=Fetal liver;								
RX	MEDLINE=83001943; PubMed=6811139;								
RA	Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;								
RT	"Structure of human immunoglobulin gamma genes: implications for								
RL	evolution of a gene family.";								
[3]									
RN	Cell 29:671-679(1982).								
RP	SEQUENCE OF 99-177 AND 310-326 FROM N.A.								
RX	TISSUE=Fetal liver;								
RA	MEDLINE=84235992; PubMed=6329676;								
RT	Krawinkel U., Rabbitts T.H.;								
RL	"Comparison of the hinge-coding segments in human immunoglobulin gamma								
RT	heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass								
genes.";									
[4]									
RN	EMBO J. 1:403-407(1982).								
RP	SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).								
RX	MEDLINE=81007873; PubMed=6774012;								
RA	Wang A.-C., Tung E., Fudenberg H.H.;								
RT	"The primary structure of a human IgG2 heavy chain: genetic,								
evolutionary, and functional implications.";									
J. Immunol. 125:1048-1054(1980).									
[5]									
RN	SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).								
RP	MEDLINE=80001357; PubMed=113060;								
RA	Connell G.E., Parr D.M., Hofmann T.;								
RT	"The amino acid sequences of the three heavy chain constant region								
domains of a human IgG2 myeloma protein.";									
Can. J. Biochem. 57:758-767(1979).									
[6]									
RN	SEQUENCE OF 238-275 (ZIE).								
RP	MEDLINE=80114419; PubMed=118920;								
RA	Hofmann T., Parr D.M.;								
RT	"A note of the amino acid sequence of residues 381-391 of human								

P01874 canis famil
P20764 mus musculu
P03988 oryctolagus
P04221 oryctolagus
P01877 homo sapien
P20758 gorilla gor
P01876 homo sapien
P01842 homo sapien
P15814 homo sapien
P01847 oryctolagus
P01840 oryctolagus
P01878 mus musculu

RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -I- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOYPIC MARKER, 97-K, & THE
CC G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE G1M(3)
CC MARKER & THE G1M (NON-1) MARKERS.
CC -I- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35-116, 198, 269 & 272.
CC -I- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -I- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198, 267&272.
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DR EMBL; J00228; AAC82527.1; ALT_INIT.
DR PIR; A02146; GHU.
DR PDB; 1FC1; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR MIM; 147100; -
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; Ig_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 223 CH2.
FT DOMAIN 224 330 CH3.
FT DISULFID 27 83
FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT MOD_RES 330 330
FT VARIANT 97 97
FT
FT
FT VARIANT 239 239
FT
FT VARIANT 241 241
FT
FT STRAND 123 126
FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164
FT STRAND 165 166
FT STRAND 175 178
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 206

FT STRAND 215 219
FT STRAND 227 234
FT STRAND 230 234
FT HELIX 238 240
FT TURN 241 242
FT STRAND 245 256
FT STRAND 260 266
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 93.5%; Score 543; DB 1; Length 330;
Best Local Similarity 90.4%; Pred. No. 2.3e-47;
Matches 103; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFUFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
|| : |||||
DB 110 PCGPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 169
|| : |||||
QY 56 AKTKPREEQNSTYRYVSVLTVLHQDLNGKEYCKVSKGLPSISIEKTSKAK 109
|||||
DB 170 AKTKPREEQNSTYRYVSVLTVLHQDLNGKEYCKVSKGLPSISIEKTSKAK 223

RESULT 3
ID GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-4 chain C region.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT constant region of a gamma 4 chain.";
RL Biochem J 117:33-47(1970).
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DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; G4HU.
DR HSSP; P01842; 7FAB.


```

FT VARIANT 227 227 S -> N (IN OMM).
FT /FTid=VAR_003894.
FT MISSING (IN ZUC).
FT /FTid=VAR_003895.
FT VARIANT 279 279 F -> Y (IN OMM).
FT /FTid=VAR_003896.
FT SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;

Query Match 86.7%; Score 504; DB 1; Length 290;
Best Local Similarity 86.8%; Pred. No. 1.6e-43;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPKPKDLMISRTPEVTCVVVDSHEDPEVKFNWYVDGVVHNAKTPREE 63
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
78 LGGPSVFLPPKPKDLMISRTPEVTCVVVDSHEDPEVKFNWYVDGVVHNAKTPREQ 137
QY : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 QYNSTRVSVLVHLQHDWMLNGEKYCKVSKNGLPSSIEKTIKSKAK 109
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
138 QFNSTRVSVLVHLQHDWMLNGEKYCKVSKNGLPSSIEKTIKSKAK 183

RESULT 5
GCB_RAT
ID GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG-like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
FT SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 72.3%; Score 420; DB 1; Length 333;
Best Local Similarity 69.8%; Pred. No. 5.1e-35;
Matches 74; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPKPKDLMISRTPEVTCVVVDSHEDPEVKFNWYVDGVVHNAKTPREE 63
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 LGGPSVFLPPKPKDLMISRTPEVTCVVVDSHEDPEVKFNWYVDGVVHNAKTPREQ 180
QY : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 QYNSTRVSVLVHLQHDWMLNGEKYCKVSKNGLPSSIEKTIKSKAK 109
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 QYNSTRVSVLVHLQHDWMLNGEKYCKVSKNGLPSSIEKTIKSKAK 226

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RESULT 6
GCB_RAT
ID GCB_RAT STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the
half-cystine joining heavy and light chains.";
RT Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
and hinge region. cyanogen bromide fragments.";
RT Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
antibodies.";
RT Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
antibodies.";
RX Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
CC Biochemistry 10:26-31(1971).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
13 INBRED GUINEA PIGS.
DR PIR; A02151; GZGP.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG-like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202

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FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
 FT DISULFID 248 308
 SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1EBA9 CRC64;

Query Match 71.8%; Score 417; DB 1; Length 329;
 Best Local Similarity 70.9%; Pred. No. 1e-34;
 Matches 78; Conservative 12; Mismatches 18; Indels 2; Gaps 1;

QY 2 PP--VAGPSVFLPPPKDKTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVGVHNAKTK 59
 || : ||||:||||||| ||||| ||||| :|||: ||||| |||||
 DB 112 PPNLGGPSVFLPPPKDKTLMISLTPRTVCVVDVSDQDEPEVQTFWVDKPNVGNATK 171
 || : ||||:||||||| ||||| ||||| :|||: ||||| |||||
 QY 60 PREQYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKSKAK 109
 || ||||:|||| ||| : ||||| ||||| ||||| ||||| |||||
 DB 172 PRVEQNTTFRVESVLPQHODWLNKGYCKVSNKGLPSSIEKTIKSKAK 221
 || ||||:|||| ||| : ||||| ||||| ||||| ||||| |||||

RESULT 7
 GC_RABIT STANDARD; PRT; 323 AA.
 ID GC_RABIT
 AC P01870;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma chain C region.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84030930; PubMed=6313520;
 RA Bernstein K.E., Alexander C.B., Mage R.G.;
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
 F-1 haplotype.";
 RL Immunogenetics 18:387-397(1983).
 RN [2]
 RP SEQUENCE OF 1-128.
 RX MEDLINE=76135469; PubMed=1243651;
 RA Pratt D.M., Mole L.E.;
 RT "Sequence studies on the constant region of the Fd sections of rabbit
 immunoglobulin G of different allotype.";
 RL Biochem. J. 151:337-349(1975).
 RN [3]
 RP SEQUENCE OF 88-266 FROM N.A.
 RX MEDLINE=83299917; PubMed=6193512;
 RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
 RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
 heavy chain and identification of two genomic C gamma genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
 RN [4]
 RP SEQUENCE OF 132-161.
 RX MEDLINE=70110015; PubMed=5461106;
 RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
 RT "Sequence studies of the Fd section of the heavy chain of rabbit
 immunoglobulin G.";
 RL Biochem. J. 116:249-259(1970).
 RN [5]
 RP SEQUENCE OF 129-131 AND 155-322.
 RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
 RL (In) Killander J. (eds.);
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
 Stockholm (1967).
 CC -I- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
 MARKERS, AND REF.5 THE E15 MARKER.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M16426; AAA31289.1;
 DR PIR; A02161; GHRB.
 DR HSP; P01857; IFC1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_cl.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IgC1; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT VARIANT 104 104 T -> M (IN D11 MARKER).
 FT VARIANT 185 185 T -> A (IN E15 MARKER).
 FT CONFLICT 48 48 N -> E (IN REF. 2).
 FT CONFLICT 71 71 V -> VPV (IN REF. 2).
 FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
 FT CONFLICT 173 173 N -> D (IN REF. 5).
 FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
 FT CONFLICT 201 201 N -> D (IN REF. 5).
 FT CONFLICT 218 218 Q -> E (IN REF. 5).
 FT CONFLICT 233 233 E -> Q (IN REF. 5).
 FT CONFLICT 246 246 N -> D (IN REF. 5).
 FT CONFLICT 256 256 E -> G (IN REF. 5).
 FT CONFLICT 260 260 N -> D (IN REF. 5).
 FT CONFLICT 266 266 N -> D (IN REF. 5).
 FT CONFLICT 280 280 Y -> W (IN REF. 5).
 FT CONFLICT 284 284 N -> S (IN REF. 5).
 SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 71.1%; Score 413; DB 1; Length 323;
 Best Local Similarity 69.1%; Pred. No. 2.5e-34;
 Matches 76; Conservative 14; Mismatches 18; Indels 2; Gaps 1;

QY 2 PP--VAGPSVFLPPPKDKTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVGVHNAKTK 59
 || : ||||:||||||| ||||| ||||| :|||: ||||| |||||
 DB 107 PPELLGGPSVFLPPPKDKTLMISRTPEVTVVVDVSDQDEPEVQTFWVWVNEQVTRAPP 166
 || : ||||:||||||| ||||| ||||| :|||: ||||| |||||
 QY 60 PREQYNSTYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKSKAK 109
 ||||:|||| ||| : ||||| ||||| ||||| ||||| |||||
 DB 167 LREQQFNSTIRVSVLTPLTHODWLNKGYCKVSNKGLPSSIEKTIKSKAK 216
 ||||:|||| ||| : ||||| ||||| ||||| ||||| |||||

RESULT 8
 GC3_MOUSE STANDARD; PRT; 329 AA.
 ID GC3_MOUSE
 AC P22436;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-3 chain C region, secreted form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85027161; PubMed=6092053;
 RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA Tucker P.W., Blattner F.R.;
 RT "Structural analysis of the murine IgG3 constant region gene.";
 RL EMBO J. 3:2041-2046(1984).
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DR EMBL; J00451; -: NOT_ANNOTATED_CDS.
DR PIR; B02156; G3MSC.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00410; IGc1; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 97
FT DOMAIN 98 113
FT DOMAIN 114 223
FT DOMAIN 224 327
FT TRANSMEM 346 362
FT DOMAIN 363 398
FT CONFLICT 333 333
FT CONFLICT 342 342
FT CONFLICT 388 388
FT SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 70.7%; Score 410.5; DB 1; Length 329;
Best Local Similarity 67.6%; Pred. No. 4.6e-34;
Matches 75; Conservative 15; Mismatches 18; Indels 3; Gaps 1;

QY 2 PP---VAGPSVLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 58
DB 112 PGNILGGPSVFIFPPKPKDLMISLTPTKTCVVVDVSDPDHVSFVFNKVEHTAWT 171
QY 59 KPREEQNSTYRVSVLTVLHODWLNKGEYCKVSKNGLPSSIEKTSKAK 109
DB 172 OPREAQNSTYRVSVLPIQHODWNRGKEFKCKVNNKALPAPIERTISPK 222

RESULT 9
GC3M_MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041483; PubMed=6314258;
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00451; AAB59655.1; -
DR EMBL; V01526; CAA24767.1; ALT_SEQ.
DR PIR; A02155; G3MSM.
DR HSSP; P01857; 1FC1.

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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 97
FT DOMAIN 98 113
FT DOMAIN 114 223
FT DOMAIN 224 327
FT TRANSMEM 346 362
FT DOMAIN 363 398
FT CONFLICT 333 333
FT CONFLICT 342 342
FT CONFLICT 388 388
FT SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 70.7%; Score 410.5; DB 1; Length 398;
Best Local Similarity 67.6%; Pred. No. 5.7e-34;
Matches 75; Conservative 15; Mismatches 18; Indels 3; Gaps 1;

QY 2 PP---VAGPSVLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 58
DB 112 PGNILGGPSVFIFPPKPKDLMISLTPTKTCVVVDVSDPDHVSFVFNKVEHTAWT 171
QY 59 KPREEQNSTYRVSVLTVLHODWLNKGEYCKVSKNGLPSSIEKTSKAK 109
DB 172 OPREAQNSTYRVSVLPIQHODWNRGKEFKCKVNNKALPAPIERTISPK 222

RESULT 10
GC1_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salser W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=78242288; PubMed=98524;

```

RA Adetugbo K.;
 RT "Evolution of immunoglobulin subclasses. Primary structure of a
 RL murine myeloma gamma chain.";
 RN J. Biol. Chem. 253:6068-6075(1978).
 [5]
 RP DISULFIDE BONDS (MOPC 21).
 RX MEDLINE=73008889; PubMed=5073237;
 RA Svasti J., Milstein C.;
 RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
 RL Biochem. J. 126:837-850(1972).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; V00793; CAA24172.1; -;
 DR EMBL; V00793; CAA24173.1; -;
 DR EMBL; V00793; CAA24174.1; -;
 DR EMBL; V00793; CAA24175.1; -;
 DR EMBL; V00795; CAA24176.1; -;
 DR PIR; A02159; GIMS.
 DR HSSP; P01842; 7FAB.
 DR GlycoSuiteDB; P01868; -;
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR003006; Igh_MHC.
 DR InterPro; IPR003597; Igh_C1.
 DR Pfam; PF00047; Igh; 3.
 DR SMART; SM00407; IghC1; 2.
 DR PROSITE; PS00290; IGH_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 110 HINGE.
 FT DOMAIN 111 217 CH2.
 FT DOMAIN 218 324 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 138 198
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
 FT FTID-CAR_000055.
 FT DISULFID 244 302
 FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
 FT CONFLICT 276 276 N -> D (IN REF. 3).
 FT CONFLICT 278 278 N -> D (IN REF. 3).
 SQ SEQUENCE 324 AA; 35704 MW; A338812F3DF2C93 CRC64;
 Query Match 68.2%; Score 396; DB 1; Length 324;
 Best Local Similarity 67.6%; Pred. No. 1.3e-32;
 Matches 69; Conservative 19; Mismatches 14; Indels 0; Gaps 0;
 QY 8 SVFLPPKPTLMISRTVEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKPREEQYNS 67
 Db 116 SVFIFFPKPDVLTITLTTPKVTVCVVVDISKDDPEYQFSNFDVDEVHTAQTPREEQNS 175
 QY 68 TVRVSVLTVLHQDWLNGKEYKCKVKNKGLPSSIEKTSKAK 109
 Db 176 TFRSVSELPIMHQDWLNGKEYKCKVKNKGLPSSIEKTSKAK 217
 RESULT 11
 GC1M_MOUSE
 ID GC1M_MOUSE STANDARD; PRT; 393 AA.
 AC P01869;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ig gamma-1 chain C region, membrane-bound form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80045036; PubMed=115593;
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
 RT gamma 1 chain gene.";
 RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 323-393 FROM N.A.
 RX MEDLINE=82197626; PubMed=6804950;
 RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
 RT "mRNA for surface immunoglobulin gamma chains encodes a highly
 RT conserved transmembrane sequence and a 28-residue intracellular
 RT domain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
 RN [3]
 RP SEQUENCE OF 323-366 FROM N.A.
 RX MEDLINE=82115295; PubMed=6799207;
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
 RA Eisenberg D., Wall R.;
 RT "Gene segments encoding transmembrane carboxyl termini of
 RT immunoglobulin gamma chains.";
 RL Cell 26:19-27(1981).
 RN [4]
 RP SEQUENCE OF 1-44 FROM N.A.
 RX MEDLINE=8222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 RT immunoglobulin gamma chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
 CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
 CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
 CC SEGMENT OF MU CHAINS.
 CC -----
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 CC -----
 DR EMBL; V00793; CAA24172.1; -;
 DR EMBL; V00793; CAA24173.1; -;
 DR EMBL; V00793; CAA24174.1; -;
 DR PIR; B02159; GIMSM.
 DR HSSP; P01842; 7FAB.
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR003006; Igh_MHC.
 DR InterPro; IPR003597; Igh_C1.
 DR Pfam; PF00047; Igh; 3.
 DR SMART; SM00407; IghC1; 2.
 DR PROSITE; PS00290; IGH_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing; Transmembrane.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 110 HINGE.
 FT DOMAIN 111 217 CH2.
 FT DOMAIN 218 324 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
 FT FTID-CAR_000055.
 FT DISULFID 244 302
 FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
 FT CONFLICT 276 276 N -> D (IN REF. 3).
 FT CONFLICT 278 278 N -> D (IN REF. 3).
 SQ SEQUENCE 324 AA; 35704 MW; A338812F3DF2C93 CRC64;

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FT DISULFID 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 N-LINKED (GLCNAC. . .).
FT CARBOHYD 174
FT DISULFID 244
FT DISULFID 302 POTENTIAL.
FT TRANSMEM 340 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 358
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7AICE27 CRC64;

Query Match 68.2%; Score 396; DB 1; Length 393;
Best Local Similarity 67.6%; Pred. No. 1.6e-32;
Matches 69; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 8 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYGVGVEVHNAKTKPREEQYNS 67
Db 116 SVFIFPPKPKDILITLTPKVCVVVDVSEEDPDVQFSEWFDVDEVHTAQTQTPREEQNS 175

QY 68 TYRVVSVLTVHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Db 176 TFRSVSELPIMHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 217

RESULT 12
GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Bruggemann M., Delmastro-Gallire P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RL Eur. J. Immunol. 18:317-319(1988).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07189; CAA30169.1;
DR PIR; S00847; S00847.
DR HSSP; P01857; 1FCL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DOMAIN 329 329
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
```

```
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 67.5%; Score 392; DB 1; Length 329;
Best Local Similarity 68.0%; Pred. No. 3.3e-32;
Matches 70; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 7 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYGVGVEVHNAKTKPREEQYN 66
Db 120 PSVFIFFPPKPKDILITLTPKVCVVVDVSEEDPDVQFSEWFDVDEVHTAQTQTPREEQLN 179

QY 67 TYRVVSVLTVHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
Db 180 GTRVYVSTLHIQDWMGSKFKCKVNNKDLPSIEKTIKPR 222

RESULT 13
GCCAB_MOUSE STANDARD; PRT; 335 AA.
ID GCCAB_MOUSE
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT IGG2aa and IGG2ab alleles of the mouse."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain C regions of Igla and Ig1b allotypic forms."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -----
CC MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSSP; P01857; 1FCL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 65.7%; Score 382; DB 1; Length 335;
Best Local Similarity 62.3%; Pred. No. 3.4e-31;
Matches 71; Conservative 17; Mismatches 20; Indels 6; Gaps 1;
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QY 2 PPVA-----GPSVFLPPPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWVVDGVEVHN 55
DB 115 PPCAAPDLGGSPVFPPKIKDVLMSLSPWTCVVVDVSEDDPDVQISFVNNVEVHT 174
QY 56 AKTKPREQYNSYRVVSVLTVLHQDWLNGKEYKCKVSKGKLPPSSIEKTISKAK 109
DB 175 AQQTQTHREDYNSLTRVVSALPIQHQDWMSGKEFKCKVNNRALSPIETISKPR 228

RESULT 14
GCB_MOUSE
ID GCB_MOUSE STANDARD; PRT; 336 AA.
AC P01866;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2B chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (A ALLELE).
RX MEDLINE=80120716; PubMed=6766534;
RA Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
RT "Complete nucleotide sequence of immunoglobulin gamma2b chain gene
RL cloned from newborn mouse DNA.";
RL Nature 283:786-789(1980).
[2]
RP SEQUENCE FROM N.A. (MPC 11).
RX MEDLINE=80081501; PubMed=117548;
RA Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;
RT "Structure of the constant and 3' untranslated regions of the murine
RL gamma 2b heavy chain messenger RNA.";
RL Science 206:1299-1303(1979).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=80081502; PubMed=117549;
RA Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
RT "Sequence of the cloned gene for the constant region of murine gamma
RL 2b immunoglobulin heavy chain.";
RL Science 206:1303-1306(1979).
[4]
RP SEQUENCE FROM N.A. (B ALLELE).
RX MEDLINE=82173203; PubMed=6803173;
RA Olio R., Rougeon F.;
RT "Mouse immunoglobulin allotypes: post-duplication divergence of gamma
RL 2a and gamma 2b chain genes.";
RL Nature 296:761-763(1982).
[5]
RP CARBOHYDRATE-LINKAGE SITE THR-105.
RX MEDLINE=94216359; PubMed=7512967;
RA Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,
RA Irimura T., Takahashi N., Kato K., Arata Y.;
RT "O-glycosylation in hinge region of mouse immunoglobulin G2b.";
RL J. Biol. Chem. 269:12345-12350(1994).
CC -1- PTM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS
CC MODIFIED WITH 2 SIALIC ACID RESIDUES.
CC -1- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA
CC CHAINS.
CC -1- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.
DR PIR: A02157; G2MS11.
DR HSP; P01857; IFC1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00410; Ig_like; 1.
DR SMART: SM00407; Ig_c1; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1

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FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 150 210
FT DISULFID 256 314
FT CARBOHYD 105 105 O-LINKED (GALNAC. . .).
FT MOD_RES 336 336 REMOVED POST-TRANSLATIONALLY (PROBABLE).
FT VARIANT 163 163 Q -> R (IN B ALLELE).
FT VARIANT 194 194 T -> A (IN B ALLELE).
FT VARIANT 300 300 N -> D (IN B ALLELE).
FT VARIANT 301 301 M -> I (IN B ALLELE).
FT CONFLICT 25 25 L -> S (IN REF. 2 AND 3).
FT CONFLICT 36 36 S -> P (IN REF. 2 AND 3).
FT CONFLICT 239 239 I -> T (IN REF. 2 AND 3).
SQ SEQUENCE 336 AA; 36658 MW; 7D879662607C356E CRC64;

Query Match 65.7%; Score 382; DB 1; Length 336;
Best Local Similarity 66.3%; Pred. No. 3.4e-31;
Matches 69; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 6 GPSVFLPPPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREQY 65
DB 126 GPSVFLPPPKDXTLMISRTPEVTCVVVDVSEDDPDVQISFVNNVEVHTAQTHREDY 185
QY 66 NSTYRVVSVLTVLHQDWLNGKEYKCKVSKGKLPPSSIEKTISKAK 109
DB 186 NSTYRVVSVLTVLHQDWLNGKEYKCKVSKGKLPPSSIEKTISKAK 229

RESULT 15
GCB_MOUSE
ID GCB_MOUSE STANDARD; PRT; 405 AA.
AC P01867;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 335-405 FROM N.A.
RX MEDLINE=82222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RL immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
[2]
RP SEQUENCE OF 335-378 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Esensberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
RL immunoglobulin gamma chains.";
RL Cell 26:19-27(1981).
CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC SEGMENT OF MU CHAINS.
CC -1- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA
CC CHAINS.
CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-335 IS ASSUMED TO BE
CC IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM.
CC -1- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.
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DR EMBL; J00462; AAB59659.1; ALT_INIT.
 DR FIR; C02154; G2MSBW.
 DR HSSP; P01857; IFC1.
 DR MGD; MGI:96445; Igh-3.
 DR InterPro; IPR003006; Iq_MHC.
 DR InterPro; IPR003597; Iq_c1.
 DR InterPro; IPR003600; Iq_like.
 DR Pfam; PF0047; Iq; 3.
 DR SMART; SM00410; Iq_like; 1.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS00290; Iq_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Transmembrane;
 KW Alternative splicing.
 FT NON_TER 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 150 210
 FT DISULFID 256 314
 FT TRANSMEM 352 369
 FT DOMAIN 370 405 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 405 AA; 44330 MW; 89B3CF0A9B6D49FA CRC64;

Query Match 65.7%; Score 382; DB 1; Length 405;
 Best Local Similarity 66.3%; Pred. No. 4.2e-31;
 Matches 69; Conservative 16; Mismatches 19; Indels 0; Gaps 0;
 QY 6 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 65
 DB 126 GPSVFIIPPNIKDVLMISLTPTKVTCTVVDVSEDDPDVQISWFINNVVHTAQQTTHREDY 185
 QY 66 NSTYRVSVLTVLHQDLNGKCKVKNKGLPSSIEKTSKAK 109
 DB 186 NSTIRVSVLTLPQHQQWMSGCKFKCKVNNKDLPSPIERTISKIK 229

Search completed: June 21, 2002, 09:00:23
 Job time: 1447 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:32:21 ; Search time 176.89 Seconds

(without alignments)
106.600 Million cell updates/sec

Title: US-09-674-857-1

Perfect score: 581

Sequence: 1 APPVAGPSVFLFPKPKDTL.....CKVSNKGLPSSIEKTISKAK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTREMBL19.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mhc.*
- 8: sp_mus.*
- 9: sp_organelle.*
- 10: sp_phage.*
- 11: sp_plant.*
- 12: sp_rodent.*
- 13: sp_virus.*
- 14: sp_vertebrate.*
- 15: sp_unclassified.*
- 16: sp_virus.*
- 17: sp_bacteriap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	543	93.5	701	4 Q96PQ8	Q96pq8 homo sapien
2	443	76.2	337	6 Q95M34	Q95m34 equus caball
3	396	68.2	437	11 Q9R1A4	Q9r1a4 mus musculus
4	396	68.2	463	11 Q9R1C4	Q9r1c4 mus musculus
5	382	65.7	473	11 Q9D8L4	Q9d8l4 mus musculus
6	382	65.7	473	11 Q9L205	Q9l205 mus musculus
7	368	63.3	468	11 Q99L31	Q99l31 mus musculus
8	368	63.3	473	11 Q99L25	Q99l25 mus musculus
9	138	23.8	375	4 Q9BSZ1	Q9bsz1 homo sapien
10	138	23.8	597	4 Q9BQB8	Q9bqb8 homo sapien
11	138	23.8	597	4 Q9BU10	Q9bu10 homo sapien
12	138	23.8	597	4 Q96BB9	Q96bb9 homo sapien
13	138	23.8	613	4 Q96EY0	Q96ey0 homo sapien
14	138	23.8	614	4 Q96G6A	Q96ga6 homo sapien
15	138	23.8	618	4 Q96AA6	Q96aa6 homo sapien
16	127.5	21.9	130	11 Q9D8W4	Q9d8w4 mus musculus

17	127.5	21.9	233	11 Q91V32	Q91v32 m adult mal
18	123.5	21.3	233	4 Q96169	Q96169 homo sapien
19	123.5	21.3	236	4 Q96E61	Q96e61 homo sapien
20	122.5	21.1	684	13 Q90544	Q90544 ginglymosto
21	121.5	20.9	235	11 Q99M11	Q99m11 mus musculus
22	119.5	20.6	384	4 Q9UP60	Q9up60 homo sapien
23	119.5	20.6	416	4 Q9NPP6	Q9npp6 homo sapien
24	119.5	20.6	494	4 Q96K68	Q96k68 homo sapien
25	119.5	20.6	496	4 Q96KX8	Q96kx8 homo sapien
26	119.5	20.6	496	4 Q96DK0	Q96dk0 homo sapien
27	115.5	19.9	500	4 Q9BRV0	Q9brv0 homo sapien
28	112.5	19.4	486	11 Q91Z07	Q91z07 mus musculus
29	112.5	19.4	487	11 Q99KA4	Q99ka4 mus musculus
30	111.5	19.2	479	11 Q99M22	Q99m22 mus musculus
31	111.5	19.2	484	11 Q99LA6	Q99la6 mus musculus
32	110.5	19.0	479	11 Q91WP5	Q91wp5 mus musculus
33	110.5	19.0	481	11 Q91WT3	Q91wt3 mus musculus
34	110.5	19.0	481	11 Q91WT1	Q91wt1 mus musculus
35	110.5	19.0	482	11 Q91X92	Q91x92 mus musculus
36	110.5	19.0	488	11 Q91WR1	Q91wr1 mus musculus
37	109.5	18.8	426	11 Q9DCD9	Q9dcd9 mus musculus
38	109.5	18.8	480	11 Q91XE1	Q91xel mus musculus
39	107	18.4	211	11 Q91XL0	Q91xl0 mus musculus
40	107	18.4	233	11 Q91WS9	Q91ws9 mus musculus
41	107	18.4	234	11 Q91WF8	Q91wf8 mus musculus
42	107	18.4	235	11 Q91W12	Q91w12 mus musculus
43	107	18.4	238	11 Q99M37	Q99m37 mus musculus
44	105	18.1	214	11 Q9R1A5	Q9ria5 mus musculus
45	103	17.7	1215	5 Q9V787	Q9v787 drosophila

ALIGNMENTS

RESULT 1

ID	Q96PQ8	PRELIMINARY;	PRT;	701 AA.
AC	Q96PQ8;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21477448; PubMed=11593034;			
RA	Hu Z., Garen A.;			
RT	"Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).			
DR	EMBL; AF272774; AAK58686.1; -.			
SQ	SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;			

Query Match	93.5%;	Score 543;	DB 4;	Length 701;
Best Local Similarity	90.4%;	Pred. No. 1.4e-51;		
Matches 103;	Conservative	2;	Mismatches 3;	Indels 6;
Gaps	1;			
QY	2 PP-----VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55			
Db	481 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 540			
QY	56 AKTKPREEQYNSTYRVVSVLTVHLQDLNGKEYCKVSNKGLPSSIEKTISKAK 109			
Db	541 AKTKPREEQYNSTYRVVSVLTVHLQDLNGKEYCKVSNKGLPSSIEKTISKAK 594			

RESULT 2

Q95M34	PRELIMINARY;	PRT;	337 AA.
ID	Q95M34		

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AC Q95M34;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IMMUNOGLOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
DE (FRAGMENT).
GN IGHC1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN 1
RP SEQUENCE FROM N.A.
RA Wagner B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN 2
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199:105-119(1998).
DR EMBL; AJ300675; CAC44624.1; --
FT NON_TER 1
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 76.2%; Score 443; DB 6; Length 337;
Best Local Similarity 73.6%; Pred. No. 6.6e-41;
Matches 78; Conservative 16; Mismatches 12; Indels 0; Gaps 0;

QY 4 VAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNQYVGVHNAKTKPREE 63
DB 123 LGGSFVFFPPPKDVLITLTKPVTCVVVDVSDQNPDKVFENYMDGVEVTRTPKKEE 182

QY 64 QYNSTRYVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTISKAK 109
DB 183 QFNSTRYVSVLTQLHQDWLNSGKEFKCKVNNQALPQPIERTITKTK 228

RESULT 3
Q9RIA4
ID Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; RAD40243.1; --
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
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Query Match 68.2%; Score 396; DB 11; Length 437;
Best Local Similarity 67.6%; Pred. No. 1.5e-35;
Matches 69; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 8 SVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNQYVGVHNAKTKPREEQYNS 67
DB 229 SVFIFFPKPKDVLITLTKPVTCVVVDISKDDPEVQFSWFDVDDVEVHTAQTQPREQFNS 288

QY 68 TYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTISKAK 109
DB 289 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIETKISKTK 330

RESULT 4
Q99LC4
ID Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; --
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 68.2%; Score 396; DB 11; Length 463;
Best Local Similarity 67.6%; Pred. No. 1.6e-35;
Matches 69; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 8 SVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNQYVGVHNAKTKPREEQYNS 67
DB 255 SVFIFFPKPKDVLITLTKPVTCVVVDISKDDPEVQFSWFDVDDVEVHTAQTQPREQFNS 314

QY 68 TYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTISKAK 109
DB 315 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIETKISKTK 356

RESULT 5
Q9D8L4
ID Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1810060009RIK PROTEIN.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzaletti J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK007918; BAB25349.1;
DR HSSP: P01842; 7FAB.
DR MGD: MGI:96443; Igh-1.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00407; Igc1; 3.
DR SMART: SM00406; Igv; 1.
DR SMART: SM00410; Ig_like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN.1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 65.7%; Score 382; DB 11; Length 473;
Best Local Similarity 62.3%; Pred. No. 5.7e-34;
Matches 71; Conservative 17; Mismatches 20; Indels 6; Gaps 1;

QY 2 PPVA-----GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFN 55
DB 253 PPCAAPDLGGPSVFIFPPKIKDVLMSISLSPMTCTVVVDVSEDDPDVQISWFNVNVEVHT 312
QY 56 AKTKPREQYNSTYRVSVLTVLDHQLNGKEYCKVKSNKGLPSSIEKTIKAK 109
DB 313 AQOTHTREDYNSTLRVVSALPIQHODWMSGKEFKCKVNNRPAPIERTISKPR 366

RESULT 6
Q91205 ID Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE HYPOTHETICAL 51.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC010327; AAH10327.1;
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

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Query Match 65.7%; Score 382; DB 11; Length 473;
Best Local Similarity 66.3%; Pred. No. 5.7e-34;
Matches 69; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 6 GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREQY 65
DB 263 GSVFIFPPKIKDVLMSISLTPKTCVVVDVSEDDPDVQISWFNVNVEVHTAQOTHTREDY 322

QY 66 NSTYRVSVSVLTVLDHQLNGKEYCKVKSNKGLPSSIEKTIKAK 109
DB 323 NSTIRVSALPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIK 366

RESULT 7
Q99L31 ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC003878; AAH03878.1;
DR HSSP: P01842; 7FAB.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00407; Igc1; 3.
DR SMART: SM00406; Igv; 1.
DR SMART: SM00410; Ig_like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN.1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 63.3%; Score 368; DB 11; Length 468;
Best Local Similarity 63.2%; Pred. No. 2e-32;
Matches 67; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREE 63
DB 256 LGGPSVFIFPPKIKDVLMSISLSPMTCTVVVDVSEDDPDVQISWFNVNVEVHTAQOTHTRE 315

QY 64 QYNSTYRVSVSVLTVLDHQLNGKEYCKVKSNKGLPSSIEKTIKAK 109
DB 316 DYNSTLRVVSALPIQHODWMSGKEFKCKVNNRPAPIERTISKPK 361

RESULT 8
Q99L25 ID Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RESULT 10
Q9BQB8 ID Q9BQB8 PRELIMINARY; PRT; 597 AA.
AC AC Q9BQB8;
DT DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE DE UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
OC OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX CX NCBI_TaxID=9606;
RN RN [1]
SEQUENCE FROM N.A.
RP RP TISSUE=RHABDOMYOSARCOMA;
RC RC Strausberg R.;
RA RA Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RL RL [2]
RN RN [2]
SEQUENCE FROM N.A.
RP RP TISSUE=Lymphoma;
RC RC Strausberg R.;
RA RA Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RL RL EMBL; BC006180; AAH06180.1; -.
DR DR EMBL; BC001872; AAH01872.1; -.
DR DR HSSP; PO1825; 7FAB.
DR DR InterPro; IPR003599; Ig.
DR DR InterPro; IPR003597; Ig_cl.
DR DR InterPro; IPR003600; Ig_like.
DR DR InterPro; IPR003006; Ig_MHC.
DR DR InterPro; IPR003596; Ig_v.
DR DR Pfam; PF00047; ig; 5.
DR DR SMART; SM00409; IG; 2.
DR DR SMART; SM00407; IGG1; 4.
DR DR SMART; SM00406; IGV; 1.
DR DR SMART; SM00410; IG_Like; 1.
DR DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 23.8%; Score 138; DB 4; Length 597;
Best Local Similarity 28.7%; Pred.No. 8, 1e-07;
Matches 29; Conservative 25; Mismatches 45; Indels 2; Gaps

QY 9 VFLFPKPKDLMISRPETVCVVDSHEDEVKFNVYDVGEVHNNAKTKEEQYNST 68
Db || || : :::: ::||:| | | | | | | | | | | | | | | |
368 VFAPIPPS-FASIFLTGSKTKLCITLDLTYY-SVTISWTRNGEAVKTHTNISESHPNAT 425

QY 69 YRVSVLTVLHDWLNGKEYCKVKSNGLPSSIETISKAK 109
Db : | : | : | : | : | : | : | : | : | : | : | : |
426 FSAVEASICEDDNWSERFTCVITHDLPLSLKITIRSPK 466

RESULT 11
Q9BU10 ID Q9BU10 PRELIMINARY; PRT; 597 AA.
AC AC Q9BU10;
DT DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE DE HYPOTHEICAL 65.3 KDA PROTEIN.
OC OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX CX NCBI_TaxID=9606;
RN RN [1]
SEQUENCE FROM N.A.
RP RP TISSUE=LYMPH, LYMPHOMA;
RC RC Strausberg R.;
RA RA Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RL RL EMBL; BC002963; AAH02963.1; -.
DR DR HSSP; PO1825; 7FAB.
DR DR InterPro; IPR003599; Ig.
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[illegible]

Query Match	23.8%	Score 138;	DB 4;	Length 618;
Best Local Similarity	28.7%	Pred. No. 8.5e-07;		
Matches	29;	Conservative 25;	Mismatches 45;	Indels 2;
Gaps	2;			

QY	9	VLEPPPKDTLMISRPPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST	68
		: : : : : : : : : : : : : : : :	
Ddb	368	VFAIPPS-FAFIFLTKSTKLTCLVTLDTLYD-SVTISWTRQNGEAVKTHNLISESHPNAT	425
		: : : : : : : : : : : : : : : :	
QY	69	YRVYSVLTVLHQDLNGCKYCKKVSNGKLPSSEIKTISKAK	109
		: : : : : : : : : : : : : : : :	
Ddb	426	FSVNGEASICEDDWNSEGTCTVTHDPLSPKLOTISRPK	466
		: : : : : : : : : : : : : : : :	

Search completed: June 21, 2002, 08:59:29
Job time: 1628 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:30:46 ; Search time 224.82 Seconds
(without alignments)
53.852 Million cell updates/sec

Title: US-09-674-857-1
Perfect score: 581
Sequence: 1 APPVAGSVFLPPPKPKDTL.....CKSVNKGLPSSIEKTISKAK 109

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	581	100.0	109	21	AA54996
2	565	97.2	462	18	AAW14933
3	565	97.2	462	18	AAW14934
4	565	97.2	463	18	AAW14939
5	565	97.2	463	18	AAW14940
6	559.5	96.3	110	21	AA54998
7	554	95.4	109	14	AAW14709
8	554	95.4	109	21	AAW14997
9	554	95.4	217	21	AAW07476
10	554	95.4	217	22	AAW67203
11	554	95.4	217	22	AAW76423

12	554	95.4	326	22	AAE02643
13	554	95.4	381	20	AA506895
14	554	95.4	432	13	AAZ26782
15	554	95.4	432	15	AAW46678
16	554	95.4	432	21	AAW85079
17	554	95.4	432	22	AAW80883
18	554	95.4	432	22	AAW67322
19	554	95.4	442	22	AAW72230
20	554	95.4	443	20	AAW31670
21	554	95.4	451	21	AAW93734
22	554	95.4	461	22	AAW72236
23	554	95.4	462	21	AAW26884
24	554	95.4	463	21	AAW93701
25	554	95.4	463	21	AAW93707
26	554	95.4	463	21	AAW93727
27	554	95.4	463	21	AAW93732
28	554	95.4	464	21	AAW93703
29	554	95.4	464	21	AAW93730
30	554	95.4	530	13	AAW26783
31	554	95.4	530	21	AAW85080
32	554	95.4	530	22	AAW80884
33	554	95.4	530	22	AAW67323
34	551	94.8	450	18	AAW34505
35	551	94.8	450	20	AAW08755
36	551	94.8	530	15	AAW46679
37	551	94.8	552	14	AAW30775
38	548	94.3	463	21	AAW93728
39	548	94.3	468	20	AAW85689
40	548	94.3	711	20	AAW85692
41	547.5	94.2	251	20	AAW05688
42	547.5	94.2	251	20	AAW97756
43	547.5	94.2	251	21	AAW07541
44	547.5	94.2	559	22	AAW85286
45	547.5	94.2	594	22	AAW04062

ALIGNMENTS

RESULT 1

AA54996
ID AA54996 standard; protein; 109 AA.

XX AC AA54996;

DT 17-FEB-2000 (first entry)

XX Mutated CH2 sequence G1deltaaab.

DE Binding molecule: CH2 sequence; complement dependent lysis; FcgammaRIIb; cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; B cell activation; mast cell degranulation; phagocytosis; vasculitis; Crohn's disease; graft-vs-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; allolimmune disorder; autoimmune haemolytic anaemia; inflammatory disease; autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis; neonatal alloimmune thrombocytopenia; Goodpasture disease; therapy; sickle cell anaemia; coronary artery occlusion.

XX Synthetic.

XX WO9958572-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB01441.

XX 08-MAY-1998; 98GB-0009951.

XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX Armour KL, Clark MR, Williamson LM;

XX

DR WPI; 2000-039075/03.
 XX Immunoglobulin-derived binding molecules that do not activate
 PT complement or trigger cytotoxic activities and maintaining desirable
 PT immunoglobulin properties -
 XX
 XX Claim 12; Fig 17; 81pp; English.
 XX
 CC This sequence represents the mutated CH2 molecule G1deltaab, and is a
 CC binding molecule of the invention. The recombinant binding molecule
 CC is capable of binding a target molecule without triggering complement
 CC dependent lysis, or the cell-mediated destruction of the target
 CC comprises: (a) a binding domain capable of binding a target molecule; and
 CC (b) an effector domain that is homologous to all or part of a constant
 CC domain of a human immunoglobulin G (IgG) heavy chain. The binding
 CC molecule is used to bind a target molecule (especially FcgammaRIIb
 CC causing inhibition of B cell activation, mast cell degranulation or
 CC phagocytosis). The binding molecule can be used to prevent or inhibit the
 CC binding of a second binding molecule, e.g. an antibody, to the target
 CC molecule. The binding molecule is useful for the treatment of
 CC graft-vs-host disease, organ transplant rejection, bone-marrow transplant
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
 CC autoimmune thrombocytopenia and arthritis), alloimmunity
 CC (e.g. foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
 CC coronary artery occlusion). The binding molecules do not activate
 CC complement or trigger cytotoxic activities through FcgammaR and desirable
 CC IgG properties have been retained. The polypeptides do not contain
 CC non-human amino acids, and are therefore likely to have reduced
 CC immunogenicity. Further, they still bind Protein A, which is consistent
 CC with being able to cross the human placenta through interaction with FcRn
 CC (neonatal Fc receptor).
 XX
 SQ Sequence 109 AA;

Query Match 100.0%; Score 581; DB 21; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.9e-52;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTP 60
 DB 1 appvagsvflfpkpkdtlmsrtpevtcvvvdvshedpevkfnkyvdgvevhnaktkp 60

QY 61 REEQNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 109
 DB 61 reeqnystyrvvsvltvlhqdmlngkeyckvsnkglpssiektiskak 109

RESULT 2
 AAW14933
 ID AAW14933 standard; Protein; 462 AA.
 XX
 AC AAW14933;
 XX
 DT 16-JUN-1997 (first entry)
 XX
 DE 2A2 (Chimeric) human G2/G4 chimeric antibody.
 XX
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX
 OS Chimeric Homo sapiens;
 OS Chimeric Mus sp.
 XX
 PN WO9711971-A1.

03-APR-1997.
 27-SEP-1996; 96WO-US15575.

PR 26-SEP-1996; 96US-0004489.
 PR 28-SEP-1995; 95US-0004489.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 XX
 DR WPI; 1997-212855/19.
 DR N-PSDB; AAT62931.
 XX
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 XX
 PS Disclosure; Page 42-44; 105pp; English.
 XX
 CC A chimeric antibody (AAW14933) comprises the C1 and hinge regions of
 CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and
 CC a murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
 CC monoclonal antibody (MAb) 2A2 heavy chain variable region sequence
 CC (see also AAW14932). The chimeric antibody is specific for porcine
 CC VCAM. It is useful for diagnosing human rejection of porcine
 CC xenotransplants and for improving xenotransplantation of porcine
 CC cells, tissues and organs into human recipients.
 XX
 SQ Sequence 462 AA;

Query Match 97.2%; Score 565; DB 18; Length 462;
 Best Local Similarity 97.2%; Pred. No. 4.8e-50;
 Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTP 60
 DB 247 appvagsvflfpkpkdtlmsrtpevtcvvvdvshedpevkfnkyvdgvevhnaktkp 306

QY 61 REEQNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKGLPSSIEKTIKAK 109
 DB 307 reeqnystyrvvsvltvlhqdmlngkeyckvsnkglpssiektiskak 355

RESULT 3
 AAW14934
 ID AAW14934 standard; Protein; 462 AA.
 XX
 AC AAW14934;
 XX
 DT 16-JUN-1997 (first entry)
 XX
 DE 2A2 (Chimeric) human G2/G4 chimeric antibody.
 XX
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX
 OS Chimeric Homo sapiens;
 OS Chimeric Mus sp.
 XX
 PN WO9711971-A1.
 PD 03-APR-1997.
 XX
 XX 27-SEP-1996; 96WO-US15575.
 XX
 PR 26-SEP-1996; 96US-0004489.
 PR 28-SEP-1995; 95US-0004489.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 XX

DR WPI; 1997-212855/19.
 DR N-PSDB; AAT62932.
 XX Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 XX
 XX
 PS Disclosure; Page 44-47; 105pp; English.
 XX
 CC A chimeric antibody (AAW14934) comprises the C1 and hinge regions of
 CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAB) and
 CC a murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
 CC monoclonal antibody (MAB) 2A2 heavy chain variable region sequence
 CC (see also AAW14932). The chimeric antibody is specific for porcine
 CC VCAM. It is useful for diagnosing human rejection of porcine
 CC xenotransplants and for improving xenotransplantation of porcine
 CC cells, tissues and organs into human recipients.
 XX
 SQ Sequence 462 AA;
 Query Match 97.2%; Score 565; DB 18; Length 462;
 Best Local Similarity 97.2%; Pred. NO. 4.8e-50;
 Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNATKTP 60
 Db 247 appvagsvflfpkpkdtlmisrtpevtcvvvdvsqdepevqfnwydgvvhnatktp 306
 QY 61 REQYNSTYRVSVLVTLVHODWLNKREYKCKVSNKGLPSSIEKTISKAK 109
 Db 307 reeqfnstyrsvsvltvlhqdwingkeyckvsnkglpssiektiskak 355
 RESULT 4
 AAW14939
 ID AAW14939 standard; Protein; 463 AA.
 AC AAW14939;
 DT 16-JUN-1997 (first entry)
 XX 3F4 (Chimeric) human G2/G4 chimeric antibody.
 XX Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX Chimeric Homo sapiens;
 OS Chimeric Mus sp.
 XX WO9711971-AL.
 XX 03-APR-1997.
 XX 27-SEP-1996; 96WO-US15575.
 XX 26-SEP-1996; 96US-0004489.
 XX 28-SEP-1995; 95US-0004489.
 XX (ALEX-) ALEXION PHARM INC.
 XX Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 XX WPI; 1997-212855/19.
 DR N-PSDB; AAT62936.
 XX Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 XX
 PS Disclosure; Page 56-57; 105pp; English.

XX A chimeric antibody (AAW14939) comprises the C1 and hinge regions of
 CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAB) and
 CC a murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
 CC monoclonal antibody (MAB) 3F4 heavy chain variable region sequence
 CC (see also AAW14938). The chimeric antibody is specific for porcine
 CC VCAM. It is useful for diagnosing human rejection of porcine
 CC xenotransplants and for improving xenotransplantation of porcine
 CC cells, tissues and organs into human recipients.
 XX
 SQ Sequence 463 AA;
 Query Match 97.2%; Score 565; DB 18; Length 463;
 Best Local Similarity 97.2%; Pred. NO. 4.8e-50;
 Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNATKTP 60
 Db 248 appvagsvflfpkpkdtlmisrtpevtcvvvdvsqdepevqfnwydgvvhnatktp 307
 QY 61 REQYNSTYRVSVLVTLVHODWLNKREYKCKVSNKGLPSSIEKTISKAK 109
 Db 308 reeqfnstyrsvsvltvlhqdwingkeyckvsnkglpssiektiskak 356
 RESULT 5
 AAW14940
 ID AAW14940 standard; Protein; 463 AA.
 AC AAW14940;
 XX 16-JUN-1997 (first entry)
 XX 3F4 (Chimeric) human G2/G4 chimeric antibody.
 XX Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX Chimeric Homo sapiens;
 OS Chimeric Mus sp.
 XX WO9711971-AL.
 XX 03-APR-1997.
 XX 27-SEP-1996; 96WO-US15575.
 XX 26-SEP-1996; 96US-0004489.
 XX 28-SEP-1995; 95US-0004489.
 XX (ALEX-) ALEXION PHARM INC.
 XX Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 XX WPI; 1997-212855/19.
 DR N-PSDB; AAT62937.
 XX Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 XX
 PS Disclosure; Page 58-61; 105pp; English.
 XX A chimeric antibody (AAW14940) comprises the C1 and hinge regions of
 CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAB) and
 CC a murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
 CC monoclonal antibody (MAB) 3F4 heavy chain variable region sequence
 CC (see also AAW14938). The chimeric antibody is specific for porcine
 CC VCAM. It is useful for diagnosing human rejection of porcine
 CC xenotransplants and for improving xenotransplantation of porcine

CC in which the heavy chain (VH) is derived from a murine source and the
 CC sequences encoding CH1, CH2 and CH3 are derived from a human source.
 CC This vector, in combination with the chimeric light chain vector,
 CC PAG4611 (see also AA043845), was transfected into SP2/0 cells and clones
 CC were isolated. 128.1 is an anti-human transferrin receptor antibody
 CC which binds to the transferrin receptor on brain capillary endothelial
 CC cells. This antibody may be used in a conjugate in which it is linked
 CC to a neuropharmaceutical or diagnostic agent. The conjugate may be
 CC used to treat or prevent neurological disorders eg. brain tumours,
 CC AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may
 CC also be used for diagnostic methods.
 XX Sequence 109 AA;

Query Match 95.4%; Score 554; DB 14; Length 109;
 Best Local Similarity 93.6%; Pred. No. 1.1e-49;
 Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 APPVAGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 DB 1 APPVAGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 QY 61 REQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
 DB 61 REQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109

RESULT 8
 AAY54997
 ID AAY54997 standard; protein; 109 AA.
 XX AAY54997;
 AC AAY54997;
 DT 17-FEB-2000 (first entry)
 XX Mutated CH2 sequence G2deltaa.

XX Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
 KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
 KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
 KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
 KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
 KW alloumune disorder; autoimmune haemolytic anaemia; inflammatory disease;
 KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
 KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;
 KW sickle cell anaemia; coronary artery occlusion.

XX Synthetic.
 OS WO9558572-A1.
 PN 18-NOV-1999.
 XX 07-MAY-1999; 99WO-GB01441.
 XX 08-MAY-1998; 98GB-0009951.
 XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX Armour KL, Clark MR, Williamson LM;
 XX WPI; 2000-039075/03.

XX Immunoglobulin-derived binding molecules that do not activate
 PT complement or trigger cytotoxic activities and maintaining desirable
 PT immunoglobulin properties -
 XX Claim 12; Fig 17; 81pp; English.
 XX This sequence represents the mutated CH2 molecule G2deltaa, and is a
 CC binding molecule of the invention. The recombinant binding molecule
 CC is capable of binding a target molecule without triggering complement

CC dependent lysis, or the cell-mediated destruction of the target
 CC comprises: (a) a binding domain capable of binding a target molecule; and
 CC (b) an effector domain that is homologous to all or part of a constant
 CC domain of a human immunoglobulin G (IgG) heavy chain. The binding
 CC molecule is used to bind a target molecule (especially FcgammaRIIb
 CC causing inhibition of B cell activation, mast cell degranulation or
 CC phagocytosis). The binding molecule can be used to prevent or inhibit the
 CC binding of a second binding molecule, e.g. an antibody, to the target
 CC molecule. The binding molecule is useful for the treatment of
 CC graft-vs-host disease, organ transplant rejection, bone-marrow transplant
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
 CC autoimmune thrombocytopenia and arthritis), alloimmunity
 CC (e.g. foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
 CC coronary artery occlusion). The binding molecules do not activate
 CC complement or trigger cytotoxic activities through FcgammaR and desirable
 CC IgG properties have been retained. The polypeptides do not contain
 CC non-human amino acids, and are therefore likely to have reduced
 CC immunogenicity. Further, they still bind Protein A, which is consistent
 CC with being able to cross the human placenta through interaction with FcRn
 CC (neonatal Fc receptor).
 XX Sequence 109 AA;

Query Match 95.4%; Score 554; DB 21; Length 109;
 Best Local Similarity 94.5%; Pred. No. 1.1e-49;
 Matches 103; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 APPVAGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 DB 1 APPVAGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 QY 61 REQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109
 DB 61 REQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 109

RESULT 9
 AAB07476
 ID AAB07476 standard; protein; 217 AA.
 XX AAB07476;
 AC AAB07476;
 XX 20-OCT-2000 (first entry)
 DT Amino acid sequence of native IgG Fc region humIgG2.
 XX IgG antibody; light chain; Fc region; effector function; cancer;
 KW allergy; asthma; LFA-1-mediated disorder; tumour; cancer.

XX Homo sapiens.
 OS WO200042072-A2.
 PN 20-JUL-2000.
 XX 14-JAN-2000; 2000WO-US009973.
 XX 15-JAN-1999; 99US-0116023.
 XX (GETH) GENENTECH INC.
 XX Presta LG;
 XX WPI; 2000-476035/41.

XX New Fc region-containing polypeptides that have altered effector
 PT function due to one or more amino acid modifications in the Fc region,
 PT useful in the treatment of cancer and allergic conditions such as
 PT asthma -
 XX

The present invention relates to a fusion protein, comprising a peptide ligand and an immunoglobulin (Ig) constant region multimerization domain (Ib). The hybrid molecules comprising the peptide ligands and their functional derivatives can be used in the same applications as, a peptide ligand can be used. For

the isolation of the peptides of the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HER2/erbB2 such as cancers, diseases of the nervous system, muscularure and epithelia, e.g. nervous system damage resulting from trauma, surgery, strokes, ischaemia infection, metabolic disorders, nutritional deficiency or toxic agents. In particular the synthetic peptide ligands may be used to treat Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease and neuropathy associated with diabetes.

the isolation of the peptides of the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HER2/erbB2 such as cancers, diseases of the nervous system, muscularure and epithelia, e.g. nervous system damage resulting from trauma, surgery, strokes, ischaemia infection, metabolic disorders, nutritional deficiency or toxic agents. In particular the synthetic peptide ligands may be used to treat Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease and neuropathy associated with diabetes.

SQ Sequence 217 AA; Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Query Match 95.4%; Score 554; DB 22; Length 217;
 Best Local Similarity 93.6%; Pred. No. 2.6e-49;
 Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 2 appvagsvflppkpkdtlmsrtpevtcvvvdvshedpevqfnvvdgvevhnaktkp 61

QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 109
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 62 reeqfstfrvsvltvvhqdwlngkeyckvsnkglpapietktsk 110

RESULT 12
 ID AAE02643 standard; Protein; 326 AA.
 XX AAE02643;
 XX 06-AUG-2001 (first entry)
 DE Human immunoglobulin G2 constant region mature protein.
 KW Human; erythropoietin; EPO; antianaemic; nephrotrophic; anti-HIV;
 KW vaccine; haemostatic; immunoglobulin G2; IgG2; EPO deficient disease;
 KW anaemia; renal failure; Human immunodeficiency Virus; HIV;
 KW haematopoietic growth factor.
 OS Homo sapiens.
 PN WO200136489-A2.
 PD 25-MAY-2001.
 XX 03-NOV-2000; 2000WO-EP10843.
 XX 12-NOV-1999; 99US-0164855.
 XX (MERE) MERCK PATENT GMBH.
 XX Hartmann A, Brandt S, Rieke E, Sobel C, Lo K, Way JC, Gillies S;
 WPI; 2001-367563/38.
 XX Novel modified erythropoietin forms such as fusion proteins, comprising
 the biological activity of erythropoietin forms
 Example 1; Page 24; 58pp; English.
 XX The present sequence is human immunoglobulin G2 (IgG2) constant region
 mature protein. IgG2 forms a fusion protein with human erythropoietin
 (EPO). EPO has improved biological activity and an extended serum half
 life greater than 20 hours. The present invention relates to modified
 EPO forms such as fusion proteins comprising a Fc portion of an
 immunoglobulin (Ig) molecule and an EPO molecule (Fc-EPO). The Fc portion
 is fused covalently through its C-terminus directly or indirectly to the
 EPO molecule, and where the Fc portion as well as EPO portion may be
 modified or mutated. The invention also relates to non-fused EPO
 molecules which have a pattern of cysteines or disulphide bonding which
 is distinct from human or animal EPO. Pharmaceutical compositions
 containing EPO are useful in the treatment of EPO deficient diseases such
 as anaemia, renal failure, HIV infection, blood loss and chronic disease
 that can be treated with haematopoietic growth factor.
 XX Sequence 326 AA;

Query Match 95.4%; Score 554; DB 22; Length 326;
 Best Local Similarity 93.6%; Pred. No. 4.3e-49;

QY 1 APPVAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 111 appvagsvflppkpkdtlmsrtpevtcvvvdvshedpevqfnvvdgvevhnaktkp 170

QY 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 109
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 171 reeqfstfrvsvltvvhqdwlngkeyckvsnkglpapietktsk 219

RESULT 13
 ID AAY06895 standard; Protein; 381 AA.
 XX AAY06895;
 XX 01-JUL-1999 (first entry)
 DE Human IL-2/Ig fusion protein.
 KW Fusion protein; vaccine; cytokine; immunoglobulin; autoimmune disease;
 KW infectious disease; inflammatory disease; neoplastic disease; cancer;
 KW immunologic disease; immune response; malaria; tuberculosis; hepatitis;
 KW AIDS; influenza; interleukin; IL-2; Ig; human.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Protein 1..153
 FT /note= "interleukin-2 (IL-2)"
 FT Protein 154..381
 FT /note= "immunoglobulin G"
 XX WO9916466-A2.
 PN 08-APR-1999.
 XX 29-SEP-1998; 98WO-US20321.
 XX 12-DEC-1997; 97US-0990180.
 XX 29-SEP-1997; 97US-0060338.
 XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX Barouch DH, Letvin NL;
 WPI; 1999-254931/21.
 N-PSDB; AAX34598.
 XX New vaccine compositions
 XX Claim 16; Fig 10A-E; 66pp; English.
 XX The invention relates to vaccine compositions comprising a vaccine and a
 timed-release formulation of a cytokine or cytokine/immunoglobulin fusion
 protein or plasmid. The formulation or device releases the cytokine
 protein or plasmid at one or more temporal points subsequent to vaccine
 administration. The vaccines can be used for treating an autoimmune
 disease, an infectious disease, an inflammatory disease, a neoplastic
 disease, or an immunologic disease in an individual. The vaccines can be
 used to elicit immune responses against diseases such as AIDS, malaria,
 tuberculosis, hepatitis C, hepatitis B, cancer or influenza. The methods
 can provide for enhancement of one or more immunologic parameters such as
 an antibody response, a cellular proliferative response as well as
 cytotoxic T-lymphocyte levels. In addition the Ig can increase the
 circulating half life of the cytokine. The present sequence represents
 a human interleukin-2 (IL-2)/Ig fusion protein.
 XX Sequence 381 AA;

Query Match 95.4%; Score 554; DB 20; Length 381;

Best Local Similarity 93.6%; Pred. No. 5.2e-49;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 166 appvagsvflfppkpkdtlmisrtpevtcvtvvdvshedpevgfnwydgvvhnaktkp 225

QY 61 REEQYNSTYRVVSVLTVLHODWLNQKEYCKVSNKGLPSSIEKTIKAK 109
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 226 reeqfnstfrvsvltvvhqdwlngkeyckvsnkglpapiektisktk 274

RESULT 14
AAR26782
ID AAR26782 standard; Protein; 432 AA.
XX AC AAR26782;
DT 06-FEB-1993 (first entry)
XX CD4-gamma2 chimeric heavy chain homodimer.
DE homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;
KW chimeric; increased serum half life; HIV infection; AIDS; ss.
XX Homo sapiens chimeric.
XX OS
FH Key Location/Qualifiers
FT Domain 1..216
FT /label= CD4
FT Domain 217..325
FT /label= CH2
FT Domain 326..433
FT /label= CH3
XX WO9213947-A.
XX 20-AUG-1992.
XX 10-FEB-1992; 92WO-US01143.
XX 08-FEB-1991; 91US-0653684.
XX (PROG-) PROGENICS PHARM INC.
XX Beaudry GA, Maddon PJ;
XX WPI; 1992-300034/36.
XX N-PSDB; AAQ28088.
PT CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for
PT treatment, prevention and diagnosis of HIV infection
XX
PS Claim 2; Fig 3; 90pp; English.
XX This sequence represents a CD4-gamma2 chimeric heavy chain homodimer.
CC It was produced by expression of the coding mutagenised CDNA
CC (produced as described in AAQ28088) in Dhfr-CHO cells. The protein is
CC efficiently assembled intracellularly and effectively secreted from
CC mammalian cells pref. CHO, COS, or myeloma cells as a homodimer,
CC enabling high recovery and purification from the medium of cells
CC expressing it. It possesses increased serum half-life and has increased
CC avidity for HIV cf. heavy chain dimers. It can inhibit HIV infection of
CC CD4+ cells and block the spread of HIV infection within a patient.
CC Attachment to a detectable marker makes it useful in an assay for HIV
CC or SIV infection, and it can also be linked to toxins, eg Diphtheria,
CC Pseudomonas exotoxin A (domains I or II) or the deglycosylated A-chain
CC of ricin.
XX
SQ Sequence 432 AA;

Query Match, 95.4%; Score 554; DB 13; Length 432;

Best Local Similarity 93.6%; Pred. No. 6.1e-49;
Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 217 appvagsvflfppkpkdtlmisrtpevtcvtvvdvshedpevgfnwydgvvhnaktkp 276

QY 61 REEQYNSTYRVVSVLTVLHODWLNQKEYCKVSNKGLPSSIEKTIKAK 109
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 277 reeqfnstfrvsvltvvhqdwlngkeyckvsnkglpapiektisktk 325

RESULT 15
AAR46678
ID AAR46678 standard; Protein; 432 AA.
XX AC AAR46678;
DT 08-AUG-1994 (first entry)
XX CD4-gamma 2 chimeric heavy chain.
DE
XX CD4; gamma; heavy chain; chimeric; chimaeric; immunoconjugate; HIV;
KW human immunodeficiency virus; radionuclide; toxin; therapy;
KW treatment; imaging; detection; targeting.
XX Homo sapiens.
XX OS
FH Key Location/Qualifiers
FT Region 1..204
FT /label= CD4 Region.
FT Region 205..216
FT /label= Hinge Region.
FT Region 217..325
FT /label= CH2 Region.
FT Region 326..432
FT /label= CH3 Region.
XX WO9403191-A.
XX 17-FEB-1994.
XX 06-AUG-1993; 93WO-US07422.
XX 07-AUG-1992; 92US-0927931.
XX (PROG-) PROGENICS PHARM INC.
XX Allaway GP, Maddon PJ;
XX WPI; 1994-065392/08.
XX N-PSDB; AAQ57750.
PT Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2
PT immunoconjugates - used to kill HIV-infected cells and to image
PT and stage HIV infection
XX
PS Disclosure; Figure 3; 142pp; English.
XX A CD4-gamma 2 chimeric heavy chain homodimer is linked to a non-
CC peptidyl toxin or a gamma radiation-emitting radionuclide of low to
CC moderate cytotoxicity. The resulting immunoconjugate comprising the
CC toxin can be used to kill HIV infected cells and to treat HIV
CC infected subjects to reduce the population of HIV infected cells.
CC It can also be used to reduce the likelihood of infection. The
CC immunoconjugate comprising the radionuclide can be used to image HIV
CC infected tissue, to calculate the stage of HIV infection or the
CC efficacy of an anti-HIV treatment using the imaging technique and
CC for determining the prognosis of an HIV infected subject.
XX
SQ Sequence 432 AA;

Query Match 95.4%; Score 554; DB 15; Length 432;
 Best Local Similarity 93.6%; Pred. NO. 6.le-49;
 Matches 102; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVYDVSHEDEPKFNNVYDGVGVHNAKTKP 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 217 appvagsvflfppkpkdtlmisrtpevtcvvvdvshdpevqfnwvydgvvhnaktkp 276
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 REEOYNSTYRVVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTIKAK 109
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 277 reeqfnstfrvsvltvvhqdwlngkeyckvsnkglpapiektisktk 325

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:00:23 ; Search time 48.19 Seconds
(without alignments)
87.579 Million cell updates/sec

Title: US-09-674-857-2

Perfect score: 580

Sequence: 1 APPVAGPSVLEFPKPKDTL.....CKVSNKGLPSSIEKTIKTK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	98.6	326	1 GC2_HUMAN	P01859 homo sapien
2	536	92.4	327	1 GC4_HUMAN	P01861 homo sapien
3	524	90.3	330	1 GC1_HUMAN	P01857 homo sapien
4	516	89.0	290	1 GC3_HUMAN	P01860 homo sapien
5	425	73.3	329	1 GC2_CAVPO	P01862 cavia porce
6	423	72.9	333	1 GCB_RAT	P20761 rattus norv
7	418	72.1	323	1 GC_RAT	P01870 oryctolagus
8	410.5	70.8	329	1 GC3_MOUSE	P22436 mus musculu
9	410.5	70.8	398	1 GC3M_MOUSE	P03987 mus musculu
10	410	70.7	324	1 GC1_MOUSE	P01868 mus musculu
11	410	70.7	393	1 GC1M_MOUSE	P01869 mus musculu
12	400	69.0	329	1 GCB_RAT	P01866 mus musculu
13	384	66.2	326	1 GC1_RAT	P20759 rattus norv
14	383	66.0	335	1 GCAB_MOUSE	P01864 mus musculu
15	383	66.0	336	1 GCB_MOUSE	P01866 mus musculu
16	383	66.0	405	1 GCBM_MOUSE	P01867 mus musculu
17	378	65.2	330	1 GCAA_MOUSE	P01863 mus musculu
18	378	65.2	399	1 GCAM_MOUSE	P01865 mus musculu
19	342	59.0	322	1 GCA_RAT	P20760 rattus norv
20	172.5	29.7	428	1 EPC_HUMAN	P01854 homo sapien
21	152	26.2	457	1 MUC_SUNMU	P20768 suncus muri
22	147	25.3	429	1 EPC_RAT	P01855 rattus norv
23	146	25.2	421	1 EPC_MOUSE	P01858 rattus norv
24	141	24.3	391	1 MUCB_HUMAN	P04220 homo sapien
25	140	24.1	454	1 MUC_HUMAN	P01871 homo sapien
26	136.5	23.5	299	1 ALC_HUMAN	P01879 oryctolagus
27	135	23.3	106	1 KAC_HUMAN	P01834 homo sapien
28	134	23.1	454	1 MUC_MESAU	P06337 mesocricetu
29	134	23.1	455	1 MUC_MOUSE	P01872 mus musculu
30	134	23.1	476	1 MUCM_MOUSE	P01873 mus musculu
31	128	22.1	103	1 LAC_CHICK	P20763 gallus gall
32	127.5	22.0	450	1 MUC_CANFA	P01874 canis fami
33	123.5	21.3	340	1 ALC2_HUMAN	P01877 homo sapien

34	123.5	21.3	353	1	ALC1_GORGO	P20758 gorilla gor
35	123.5	21.3	353	1	ALC1_HUMAN	P01876 homo sapien
36	121	20.9	458	1	MUC_RABIT	P03988 oryctolagus
37	121	20.9	479	1	MUCM_RABIT	P04221 oryctolagus
38	120.5	20.8	105	1	LAC1_MOUSE	P01843 mus musculu
39	120.5	20.8	105	1	LAC_HUMAN	P01842 homo sapien
40	119.5	20.6	105	1	LAC5_MUSSP	P20765 mus spretus
41	115.5	19.9	105	1	LAC5_MOUSE	P20764 mus musculu
42	112.5	19.4	370	1	HVC1_HETFR	P23084 heterodontu
43	110.5	19.1	213	1	ILL1_HUMAN	P015814 homo sapien
44	109.5	18.9	103	1	KAC4_RABIT	P01840 oryctolagus
45	107.5	18.5	344	1	ALC_MOUSE	P01878 mus musculu

ALIGNMENTS

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RESULT 1
GC2_HUMAN
ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
RT heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
RT evolution of a gene family.";
RL Cell 29:671-679(1982).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT genes.";
RL EMBO J. 1:403-407(1982).
RN [4]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The amino acid sequences of the three heavy chain constant region
RT domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
RN [6]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Farr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human

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immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
[7]
REVISONS TO 25; 59; 60 AND 264-268 (ZIE).
R Hofmann T., Parr D.M.;
RA Submitted (MAR-1980) to the PIR data bank.
RL [8]
SEQUENCE OF 1-121 (DOT).
RP MEDLINE=9525298; PubMed=7737190;
RX Stopini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RA "Characterization of the two unique human anti-flavin monoclonal
immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
RP [9]
DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RP [10]
DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
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CC -----
DR EMBL; J00230; AAB59393.1; -
DR PIR; A02148; G2HU;
DR HSSP; P01857; IFCL;
DR MIM; 147110; -
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 98
FT DOMAIN 1 98
FT DOMAIN 99 110
FT DOMAIN 111 219
FT DOMAIN 220 326
FT DISULFID 14 14
FT DISULFID 27 83
FT DISULFID 102 102
FT DISULFID 103 103
FT DISULFID 106 106
FT DISULFID 109 109
FT DISULFID 140 200
FT DISULFID 246 304
FT SITE 156 156
FT MOD_RES 326 326
FT VARIANT 60 60
FT CONFLICT 109 109
SQ SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;

Query Match 98.6%; Score 572; DB 1; Length 326;
Best Local Similarity 98.2%; Pred. No. 4.7e-51;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYDGVVHNAKTKP 60
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Db 111 APPVAGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYDGVVHNAKTKP 170
QY 61 REEQFNSTRVSVLTVVHODMLNGKEYCKVSKNGLPSSIEKTSKTK 109
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Db 171 REEQFNSTRVSVLTVVHODMLNGKEYCKVSKNGLPAPIEKTSKTK 219
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RESULT 2
GC4_HUMAN GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-4 chain C region.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; G4HU.
DR HSSP; P01842; 7FAB.
DR MIM; 147130; -
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 98
FT DOMAIN 1 98
FT DOMAIN 99 110
FT DOMAIN 111 220
FT DOMAIN 221 327
FT DISULFID 14 14
FT DISULFID 27 83
FT DISULFID 106 106
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FT DISULFID 247 305
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Best Local Similarity 94.3%; Pred. No. 2.2e-47;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYDGVVHNAKTKPREE 63
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Db 115 LGGSVFLFPKPKDTLMISRTPEVTCVVVDVSOEDDEVQFNWYGVHNAKTPREE 174
QY 64 QFNSTFRVSVLTIVVHODWLNKEYKCKVSNKGLPSSIEKTIKTK 109
Db 175 QFNSTFRVSVLTIVVHODWLNKEYKCKVSNKGLPSSIEKTIKAK 220
RESULT 3
GC1_HUMAN
ID GC1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
[2]
RN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RP MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
[3]
RN SEQUENCE OF 136-329 (EU).
RP MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
[4]
RN SEQUENCE (MYELOMA PROTEIN NIE).
RP MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a
RT monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
RT chymotryptic peptides of the H-chain, alignment of the tryptic
RT peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
[5]
RN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RP MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
[6]
RN DISULFIDE BONDS.
RP MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
[7]
RN DISULFIDE BONDS.
RP MEDLINE=77070267; PubMed=1002129;
RA Breker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie). I: Purification and
RT characterization of the protein, the L- and H-chains, the

RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
[8]
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RP MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -1- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, & THE
CC G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE G1M(3)
CC MARKER & THE G1M (NON-1) MARKERS.
CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35,116,198,269 & 272.
CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198,267&272.
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CC
CC EMBL; J00228; AAC82527.1; ALT_INIT.
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DR PDB; 1FC1; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR MIM; 147100; -.
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DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00230; Ig_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW 3D-structure.
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FT DISULFID 144 204
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FT DISULFID 180 180
FT CARBOHYD 330 330
FT MOD_RES 97 97
FT VARIANT 239 239
FT VARIANT 241 241
FT STRAND 123 126
FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164
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FT TURN 198 199
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REMOVED POST-TRANSLATIONALLY.
K -> R (IN G1M(3) MARKER).
D -> E (IN G1M(NON-1) MARKER).
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/FTid=VAR_003887.
L -> M (IN G1M(NON-1) MARKER).
/FTid=VAR_003888.


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FT MISSING (IN ZUC).
FT FTID-VAR_003895.
FT VARIANT 279 279 F -> Y (IN OMM).
FT FTID-VAR_003896.
FT SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;

Query Match 89.0%; Score 516; DB 1; Length 290;
Best Local Similarity 89.6%; Pred. No. 2.1e-45;
Matches 95; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNNAKTKPRE 63
DB 78 LGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNNAKTKPREQ 137
QY 64 QFNSTFRVSVLVTHQWDLNGKEYCKVKVSNKGLPSSIEKTSKTK 109
DB 138 QFNSTFRVSVLVTHQWDLNGKEYCKVKVSNKGLPSSIEKTSKTK 183

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 01, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF I-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";

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RL Biochemistry 10:26-31(1971).
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DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 73.3%; Score 425; DB 1; Length 329;
Best Local Similarity 72.7%; Pred. No. 4.4e-36;
Matches 80; Conservative 11; Mismatches 17; Indels 2; Gaps 1;

QY 2 PP--VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNNAKTK 59
DB 112 PPNELGGSPSVFIIPKPKDTLMISLTPTVTCVVVDVSDPEVQFTWFDVKNKPVGNAETK 171
QY 60 PREQFNSTFRVSVLVTHQWDLNGKEYCKVKVSNKGLPSSIEKTSKTK 109
DB 172 PRVEQYNTFRVSVLVTHQWDLNGKEYCKVKVSNKGLPSSIEKTSKTK 221

RESULT 6
GCB_RAT STANDARD; PRT; 333 AA.
ID GCB_RAT
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).

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FT DISULFID 147 207
 FT DISULFID 253 311
 SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 72.9%; Score 423; DB 1; Length 333;
 Best Local Similarity 70.8%; Pred. No. 7.1e-36;
 Matches 75; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPRE 63
 Db 121 LGGPSVFIFPPKPKDILLISQNAKVTCTVVDVSEEDPQFSWFNNVEHTAQTPRE 180

QY 64 QNSTFRVSVLTVVHODWLNKGEYCKVSKNGLPSSIEKTSKTK 109
 Db 181 OYNSTFRVSVLPIQHODWMSGKFKCKVNNKALPSPIEKTSKPK 226

RESULT 7
 GC_RABIT STANDARD; PRT; 323 AA.
 AC P01870;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma chain C region.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84030930; PubMed=6313520;
 RA Bernstein K.E., Alexander C.B., Mage R.G.;
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
 F-1 haplotype.";
 RL Immunogenetics 18:387-397(1983).
 RN [2]
 RP SEQUENCE OF 1-128.
 RX MEDLINE=76135469; PubMed=1243651;
 RA Pratt D.M., Mole L.E.;
 RT "Sequence studies on the constant region of the Fd sections of rabbit
 immunoglobulin G of different allotype.";
 RL Biochem. J. 151:337-349(1975).
 RN [3]
 RP SEQUENCE OF 88-266 FROM N.A.
 RX MEDLINE=83299917; PubMed=6193512;
 RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
 RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
 heavy chain and identification of two genomic C gamma genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
 RN [4]
 RP SEQUENCE OF 132-161.
 RX MEDLINE=70110015; PubMed=5461106;
 RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
 RT "Sequence studies of the Fd section of the heavy chain of rabbit
 immunoglobulin G.";
 RL Biochem. J. 116:249-259(1970).
 RN [5]
 RP SEQUENCE OF 129-131 AND 155-322.
 RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
 RL (in) Killander J. (eds.);
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
 Stockholm (1967).
 CC -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
 CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
 CC MARKERS AND REF.5 THE E15 MARKER.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M16426; AAA31289.1; -.
 DR PIR; A02161; GHRB.
 DR HSP; P01857; lPCL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_C1.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IgC1; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT VARIANT 104 104 T -> M (IN D11 MARKER).
 FT VARIANT 185 185 T -> A (IN E15 MARKER).
 FT CONFLICT 48 48 N -> E (IN REF. 2).
 FT CONFLICT 71 71 V -> VPV (IN REF. 2).
 FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
 FT CONFLICT 173 173 N -> D (IN REF. 5).
 FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
 FT CONFLICT 201 201 N -> D (IN REF. 5).
 FT CONFLICT 218 218 Q -> E (IN REF. 5).
 FT CONFLICT 233 233 E -> Q (IN REF. 5).
 FT CONFLICT 246 246 N -> D (IN REF. 5).
 FT CONFLICT 256 256 E -> G (IN REF. 5).
 FT CONFLICT 260 260 N -> D (IN REF. 5).
 FT CONFLICT 266 266 N -> D (IN REF. 5).
 FT CONFLICT 280 280 Y -> W (IN REF. 5).
 FT CONFLICT 284 284 N -> S (IN REF. 5).
 SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 72.1%; Score 418; DB 1; Length 323;
 Best Local Similarity 70.0%; Pred. No. 2.2e-35;
 Matches 77; Conservative 12; Mismatches 15; Indels 2; Gaps 1;

QY 2 PP-VAGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATK 59
 Db 107 PELLGGPSVFIFPPKPKDTLMISRTPEVTCVVDVSDQDPEVQFTWINNQVTRAPP 166

QY 60 PREQFNSTFRVSVLTVVHODWLNKGEYCKVSKNGLPSSIEKTSKTK 109
 Db 167 LREQQFNSTFRVSVLTPIHODWLNKGEYCKVSKNGLPAPIEKTSKAR 216

RESULT 8
 GC3_MOUSE STANDARD; PRT; 329 AA.
 ID GC3_MOUSE
 AC P22436;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-3 chain C region, secreted form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85027161; PubMed=6092053;
 RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA Tucker P.W., Blattner F.R.;
 RT "Structural analysis of the murine IgG3 constant region gene.";
 RL EMBO J. 3:2041-2046(1984).
 CC -----
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DR EMBL: J00451; -: NOT_ANNOTATED_CDS.
DR PIR: B02156; G3MSC.
DR HSSP: P01857; 1FC1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_C1.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00410; Ig_like.
DR SMART: SM00407; Ig_3.
DR SMART: SM00410; Ig_like; 1.
DR SMART: SM00407; IgC1; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 70.8%; Score 410.5; DB 1; Length 329;
Best Local Similarity 67.6%; Pred. No. 1.3e-34;
Matches 75; Conservative 15; Mismatches 18; Indels 3; Gaps 1;

QY 2 PP---VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQNWYDGVGVHNAKT 58
DB 112 PGNILGGPSVFIFPPKPKDLMISLTPTKVTCTVVDVSEDDPDVHVSWFVDNKEVHTAWT 171
QY 59 KPREEQFNSTFRVSVLTVVHQQDLNGKEYCKVSKNGLPSSIEKTSKTK 109
DB 172 QPREAQYNSTFRVVSALPTQHQDMRGKFEKCKVNNKALPAPIERTISPKK 222

RESULT 9
GC3M_MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041483; PubMed=6314258;
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: J00451; AAB59655.1; -.
DR EMBL: V01526; CAA24767.1; ALT_SEQ.
DR PIR: A02155; G3MSM.
DR HSSP: P01857; 1FC1.
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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_C1.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00410; Ig_like; 1.
DR SMART: SM00407; IgC1; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 70.8%; Score 410.5; DB 1; Length 398;
Best Local Similarity 67.6%; Pred. No. 1.6e-34;
Matches 75; Conservative 15; Mismatches 18; Indels 3; Gaps 1;

QY 2 PP---VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQNWYDGVGVHNAKT 58
DB 112 PGNILGGPSVFIFPPKPKDLMISLTPTKVTCTVVDVSEDDPDVHVSWFVDNKEVHTAWT 171
QY 59 KPREEQFNSTFRVSVLTVVHQQDLNGKEYCKVSKNGLPSSIEKTSKTK 109
DB 172 QPREAQYNSTFRVVSALPTQHQDMRGKFEKCKVNNKALPAPIERTISPKK 222

RESULT 10
GC1_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salser W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=78242288; PubMed=98524;
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Adetugbo K.;
 "Evolution of immunoglobulin subclasses. Primary structure of a murine myeloma gamma1 chain."
 J. Biol. Chem. 253:6068-6075(1978).
 [5]
 DISULFIDE BONDS (MOPC 21).
 MEDLINE=73008889; PubMed=5073237;
 Svasti J., Milstein C.;
 "The disulphide bridges of a mouse immunoglobulin G1 protein."
 Biochem. J. 126:837-850(1972).

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 EMBL; V00793; CAA24172.1; -
 EMBL; V00793; CAA24173.1; -
 EMBL; V00793; CAA24174.1; -
 EMBL; V00793; CAA24175.1; -
 EMBL; V00795; CAA24176.1; -
 PIR; A02159; GIMS.
 HSP; P01842; 7FAB.
 GlycosuiteDB; P01868; -
 MGI; 96446; Igh-4.
 InterPro; IPR003006; Igh_MHC.
 InterPro; IPR003597; Igh-cl.
 Pfam; PF00047; Igh-3.
 SMART; SM00407; Igh-2.
 PROSITE; PS00290; Igh_MHC; 1.
 Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 Alternative splicing.
 NON_TER 1
 DOMAIN 1 97
 CH1.
 HINGE.
 DOMAIN 110 217
 CH2.
 DOMAIN 218 324
 CH3.
 DISULFID 27 82
 DISULFID 102 102
 DISULFID 104 104
 DISULFID 107 107
 DISULFID 109 109
 DISULFID 138 138
 CARBOHYD 174 174
 N-LINKED (GLCNAC. . .).
 /FTIQ-CAR_000055.
 REMOVED POST-TRANSLATIONALLY.
 N -> D (IN REF. 3).
 N -> D (IN REF. 3).
 SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;

 Query Match 70.7%; Score 410; DB 1; Length 324;
 Best Local Similarity 71.6%; Pred. No. 1.4e-34;
 Matches 73; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

 QY 8 SVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFVYVGVHNAKTPREEQFNS 67
 Db 116 SVFIIPKPKDVTITLTPKVCVVVDISKDDPEVQFSEFVDDVEVHTAQTPREEQFNS 175

 QY 68 TFRVSVLTVHVDWLNGKEYCKVSNKGLPSSIEKTSKTK 109
 Db 176 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTSKTK 217

 RESULT 11
 GC1M.MOUS
 ID GC1M.MOUS
 AC P01869;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 OS Ig gamma-1 chain C region, membrane-bound form.
 OC Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80045036; PubMed=115593;
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
 RT gamma 1 chain gene."
 RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 323-393 FROM N.A.
 RX MEDLINE=82197626; PubMed=6804950;
 RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
 RT "mRNA for surface immunoglobulin gamma chains encodes a highly
 RT conserved transmembrane sequence and a 28-residue intracellular
 RT domain."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
 RN [3]
 RP SEQUENCE OF 323-366 FROM N.A.
 RX MEDLINE=82115295; PubMed=6799207;
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
 RA Eisenberg D., Wall R.;
 RT "Gene segments encoding transmembrane carboxyl termini of
 RT immunoglobulin gamma chains."
 RL Cell 26:19-27(1981).
 RN [4]
 RP SEQUENCE OF 1-44 FROM N.A.
 RX MEDLINE=82222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 RT immunoglobulin gamma chains."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
 CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
 CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
 CC SEGMENT OF MU CHAINS.

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 or send an email to license@isb-sib.ch).

 EMBL; V00793; CAA24172.1; -
 EMBL; V00793; CAA24173.1; -
 EMBL; V00793; CAA24174.1; -
 PIR; B02159; GIMSM.
 HSP; P01842; 7FAB.
 MGI; 96446; Igh-4.
 InterPro; IPR003006; Igh_MHC.
 InterPro; IPR003597; Igh-cl.
 Pfam; PF00047; Igh-3.
 SMART; SM00407; Igh-2.
 PROSITE; PS00290; Igh_MHC; 1.
 Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 Alternative splicing; Transmembrane.
 NON_TER 1
 DOMAIN 1 97
 CH1.
 DOMAIN 98 110
 HINGE.
 DOMAIN 111 217
 CH2.
 DOMAIN 218 324
 CH3.
 DISULFID 27 82
 DISULFID 102 102
 INTERCHAIN (WITH A LIGHT CHAIN).
 INTERCHAIN (WITH A HEAVY CHAIN).
 INTERCHAIN (WITH A HEAVY CHAIN).
 INTERCHAIN (WITH A HEAVY CHAIN).
 N-LINKED (GLCNAC. . .).
 /FTIQ-CAR_000055.
 REMOVED POST-TRANSLATIONALLY.
 N -> D (IN REF. 3).
 N -> D (IN REF. 3).
 SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;

 Query Match 70.7%; Score 410; DB 1; Length 324;
 Best Local Similarity 71.6%; Pred. No. 1.4e-34;
 Matches 73; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

 QY 8 SVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFVYVGVHNAKTPREEQFNS 67
 Db 116 SVFIIPKPKDVTITLTPKVCVVVDISKDDPEVQFSEFVDDVEVHTAQTPREEQFNS 175

 QY 68 TFRVSVLTVHVDWLNGKEYCKVSNKGLPSSIEKTSKTK 109
 Db 176 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTSKTK 217

 RESULT 11
 GC1M.MOUS
 ID GC1M.MOUS
 AC P01869;
 DT 21-JUL-1986 (Rel. 01, Created)

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FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174
FT DISULFID 244 302
FT TRANSMEM 340 357
FT DOMAIN 358 393
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7AICE27 CRC64;

Query Match 70.7%; Score 410; DB 1; Length 393;
Best Local Similarity 71.6%; Pred. No. 1.8e-34;
Matches 73; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 8 SVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVHNNAKTKPREQFNS 67
Db 116 SVFIFFPKPKDVLITLTPKVTVCVVVDISKDPEVQFSFVDDVEVHTAQTQPREQFNS 175

QY 68 TFRVSVLTIVVHODWLNKGEYCKVSNKGLPSSIEKTSKTK 109
Db 176 TFRSVSELPIMHODWLNKGEYCKVSNKGLPSSIEKTSKTK 217

RESULT 12
GCC_RAT ID GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
CC -----
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CC -----
DR EMBL; X07189; CAA30169.1; -
DR PIR; S00847; S00847.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203

QY 8 SVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVHNNAKTKPREQFNS 67
Db 116 SVFIFFPKPKDVLITLTPKVTVCVVVDISKDPEVQFSFVDDVEVHTAQTQPREQFNS 175

QY 68 TFRVSVLTIVVHODWLNKGEYCKVSNKGLPSSIEKTSKTK 107
Db 178 TFRSVSELPILHODWLNKGEYCKVSNKGLPSSIEKTSKTK 217

RESULT 14
```

```
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 69.0%; Score 400; DB 1; Length 329;
Best Local Similarity 69.9%; Pred. No. 1.5e-33;
Matches 72; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 7 PSVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVHNNAKTKPREQFNS 66
Db 120 PSVFIFFPKPKDLMITLTPKVTVCVVVDSEEPDQVQFSFVDDVEVHTAQTQPREQFNS 179

QY 67 TFRVSVLTIVVHODWLNKGEYCKVSNKGLPSSIEKTSKTK 109
Db 180 GTFRVVSTLHIQHDWMSGKEFKCKVNNKDLPSPIEKTSKPR 222

RESULT 13
GCC_RAT ID GCC_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176
FT SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 66.2%; Score 384; DB 1; Length 326;
Best Local Similarity 68.0%; Pred. No. 6.4e-32;
Matches 68; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 8 SVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVHNNAKTKPREQFNS 67
Db 118 SVFIFFPKPKDVLITLTPKVTVCVVVDISKDPEVQFSFVDDVEVHTAQTQPREQFNS 177

QY 68 TFRVSVLTIVVHODWLNKGEYCKVSNKGLPSSIEKTSKTK 107
Db 178 TFRSVSELPILHODWLNKGEYCKVSNKGLPSSIEKTSKTK 217

RESULT 14
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Query Match 66.0%; Score 383; DB 1; Length 336;
Best Local Similarity 66.3%; Pred. No. 8.4e-32;
Matches 69; Conservative 16; Mismatches 19; Indels 0; Gaps 0;
QY 6 GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREEQF 65
Db 126 GPSVFIFFPNIKDVLMLISLTPKVCVVVDVSEDDPDVQISWFEVNNVEVHTAQTTHREDY 185
QY 66 NSTFRVSVLTVVHODWLNKKEYCKVSNKGLPSSIEKTIKTK 109
Db 186 NSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIK 229

Search completed: June 21, 2002, 09:00:23
Job time: 1447 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:59:29 ; Search time 176.89 Seconds

(without alignments)
106.600 Million cell updates/sec

Title: US-09-674-857-2

Perfect score: 580

Sequence: 1 APPVAGSVFLFPPKPKDTL.....CKVSNKGLPSSIEKTIKTK 109

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	524	90.3	701	4 Q96PQ8	Q96PQ8 homo sapien
2	443	76.4	337	6 Q95M34	Q95M34 equus caball
3	410	70.7	437	11 Q9R1A4	Q9R1A4 mus musculus
4	410	70.7	463	11 Q99LC4	Q99LC4 mus musculus
5	383	66.0	473	11 Q9D8L4	Q9D8L4 mus musculus
6	383	66.0	473	11 Q91Z05	Q91Z05 mus musculus
7	369	63.6	468	11 Q99L31	Q99L31 mus musculus
8	369	63.6	473	11 Q99L25	Q99L25 mus musculus
9	140	24.1	375	4 Q9BS21	Q9BS21 homo sapien
10	140	24.1	597	4 Q9QB88	Q9QB88 homo sapien
11	140	24.1	597	4 Q9BU10	Q9BU10 homo sapien
12	140	24.1	597	4 Q96BB9	Q96BB9 homo sapien
13	140	24.1	613	4 Q96EY0	Q96EY0 homo sapien
14	140	24.1	614	4 Q96GA6	Q96GA6 homo sapien
15	140	24.1	618	4 Q96AA6	Q96AA6 homo sapien
16	125.5	21.6	233	4 Q96169	Q96169 homo sapien

17	125.5	21.6	236	4 Q96E61	Q96E61 homo sapien
18	123.5	21.3	384	4 Q90P60	Q90P60 homo sapien
19	123.5	21.3	416	4 Q9NPP6	Q9NPP6 homo sapien
20	123.5	21.3	494	4 Q96K68	Q96K68 homo sapien
21	123.5	21.3	496	4 Q96KX8	Q96KX8 homo sapien
22	123.5	21.3	496	4 Q96DK0	Q96DK0 homo sapien
23	123.5	20.8	130	11 Q9D8W4	Q9D8W4 mus musculus
24	120.5	20.8	233	11 Q91V32	Q91V32 m adult mal
25	119.5	20.6	500	4 Q9BRV0	Q9BRV0 homo sapien
26	113.5	19.6	235	11 Q99M11	Q99M11 mus musculus
27	113.5	19.6	684	13 Q90544	Q90544 ginglymosto
28	108.5	18.7	486	11 Q91Z07	Q91Z07 mus musculus
29	108.5	18.7	487	11 Q99KA4	Q99KA4 mus musculus
30	107.5	18.5	479	11 Q99M22	Q99M22 mus musculus
31	107.5	18.5	484	11 Q99LA6	Q99LA6 mus musculus
32	106.5	18.4	479	11 Q91WP5	Q91WP5 mus musculus
33	106.5	18.4	481	11 Q91WT3	Q91WT3 mus musculus
34	106.5	18.4	481	11 Q91WT1	Q91WT1 mus musculus
35	106.5	18.4	482	11 Q91X92	Q91X92 mus musculus
36	106.5	18.4	488	11 Q91WR1	Q91WR1 mus musculus
37	105.5	18.2	426	11 Q9DCD9	Q9DCD9 mus musculus
38	105.5	18.2	480	11 Q91XE1	Q91XE1 mus musculus
39	100	17.2	211	11 Q91XL0	Q91XL0 mus musculus
40	100	17.2	233	11 Q91WS9	Q91WS9 mus musculus
41	100	17.2	234	11 Q91WF8	Q91WF8 mus musculus
42	100	17.2	235	11 Q91W12	Q91W12 mus musculus
43	100	17.2	238	11 Q99M37	Q99M37 mus musculus
44	99	17.1	1215	5 Q9V787	Q9V787 drosophila
45	98	16.9	214	11 Q9R1A5	Q9R1A5 mus musculus

ALIGNMENTS

RESULT 1

Q96PQ8	PRELIMINARY;	PRT;	701 AA.
ID Q96PQ8			
AC Q96PQ8			
DT 01-DEC-2001 (Tremblrel. 19, Created)			
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RP [1]			
RN SEQUENCE FROM N.A.			
RX MEDLINE=21477448; PubMed=11593034;			
RA Hu Z., Garen A.;			
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor			
RT cells for immunotherapy in mouse models of prostatic cancer.";			
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).			
DR EMBL; AF272774; AAK58686.1; -.			
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;			

Query Match 90.3%; Score 524; DB 4; Length 701;
Best Local Similarity 86.0%; Pred. No. 3.9e-50;
Matches 98; Conservative 6; Mismatches 4; Indels 6; Gaps 1;

Qy 2 PP-----VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHN 55

Db 481 PPCPAELGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHN 540

Qy 56 AKTKPREQNSFRVYVSVLTVDHQLNGKEYCKVSNKGLPSSIEKTIKTK 109

Db 541 AKTKPREQNSFRVYVSVLTVDHQLNGKEYCKVSNKGLPSSIEKTIKTK 594

RESULT 2

Q95M34	PRELIMINARY;	PRT;	337 AA.
ID Q95M34			

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AC Q95M34;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE IMMUNOGLOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
DE (FRAGMENT).
GN IGHC1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Wagner B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B.; Overesch G.; Sheoran A.; Holmes M.; Richards C.;
RA Leibold W.; Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199;103-119(1998).
DR EMBL; AJ300675; CAC44624.1; -.
FT NON_TER 1
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 76.4%; Score 443; DB 6; Length 337;
Best Local Similarity 73.6%; Pred. No. 1.9e-41;
Matches 78; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYGVGVEVHNAKTKPREE 63
Db 123 LGGPSVFIFPPPKDLMITRTPEVTCVVVDVSHEDPEVKFNWYGVGVEVHNAKTKPREE 182

QY 64 QFNSTRVSVLVTHQDHLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 183 QFNSTRVSVLVTHQDHLNGKEYCKVSNKGLPSSIEKTIKTK 228

RESULT 3
Q9RIA4 PRELIMINARY; PRT; 437 AA.
ID Q9RIA4;
AC Q9RIA4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G.; Yu X.; Ekramoddoullah A.K.M.; Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFV).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
```

```
Query Match 70.7%; Score 410; DB 11; Length 437;
Best Local Similarity 71.6%; Pred. No. 1.3e-37;
Matches 73; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 8 SYVLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYGVGVEVHNAKTKPREEQFNS 67
Db 229 SVFIFPPKPKDLMITRTPEVTCVVVDVSHEDPEVFQFNWYGVGVEVHNAKTKPREEQFNS 288

QY 68 TFRVSVLVTHQDHLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 289 TFRVSVLVTHQDHLNGKEYCKVSNKGLPSSIEKTIKTK 330

RESULT 4
Q99LC4 PRELIMINARY; PRT; 463 AA.
ID Q99LC4;
AC Q99LC4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 70.7%; Score 410; DB 11; Length 463;
Best Local Similarity 71.6%; Pred. No. 1.4e-37;
Matches 73; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 8 SYVLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYGVGVEVHNAKTKPREEQFNS 67
Db 255 SVFIFPPKPKDLMITRTPEVTCVVVDVSHEDPEVFQFNWYGVGVEVHNAKTKPREEQFNS 314

QY 68 TFRVSVLVTHQDHLNGKEYCKVSNKGLPSSIEKTIKTK 109
Db 315 TFRVSVLVTHQDHLNGKEYCKVSNKGLPSSIEKTIKTK 356

RESULT 5
Q9D8L4 PRELIMINARY; PRT; 473 AA.
ID Q9D8L4;
AC Q9D8L4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 1810060009RIK-PROTEIN.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

RP SEQUENCE FROM N.A.
RC STRAN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN1.
DR SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 66.0%; Score 383; DB 11; Length 473;
Best Local Similarity 62.3%; Pred. No. 1.5e-34;
Matches 71; Conservative 17; Mismatches 20; Indels 6; Gaps 1;

QY 2 PPVA-----GPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVFQFNVYDGVGVHN 55
Db 253 PPCAAPDLLGGPSVFIPPKIKDVLMSLSPMTVCVVVDVSEDDPDVQISFWNNVEVHT 312
QY 56 AKTKPREQFNSTFRVSVLTVVHODWLNKGYCKVSKNKGLPSSIEKTSKTK 109
Db 313 AQQTREDYNTSLRVVSALPIQHDWMSGKEFKCKVNNRALSPIERTISKPR 366

RESULT 6
Q91205 ID Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 51.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH0327.1; -
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 66.0%; Score 383; DB 11; Length 473;
Best Local Similarity 66.3%; Pred. No. 1.5e-34;
Matches 69; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 6 GPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVFQFNVYDGVGVHNKTKPREEQF 65
Db 263 GPSVFIPPNKIDVLMISLTPKVTVCVVVDVSEDDPDVQISFWNNVEVHTAQQTREDY 322

QY 66 NSTFRVSVLTVVHODWLNKGYCKVSKNKGLPSSIEKTSKTK 109
Db 323 NSTIRVVSALPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIK 366

RESULT 7
Q99L31 ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN1.
DR SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 63.6%; Score 369; DB 11; Length 468;
Best Local Similarity 63.2%; Pred. No. 5.5e-33;
Matches 67; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVFQFNVYDGVGVHNKTKPREE 63
Db 256 LGGPSVFIPPKIKDVLMSLSPMTVCVVVDVSEDDPDVQISFWNNVEVHTAQQTRE 315

QY 64 QFNSTFRVSVLTVVHODWLNKGYCKVSKNKGLPSSIEKTSKTK 109
Db 316 DYNSTLRVVSALPIQHDWMSGKEFKCKVNNKALPAPIERTISKPR 361

RESULT 8
Q99L25 ID Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

Search completed: June 21, 2002, 08:59:30
Job time: 1629 sec

Best Local Similarity 94.5%; Pred. No. 3.9e-48;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
II : |||||
Db 39 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 98
II : |||||

QY 61 PREEQNSTYRVVSVLTVHLQDWLNKEYKCKVSNKGLPSSIEKTIKSAK 110
II : |||||
Db 99 PREEQNSTYRVVSVLTVHLQDWLNKEYKCKVSNKGLPSSIEKTIKSAK 148
II : |||||

RESULT 3
GHU

Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:CROSS-references: EMBL:Z17370
A:Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers,
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:CROSS-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:CROSS-references: EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A:Reference number: A90563; MUID:71064024
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96,'R',98-135 <CUN>
A:Note: this sequence has the Glm(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
A:Reference number: A90564; MUID:71064025
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A:Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primaerstruktur.
A:Reference number: A91668; MUID:77070269
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A:Note: this sequence has the Glm(17) and Glm(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983

A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <
A:Note: this sequence has the Glm(3) and Glm(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul
A:Reference number: A90565; MUID:71064027
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunog
enbromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:CROSS-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-204,250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 94.9%; Score 557; DB 1; Length 330;
Best Local Similarity 94.5%; Pred. No. 5.3e-48;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
II : |||||
Db 114 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 173
II : |||||

QY 61 PREEQNSTYRVVSVLTVHLQDWLNKEYKCKVSNKGLPSSIEKTIKSAK 110
II : |||||
Db 174 PREEQNSTYRVVSVLTVHLQDWLNKEYKCKVSNKGLPSSIEKTIKSAK 223
II : |||||

RESULT 4
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687
A:Accession: S69339
A:Molecule type: mRNA
A:Status: preliminary
A:Residues: 1-374 <KHA>
A:CROSS-references: EMBL:X81695
R:Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140,'C',142-374 <KH2>
A:CROSS-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Qy	1	APPVAGPSPFLPPKPKD	TLMSRPEVTCVVVDVSHEDPEVKFNNYV	DGVEVHNAKTK	60
Db	111	APPVA-GPSPFLPPKPKD	TLMSRPEVTCVVVDVSHEDPEVKFNNYV	DGVEVHNAKTK	169
Qy	61	PREQYNSTRYVSVLT	VHQDWLNKGEYCKVSNRGLPSSIEKTK	ISAK	110
Db	170	PREQYNSTRYVSVLT	VHQDWLNKGEYCKVSNRGLPAPTEKTK	ISKTK	219

```

RESULT 7
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an
A:Reference number: A60764; MUID:90007613
A:Accession: A60764
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

```

Query Match 91.8%; Score 539; DB 2; Length 377;
Best Local Similarity 90.9%;
Pred. NO. 3.9e-46;
Matches 100; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

[illegible]

```

RESULT      8
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:C.Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:C.Accession: A23511
R:R.Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene
A:Reference Number: A23511; MUID:86148507
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

```

Query Match 91.8%; Score 539; DB 2; Length 377;
Best Local Similarity 90.9%; Pred. No. 3.9e-46;
Matches 100; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 APPVAGGPSVFLLFPKPKDTLMISTPEVTCVVVDVSHEDPEVKFWYDGVGEVHNAKTK 60
 " : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Dd 161 APELLGGPSVFLFPPKPKDTLMISTPEVTCVVVDVSHEDPEVQFKWYDGVGEVHNAKT 220

4.

QY	61	PREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEK	110
		: : : : : : :	
Db	221	PREEQYNSTFRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK	270

RESULT 9
G3HUW1
Ig gamma-3 heavy chain disease proteins - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1979 #sequence.revision 23-Oct-1981 #text_change 16-Jul-1999
C:Accession: A90442; A92219; A90198; A93915; A92149
R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 head
A:Reference number: A90442; MUID:81021548
A:Contents: heavy chain disease protein Wis
A:Accession: A90442
A:Molecule type: protein
A:Residues: 1-289 <PRA>
A:Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch
A:Note: this protein lacks most of the V region and all of the CH1 region. Residue 12
A:Note: the sequence of residues 42-76 was taken from the reference that follows
R:Michaelisen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977

A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplicate segment (12-28)
A:Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form in R.Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
A:Reference number: A92219; MUID:77118561
A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein A:Accession: A92219
A:Molecule type: protein
A:Residues: 12-97 <MIC>
A:Note: the hinge region in gamma-3 chains is about four times as long as in other gamma-3 chains

A:Molecule type: protein
A:Residues: 59-125,'EG',128-226,228-289 <WOL>
A:Note: this protein lacks most of the V region, all of the CH1 region, and part of t
R:Alexander, A.; Steinmetz, A.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood,
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A:Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deleti
A:Reference number: A93915; MUID:82247835
A:Contents: heavy chain disease protein Omm
A:Accession: A93915
A:Molecule type: mRNA
A:Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-
A:Note: a carboxyl-terminal Lys is removed posttranslationally
A:Note: this sequence may represent an allelic form or another gamma chain subclass
A:Comment: The heavy chain disease protein Wls is shown.

C:Genetics: A:Gene: GDB:IGHG3
 C:Cross-references: GDB:I19339; OMIM:147120
 A:Map position: 14q32.33-14q32.33
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
 C:Domain: immunoglobulin homology <IMM>
 C:Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 C:Binding site: pyrrolidone (Asn) (covalent) #status experimental

Query Match	88.4%;	Score 519;	DB 1;	Length 289;
Best Local Similarity	86.4%;	Pred. No. 2.8e-44;		

```

1 APPVAGGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVFKNVYDGVGVHNAKTK 60
  || : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
74 APELLGGSPVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFKVYDGVGVHNAKTK 133
                                     ||
61 PREQEQNSIYRVVSVLTVLHQDWLNGKEYCKVKSNKGLPSSIETISKAK 110

```

QY 2 PPVAGGSPSVFLPPKPKDTLMTISRTPEVTCVVVDVSHEDPEVKFNWYVDGEVHHNAKTKP 61
 | : |||||:||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
pB 253 PELGGGPSVFLEPPKPKDTLTLSGTPEVTCVVVDVGHDDPEVKFSNFDVEVNTATIKP 312

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:00:23 ; Search time 48.19 Seconds
(without alignments)
88.382 Million cell updates/sec

Title: US-09-674-857-3

Perfect score: 587

Sequence: 1 APPVAGGSPVFLPPPKPKDT.....CKVSNKGLPSSIEKTIKAK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	94.9	330	1 GCL_HUMAN	P01857 homo sapien
2	553	94.2	327	1 GC4_HUMAN	P01861 homo sapien
3	543.5	92.6	326	1 GC2_HUMAN	P01859 homo sapien
4	519	88.4	290	1 GC3_HUMAN	P01860 homo sapien
5	431	73.4	333	1 GCB_RAT	P02761 rattus norv
6	421	71.7	323	1 GC_RABIT	P01870 oryctolagus
7	421	71.7	329	1 GC2_CAVPO	P01862 cavia porce
8	418	71.2	329	1 GC3_MOUSE	P22436 mus musculu
9	418	71.2	398	1 GC3M_MOUSE	P03987 mus musculu
10	397	67.6	336	1 GCB_MOUSE	P01866 mus musculu
11	397	67.6	405	1 GCBM_MOUSE	P01867 mus musculu
12	386	67.5	324	1 GCL_MOUSE	P01868 mus musculu
13	396	67.5	329	1 GCC_RAT	P20762 rattus norv
14	396	67.5	393	1 GC1M_MOUSE	P01869 mus musculu
15	394	67.1	335	1 GCAB_MOUSE	P01864 mus musculu
16	391	66.6	330	1 GCAA_MOUSE	P01863 mus musculu
17	391	66.6	399	1 GCBM_MOUSE	P01865 mus musculu
18	380	64.7	326	1 GCL_RAT	P20759 rattus norv
19	339	57.8	322	1 GCA_RAT	P20760 rattus norv
20	166.5	28.4	428	1 EPC_HUMAN	P01854 homo sapien
21	153	26.1	429	1 EPC_RAT	P01855 rattus norv
22	153	26.1	457	1 MUC_SUNMU	P02768 suncus muri
23	138	23.5	421	1 EPC_MOUSE	P06336 mus musculu
24	138	23.5	454	1 MUC_HUMAN	P01871 homo sapien
25	137.5	23.4	299	1 ALC_RABIT	P01879 oryctolagus
26	136	23.2	391	1 MUCB_HUMAN	P04220 homo sapien
27	132	22.5	454	1 MUC_MESAU	P06337 mesocricetu
28	132	22.5	455	1 MUC_MOUSE	P01872 mus musculu
29	132	22.5	476	1 MUCB_MOUSE	P01873 mus musculu
30	131	22.3	106	1 KAC_HUMAN	P01834 homo sapien
31	130	22.1	103	1 LAC_CHICK	P20763 gallus gall
32	125	21.3	450	1 MUC_CANFA	P01874 canis famil
33	121.5	20.7	105	1 LAC1_MOUSE	P01843 mus musculu

ALIGNMENTS

RESULT 1

ID	GCL_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	IGHG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a			
RL	monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The			
RT	chymotryptic peptides of the H-chain, alignment of the tryptic			
RT	peptides and discussion of the complete structure.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary			
RL	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

P20765 mus spretus
P03988 oryctolagus
P04221 oryctolagus
P01877 homo sapien
P20758 gorilla gor
P01876 homo sapien
P20764 mus musculu
P01840 oryctolagus
P01878 mus musculu
P23086 heterodontu
P15814 homo sapien
P01842 homo sapien

RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196(1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Delsenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from *Staphylococcus*
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -I- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -I- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35, 116, 198, 269 & 272.
 CC -I- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -I- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198, 267 & 272.
 CC -----
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 DR EMBL; J00228; AAC82527.1; ALT_INIT.
 DR PIR; A02146; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR MTM; 147100; -
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; Ig_like; 1.
 DR SMART; SM00407; IGL1; 2.
 DR PROSITE; PS00290; Ig_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT VARIANT 241 241
 FT STRAND 123 126
 FT HELIX 130 134
 N-LINKED (GLCNAC...).
 REMOVED POST-TRANSLATIONALLY.
 K -> R (IN GIM(3) MARKER).
 D -> E (IN GIM(NON-1) MARKER).
 L -> M (IN GIM(NON-1) MARKER).
 /FTid=VAR_003886.
 /FTid=VAR_003887.
 /FTid=VAR_003888.

FT TURN 136 137
 FT STRAND 141 148
 FT STRAND 158 162
 FT TURN 163 164
 FT STRAND 165 166
 FT STRAND 175 178
 FT STRAND 183 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 206
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 240
 FT TURN 241 242
 FT STRAND 245 256
 FT STRAND 260 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 324
 SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;
 Query Match 94.9%; Score 557; DB 1; Length 330;
 Best Local Similarity 94.5%; Pred. No. 6.4e-49;
 Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 APPVAGGSPVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATK 60
 || : |||||
 Db 114 APPELLGGSPVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATK 173
 QY 61 PREEQYNSTIRYVSVLTVLHQDLNGKEYCKVSKNGLPSSIEKTIISRAK 110
 |||||
 Db 174 PREEQYNSTIRYVSVLTVLHQDLNGKEYCKVSKNGLPAPIEKTIISRAK 223
 RESULT 2
 GC4_HUMAN
 ID GC4_HUMAN STANDARD; PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-4 chain C region.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85157104; PubMed=6299662;
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 1:11-18(1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE=70207560; PubMed=4192699;
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 RT constant region of a gamma 4 chain.";
 RL Biochem. J. 117:33-47(1970).
 CC -----
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DR EMBL: K01316; AAB59394.1; ALT_INIT.
 DR PIR: A02150; G4HU.
 DR HSP; P01842; 7FAB.
 DR MIM; 147130; -.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_cl.
 DR InterPro: IPR003600; Ig_like.
 DR Pfam: PF00047; Ig; 3
 DR SMART: SM00410; Ig_like; 1.
 DR SMART; SM00410; IGL; 2.
 DR PROSITE; PS00290; Ig_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT DOMAIN 1 98 CHI.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 220 CH2.
 FT DOMAIN 221 327 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 141 201
 FT DISULFID 247 305
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 94.2%; Score 553; DB 1; Length 327;
 Best Local Similarity 94.5%; Pred. No. 1.6e-48;
 Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNQYVGVVHNAKTK 60
 || |||||
 Db 111 APFELGSPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNQYVGVVHNAKTK 170
 |||||
 QY 61 PREEQNSTYRVSVLTFLVQLHQLWLNQKEYCKVSNKGLPSSIEKTSKAK 110
 |||||
 Db 171 PREEQNSTYRVSVLTFLVQLHQLWLNQKEYCKVSNKGLPSSIEKTSKAK 220
 |||||

RESULT 3

GC2_HUMAN STANDARD; PRT; 326 AA.
 ID GC2_HUMAN
 AC P01859;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-2 chain C region.
 GN IGHG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE OF 2-326 FROM N.A.
 RP MEDLINE-82197621; PubMed-6804948;
 RA Ellison J.W., Hood L.E.;
 RT "Linkage and sequence homology of two human immunoglobulin gamma
 RT heavy chain constant region genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
 RL [2]
 RP SEQUENCE OF 88-115 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE-83001943; PubMed-6811139;
 RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
 RT "Structure of human immunoglobulin gamma genes: implications for
 RT evolution of a gene family.";

RL Cell 29:671-679(1982).
 RN [3]
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE-84235992; PubMed-6329676;
 RA Krawinkel U., Rabbitts T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 RT genes.";
 RL EMBO J. 1:403-407(1982).
 RN [4]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE-81007873; PubMed-6774012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 myeloma protein.";
 RT evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE-80001357; PubMed-113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 RT domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE-80114419; PubMed-118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 RT immunoglobulins gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE-95255298; PubMed-7737190;
 RA Stoppini M., Ballotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 RT immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE-72033500; PubMed-4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE-69064124; PubMed-5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
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 CC -----
 DR EMBL: J00230; AAB59393.1; -.
 DR PIR; A02148; G2HU.
 DR HSP; P01857; 1FC1.
 DR MIM; 147110; -.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_cl.
 DR InterPro: IPR003600; Ig_like.
 DR Pfam: PF00047; Ig; 3.
 DR SMART; SM00410; IG_like; 1.
 DR SMART; SM00407; IGL; 2.

DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT SITE 156 156 AT OR NEAR THE COMPLEMENT-BINDING SITE.
 FT MOD_RES 326 326 REMOVED POST-TRANSLATIONALLY (PROBABLE).
 FT VARIANT 60 60 S -> A (IN MYELOMA PROTEINS TIL & ZIE).
 FT CONFLICT 109 109 /FTid=VAR_003889.
 FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
 SQ

Query Match 92.68; Score 543.5; DB 1; Length 326;
 Best Local Similarity 92.78; Pred. No. 1.5e-47;
 Matches 102; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
 QY 1 APPVAGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTK 60
 DB 111 APPVA-GPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNKYVDGVEVHNAKTK 169
 QY 61 PREEQYNSTRVSVLVHQLDNLNGKEYKCKVSNKGLPSSIEKTSKAK 110
 DB 170 PREEQFNSTRVSVLVHQLDNLNGKEYKCKVSNKGLPAPIEKTSKTK 219

RESULT 4
 GC3_HUMAN STANDARD; PRT; 290 AA.
 AC P01860;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
 GN IGHG3
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (DISEASE PROTEIN WIS).
 RX MEDLINE=81021548; PubMed=6774747;
 RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
 RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
 RL gamma 3 heavy-chain disease protein Wis.";
 RL Biochemistry 19:4304-4308(1980).
 RN [2]
 RP REVISIONS TO 12-97 OF PROTEIN WIS.
 RX MEDLINE=77118561; PubMed=402363;
 RA Michaelson T.E., Frangione B., Franklin E.C.;
 RT "Primary structure of the 'hinge' region of human IgG3. Probable
 RL quadruplication of a 15-amino acid residue basic unit.";
 RL J. Biol. Chem. 252:883-889(1977).
 RN [3]
 RP REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC).
 RX MEDLINE=77021516; PubMed=823945;
 RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
 RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
 RL Structure of the Fc fragment of immunoglobulin G3";
 RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
 RN [4]
 RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
 RX MEDLINE=82247835; PubMed=6808505;

RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
 RA Franklin E.C., Hood L., Buxbaum J.N.;
 RT "Gamma heavy chain disease in man: cDNA sequence supports partial
 RT gene deletion model.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
 CC -1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
 CC INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
 CC NORMALLY PRESENT IN THE HINGE REGION.
 CC -1- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
 CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
 CC REF. 2.
 CC -1- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
 CC AND ALL OF THE CH1 REGION.
 CC -1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
 CC OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
 CC GAMMA-3 HEAVY CHAINS.
 CC -1- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
 CC OR ANOTHER GAMMA CHAIN SUBCLASS.
 CC -1- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
 CC TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
 CC IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
 CC SEGMENT (12-28).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J00231; AAA52805.1; ALT_SEQ.
 DR PIR; A02149; G3HUWI.
 DR HSSP; P01857; LFC1.
 DR MIM; 147120; -
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00410; IG-like; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.
 FT DOMAIN 12 73 HINGE.
 FT DOMAIN 74 183 CH2.
 FT DOMAIN 184 289 CH3.
 FT REPEAT 29 43
 FT REPEAT 44 58
 FT REPEAT 59 73
 FT MOD_RES 1 1
 FT CARBOHYD 6 6
 FT DISULFID 7 7
 FT DISULFID 24 24 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 27 27 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 33 33 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 39 39 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 42 42 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 48 48 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 54 54 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 57 57 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 63 63 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 69 69 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 72 72 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC...).
 FT MOD_RES 290 290 REMOVED POST-TRANSLATIONALLY.
 FT VARIANT 126 127 QV -> EB (IN ZUC).
 FT VARIANT 134 134 /FTid=VAR_003890.
 FT VARIANT 139 139 P -> L (IN OMM).
 FT VARIANT 182 182 /FTid=VAR_003891.
 FT VARIANT 182 182 F -> Y (IN OMM).
 FT VARIANT 182 182 /FTid=VAR_003892.
 FT VARIANT 182 182 T -> A (IN OMM).
 FT VARIANT 182 182 /FTid=VAR_003893.

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FT VARIANT 227 227 S -> N (IN OMM).
FT /FTID=VAR_003894.
FT VARIANT 227 227 MISSING (IN ZUC).
FT /FTID=VAR_003895.
FT VARIANT 279 279 F -> Y (IN OMM).
FT /FTID=VAR_003896.
SQ SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;

Query Match 88.4%; Score 519; DB 1; Length 290;
Best Local Similarity 86.4%; Pred. No. 3.7e-45;
Matches 95; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 APPVAGSPVFLPPPKDPTLMSRPTVTCVVVDVSHEDPEVKENWYVDGVEVHNKATK 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 74 ABELGGPSVFLPPPKDPTLMSRPTVTCVVVDVSHEDPEVKENWYVDGVEVHNKATK 133
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 PREEQNSTYRVSVLTVLHQDLNGLNGKEYCKVSKNKGFLPSSIEKTIISKAK 110
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 134 PREQQFNSTFRVSVLTVLHQDLNGLNGKEYCKVSKNKGFLPSSIEKTIISKAK 183
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
GCB_RAT
ID GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Bruggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; Ig_C1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 73.4%; Score 431; DB 1; Length 333;
Best Local Similarity 69.7%; Pred. No. 3.2e-36;
Matches 76; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 2 PPVAGSPVFLPPPKDPTLMSRPTVTCVVVDVSHEDPEVKENWYVDGVEVHNKATK 61
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Db 118 PELLGSPVFIPLPPKDKLLISQNAKVTCTVVDVSEEPDQFQFVNNVEVHTAQTP 177
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QY 62 REEQNSTYRVSVLTVLHQDLNGLNGKEYCKVSKNKGFLPSSIEKTIISKAK 110
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 178 REEQNSTYRVSVLTVLHQDLNGLNGKEYCKVSKNKGFLPSSIEKTIISKAK 226
```

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RESULT 6
GCB_RAT
ID GCB_RAT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8403030; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G.";
RL Biochem. J. 116:249-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RT (In) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell, Stockholm (1967).
CC -!- MISCELLANEOUS; REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER.
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15 MARKERS AND REF.5 THE E15 MARKER.
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CC -----
DR EMBL; M16426; AAA31289.1; -.
DR PIR; A02161; GHRB.
DR HSSP; P01857; IFC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Ig_C1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
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FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 71.7%; Score 421; DB 1; Length 323;
Best Local Similarity 69.7%; Pred. No. 3.1e-35;
Matches 76; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 2 PPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
DB 108 PELLGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSDQDPEVQFTWYINNEQVRTARPPL 167

QY 62 REEQYNSTRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTSKAK 110
DB 168 REQQFNSTRVSVLTPLTHODWLRGKFEKCKVHNKALPAPIEKTSKAR 216

RESULT 7
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN 1;
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN 12;
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN 13;
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN 14;
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN 15;
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
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RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN 16;
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC 1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 16 16 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 28 79 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202 N-LINKED (GLCNAC. .).
FT CARBOHYD 178 178
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 71.7%; Score 421; DB 1; Length 329;
Best Local Similarity 71.6%; Pred. No. 3.2e-35;
Matches 78; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 2 PPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
DB 113 PENLGGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSDQDPEVQFTWFDNKPVGNAETKP 172

QY 62 REEQYNSTRVSVLTVLHODWLNKGKEYCKVSNKGLPSSIEKTSKAK 110
DB 173 RVEQNTFRVSVLPVPIQHDWLRGKFEKCKVHNKALPAPIEKTSKTK 221

RESULT 8
GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
CC 1;
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CC or send an email to license@isb-sib.ch).
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DR EMBL: J00451; ; NOT_ANNOTATED_CDS.
DR PIR: B02156; G3MSC.
DR HSSP: P01857; 1FC1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_C1.
DR Pfam: PF00047; Ig_3.
DR InterPro: IPR003600; Ig_like.
DR SMART: SM00410; IgC1; 2.
DR SMART: SM00407; IgC1; 2.
DR PROSITE: PS00290; IG_MHC; 1.
DR PROSITE: PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
FT Transmembrane; Alternative splicing.
FT NON_TER 1 97
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362
FT DOMAIN 363 398 POTENTIAL.
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 71.2%; Score 418; DB 1; Length 329;
Best Local Similarity 68.5%; Pred. No. 6.4e-35;
Matches 76; Conservative 15; Mismatches 18; Indels 2; Gaps 1;

QY 2 PP--VAGGSPVLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKT 59
DB 112 PGNILGGSPVFIFFPKPKDALMISLTPTKVTCTVVDVSEDDPDVHVSFVDNKEVHTAWT 171
QY 60 KPREEQNSTYRVSVLTVLHODWLNKGKEYCKVSKNGKLPSSIEKTIKSAK 110
DB 172 QPREAQNSTFRVVSALPTQHQDWRGKEFKCKVNNKALPAPIERTISRPK 222

RESULT 9
GC3M_MOUSE
ID GC3M_MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041483; PubMed=6314258;
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00451; AAB59655.1; -.
DR EMBL: V01526; CAA24767.1; ALT_SEQ.
DR PIR: A02155; G3MSM.
DR HSSP: P01857; 1FC1.
```

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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00410; IgC1; 1.
DR SMART: SM00407; IgC1; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
FT Transmembrane; Alternative splicing.
FT NON_TER 1 97
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362
FT DOMAIN 363 398 POTENTIAL.
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 71.2%; Score 418; DB 1; Length 398;
Best Local Similarity 68.5%; Pred. No. 7.9e-35;
Matches 76; Conservative 15; Mismatches 18; Indels 2; Gaps 1;

QY 2 PP--VAGGSPVLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKT 59
DB 112 PGNILGGSPVFIFFPKPKDALMISLTPTKVTCTVVDVSEDDPDVHVSFVDNKEVHTAWT 171
QY 60 KPREEQNSTYRVSVLTVLHODWLNKGKEYCKVSKNGKLPSSIEKTIKSAK 110
DB 172 QPREAQNSTFRVVSALPTQHQDWRGKEFKCKVNNKALPAPIERTISRPK 222

RESULT 10
GC3M_MOUSE
ID GC3M_MOUSE STANDARD; PRT; 336 AA.
AC P01866;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2B chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (A ALLELE).
RX MEDLINE=80120716; PubMed=6766534;
RA Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
RT "Complete nucleotide sequence of immunoglobulin gamma2b chain gene
cloned from newborn mouse DNA.";
RL Nature 283:786-789(1980).
RN [2]
RP SEQUENCE FROM N.A. (MPC 11).
RX MEDLINE=80081501; PubMed=117548;
RA Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;
RT "Structure of the constant and 3' untranslated regions of the murine
gamma 2b heavy chain messenger RNA.";
RL Science 205:1299-1303(1979).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=80081502; PubMed=117549;
RA Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
RT "Sequence of the cloned gene for the constant region of murine gamma
2b immunoglobulin heavy chain.";
RL Science 205:1303-1306(1979).
RN [4]
RP SEQUENCE FROM N.A. (B ALLELE).
RX MEDLINE=82173203; PubMed=6803173;
RA Ollo R., Rougeon F.;
RT "Mouse immunoglobulin allotypes: post-duplication divergence of gamma
```

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RT 2a and gamma 2b chain genes."
RL Nature 296:761-763(1982).
RN [5]
RA CARBOHYDRATE-LINKAGE SITE THR-105.
RX MEDLINE=94216359; PubMed=7512967.
RA Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,
RA Irimura T., Takahashi N., Kato K., Arata Y.;
RT "O-glycosylation in hinge region of mouse immunoglobulin G2b.";
RL J. Biol. Chem. 269:12345-12350(1994).
CC -!- PTM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS
CC MODIFIED WITH 2 SIALIC ACID RESIDUES.
CC -!- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLGY WITH OTHER IG GAMMA
CC CHAINS.
CC -!- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.
DR PIR: A02157; G2MS11.
DR HSSP: P01857; IFC1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00410; Ig-like; 1.
DR SMART: SM00407; IGcl; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 150 210 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 256 314
FT CARBOHYD 105 105 O-LINKED (GALNAC...).
FT MOD_RES 336 336 REMOVED POST-TRANSLATIONALLY (PROBABLE).
FT VARIANT 163 163 Q -> R (IN B ALLELE).
FT VARIANT 194 194 T -> A (IN B ALLELE).
FT VARIANT 300 300 N -> D (IN B ALLELE).
FT VARIANT 301 301 M -> I (IN B ALLELE).
FT CONFLICT 25 25 L -> S (IN REF. 2 AND 3).
FT CONFLICT 36 36 S -> P (IN REF. 2 AND 3).
FT CONFLICT 239 239 I -> T (IN REF. 2 AND 3).
SQ SEQUENCE 336 AA; 36658 MW; 7D879662607C356E CRC64;

Query Match 67.6%; Score 397; DB 1; Length 336;
Best Local Similarity 65.5%; Pred. No. 8.5e-33;
Matches 72; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDITLMSRTPETVTVVVDVSHEDPEVKFNWYDGVGVHNAKTK 60
Db 120 APNLEGGPSVFIFPPNKKDVLMSLPKVTCTVVDVSEDDPDVQISWVNNVEVHTAQ 179
QY 61 PREEQYNSTYRVSVTLVTLHQLDNLNGKEYCKVSKNGLPSSIEKTSKAK 110
Db 180 THREDYNSTIRVSTLPIQHDQWMSGKEFKCKVNNKDLPSPIERTISKIK 229

RESULT 11
GCBM_MOUSE
ID CCBM_MOUSE STANDARD; PRT: 405 AA.
AC F01867;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2b chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 335-405 FROM N.A.
RX MEDLINE=8222190; PubMed=6283537;

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RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RL immunoglobulin gamma chains.";
RN Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
RP SEQUENCE OF 335-378 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
RL immunoglobulin gamma chains.";
RL Cell 26:19-27(1981).
CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC SEGMENT OF MU CHAINS.
CC -!- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLGY WITH OTHER IG GAMMA
CC CHAINS.
CC -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-335 IS ASSUMED TO BE
CC IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM.
CC -!- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL: J00462; AAB59659.1; ALT_INIT.
DR PIR: C02154; G2MSBM.
DR HSSP: P01857; IFC1.
DR MGD: MGI:96445; Igh-3.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00410; Ig-like; 1.
DR SMART: SM00407; IGcl; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Transmembrane;
KW Alternative splicing.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 150 210 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 256 314
FT TRANSMEM 352 369
FT DOMAIN 370 405
FT SEQUENCE 405 AA; 44330 MW; 89B3CF0A9BD6D49FA CRC64;

Query Match 67.6%; Score 397; DB 1; Length 405;
Best Local Similarity 65.5%; Pred. No. 1.1e-32;
Matches 72; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDITLMSRTPETVTVVVDVSHEDPEVKFNWYDGVGVHNAKTK 60
Db 120 APNLEGGPSVFIFPPNKKDVLMSLPKVTCTVVDVSEDDPDVQISWVNNVEVHTAQ 179
QY 61 PREEQYNSTYRVSVTLVTLHQLDNLNGKEYCKVSKNGLPSSIEKTSKAK 110
Db 180 THREDYNSTIRVSTLPIQHDQWMSGKEFKCKVNNKDLPSPIERTISKIK 229

RESULT 12

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GCL_MOUSE STANDARD; PRT; 324 AA.

AC P01868;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Ig gamma-1 chain C region.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=80045036; PubMed=115593;

RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.;

RA "Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene.";

RT Cell 18:559-568(1979).

RL [2]

RN [2]

RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).

RX MEDLINE=80202559; PubMed=6769752;

RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;

RA "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";

RT Gene 9:87-97(1980).

RL [3]

RN [3]

RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).

RX MEDLINE=80012837; PubMed=113776;

RA Rogers J., Clarke P., Salser W.;

RA "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain.";

RT Nucleic Acids Res. 6:3305-3321(1979).

RL [4]

RN [4]

RP SEQUENCE (MYELOMA PROTEIN MOPC 21).

RX MEDLINE=78242288; PubMed=98524;

RA Adetugbo K.;

RA "Evolution of immunoglobulin subclasses. Primary structure of a murine myeloma gamma chain.";

RT J. Biol. Chem. 253:6068-6075(1978).

RL [5]

RN [5]

RP DISULFIDE BONDS (MOPC 21).

RX MEDLINE=73008889; PubMed=5073237;

RA Svasti J., Milstein C.;

RA "The disulphide bridges of a mouse immunoglobulin G1 protein.";

RT Biochem. J. 126:837-850(1972).

RL [6]

RN [6]

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CC EMBL; V00793; CAA24172.1; -

DR EMBL; V00793; CAA24173.1; -

DR EMBL; V00793; CAA24174.1; -

DR EMBL; V00793; CAA24175.1; -

DR EMBL; V00795; CAA24176.1; -

DR PIR; A02159; GIMS.

DR HSSP; P01842; 7FAB.

DR GDC; MGI:96446; Igh-4.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003597; Ig_C1.

DR Pfam; PF00047; ig; 3.

DR SMART; SM00407; IGcl; 2.

DR PROSITE; PS00290; IG_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Alternative splicing.

FT NON_TER 1 1

FT DOMAIN 1 97 CH1.

FT DOMAIN 98 110 HINGE.

FT DOMAIN 111 217 CH2.

FT DOMAIN 218 324 CH3.

FT DISULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 N-LINKED (GLCNAC. .).

FT DISULFID 138 198 /FTIG-CAR_000055.

FT CARBOHYD 174 174

FT DISULFID 244 302 REMOVED POST-TRANSLATIONALLY.

FT MOD_RES 324 324 N -> D (IN REF. 3).

FT CONFLICT 276 276 N -> D (IN REF. 3).

FT CONFLICT 278 278

SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;

Query Match 67.5%; Score 396; DB 1; Length 324;

Best Local Similarity 67.6%; Pred. No. le-32;

Matches 69; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 9 SVFLPPPKPKDILMISRTPEVTCVVVDVSHEDPEVFNNVVDGVEVHNKTKPREQYNS 68

DB 116 SVFIPPKPKDVLITLTPKVCVVVDISKDDPEVQSFVDDVEVHTAQTQPREQFNS 175

QY 69 TYRVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSAK 110

DB 176 TFRSVSELPIMHQDWLNGKEYKCRVNSAAPPAPIETISKTK 217

RESULT 13

GCC_RAT STANDARD; PRT; 329 AA.

AC P20762;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig gamma-2C chain C region.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88166903; PubMed=3127222;

RA Bruggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;

RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant region cDNA: extensive homology to mouse gamma 3.";

RL Eur. J. Immunol. 18:317-319(1988).

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CC EMBL; X07189; CAA30169.1; -

DR PIR; S00847; S00847.

DR HSSP; P01857; IFCL.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003597; Ig_C1.

DR InterPro; IPR003600; Ig_Like.

DR Pfam; PF00047; ig; 3.

DR SMART; SM00410; IG_Like; 1.

DR PROSITE; PS00407; IGcl; 2.

DR PROSITE; PS00290; IG_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region.

FT NON_TER 1 1

FT DOMAIN 1 97 CH1.

```
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 203 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 249 307 INTERCHAIN (WITH A HEAVY CHAIN).
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 67.5%; Score 396; DB 1; Length 329;
Best Local Similarity 67.6%; Pred. No. 1e-32;
Matches 71; Conservative 17; Mismatches 17; Indels 0; Gaps 0;

QY 6 GGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 65
DB 118 GRPSVFIFPKPKDILMITLTPKVTCTVVVDVSEEDPVQSFVDFVNRVFTAQTPHEEQ 177
QY 66 NYSYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTSISKAK 110
DB 178 LNSGFRVSVLTSLHODWLNKGYKCKVSNKGLPSSIEKTSISKPR 222

RESULT 14
GCIM_MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RA "mRNA for surface immunoglobulin gamma chains encodes a highly
RT conserved transmembrane sequence and a 28-residue intracellular
RT domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
RT immunoglobulin gamma chains.";
RL Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=8222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC GAMMA CHAINS, A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
```

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CC SEGMENT OF MU CHAINS.
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CC -----
DR EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR PIR; B02159; GIMSM.
DR HSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 104 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198 N-LINKED (GLCNAC. . .).
FT CARBOHYD 174 174 POTENTIAL.
FT DISULFID 244 302 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 340 357
FT DOMAIN 358 393
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7ALCE27 CRC64;

Query Match 67.5%; Score 396; DB 1; Length 393;
Best Local Similarity 67.6%; Pred. No. 1.3e-32;
Matches 69; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 9 SVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 68
DB 116 SVFIFFPKPKDVLTLTPKVTCTVVVDISKDDPEVQFSWFDVDDVEVHTAQTPREEQNS 175
QY 69 TYRVVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTSISKAK 110
DB 176 TFRSVSELPIMHQDWLNKGYKCKVSNKGLPSSIEKTSISKAK 217

RESULT 15
GCAB_MOUSE STANDARD; PRT; 335 AA.
ID GCAB_MOUSE
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT IgG2aa and IgG2ab alleles of the mouse.";
```


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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:59:30 ; Search time 176.89 Seconds

(without alignments)
107.578 Million cell updates/sec

Title: US-09-674-857-3

Perfect score: 587

Sequence: 1 APPVAGGPSVFLPPPKPDKT.....CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTEMBL19.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriopl.*
- 17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	94.9	701	4 Q96PQ8	Q96PQ8 homo sapien
2	458	78.0	337	6 Q95M34	Q95M34 equus caball
3	397	67.6	473	11 Q91Z05	Q91Z05 mus musculus
4	396	67.5	437	11 Q9R1A4	Q9R1A4 mus musculus
5	396	67.5	463	11 Q99LCA	Q99LCA mus musculus
6	394	67.1	473	11 Q9D8L4	Q9D8L4 mus musculus
7	382	65.1	468	11 Q99L31	Q99L31 mus musculus
8	382	65.1	473	11 Q99L25	Q99L25 mus musculus
9	138	23.5	375	4 Q9BSZ1	Q9BSZ1 homo sapien
10	138	23.5	597	4 Q9BQ88	Q9BQ88 homo sapien
11	138	23.5	597	4 Q9BU10	Q9BU10 homo sapien
12	138	23.5	597	4 Q9BBB9	Q9BBB9 homo sapien
13	138	23.5	613	4 Q96EY0	Q96EY0 homo sapien
14	138	23.5	614	4 Q96GA6	Q96GA6 homo sapien
15	138	23.5	618	4 Q96AA6	Q96AA6 homo sapien
16	122.5	20.9	684	13 Q90544	Q90544 ginglymosto

17	121.5	20.7	130	11 Q9D8W4	Q9D8W4 mus musculus
18	121.5	20.7	233	11 Q91V32	Q91V32 m adult mal
19	119.5	20.4	384	4 Q9UP60	Q9UP60 homo sapien
20	119.5	20.4	416	4 Q9NPP6	Q9NPP6 homo sapien
21	119.5	20.4	494	4 Q96K68	Q96K68 homo sapien
22	119.5	20.4	496	4 Q96KX8	Q96KX8 homo sapien
23	119.5	20.4	496	4 Q96DK0	Q96DK0 homo sapien
24	116.5	19.8	235	11 Q99M11	Q99M11 mus musculus
25	115.5	19.7	500	4 Q9BRV0	Q9BRV0 homo sapien
26	114.5	19.5	233	4 Q96169	Q96169 homo sapien
27	114.5	19.5	236	4 Q96E61	Q96E61 homo sapien
28	112.5	19.2	486	11 Q91Z07	Q91Z07 mus musculus
29	112.5	19.2	487	11 Q99KA4	Q99KA4 mus musculus
30	111.5	19.0	479	11 Q99M22	Q99M22 mus musculus
31	111.5	19.0	484	11 Q99LA6	Q99LA6 mus musculus
32	110.5	18.8	479	11 Q91WP5	Q91WP5 mus musculus
33	110.5	18.8	481	11 Q91WT3	Q91WT3 mus musculus
34	110.5	18.8	481	11 Q91WT1	Q91WT1 mus musculus
35	110.5	18.8	482	11 Q91X92	Q91X92 mus musculus
36	110.5	18.8	488	11 Q91WR1	Q91WR1 mus musculus
37	109.5	18.7	426	11 Q9DCD9	Q9DCD9 mus musculus
38	109.5	18.7	480	11 Q91XE1	Q91XE1 mus musculus
39	105	17.9	235	11 Q91WL2	Q91WL2 mus musculus
40	103	17.5	211	11 Q91XL0	Q91XL0 mus musculus
41	103	17.5	233	11 Q91WS9	Q91WS9 mus musculus
42	103	17.5	234	11 Q91WF8	Q91WF8 mus musculus
43	103	17.5	238	11 Q99M37	Q99M37 mus musculus
44	103	17.5	1215	5 Q9V787	Q9V787 drosophila
45	101	17.2	214	11 Q9R1A5	Q9R1A5 mus musculus

ALIGNMENTS

RESULT 1

Q96PQ8 ID Q96PQ8 PRELIMINARY; PRT; 701 AA.

AC Q96PQ8; DT 01-DEC-2001 (TEMBLrel. 19, Created)

DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)

DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21477448; PubMed=11593034;

RA Hu Z., Garen A.;

RT "Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).

DR EMBL: AF272774; AAK58686.1; .

SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 94.9%; Score 557; DB 4; Length 701;

Best Local Similarity 94.5%; Pred. No. 3.3e-53;

Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

|| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 485 APELLGGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 544

QY 61 PREEQNSTYRVVSVLTVTLQHDWLNQKEYCKVSNKGLPSSIEKTISKAK 110

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 545 PREEQNSTYRVVSVLTVTLQHDWLNQKEYCKVSNKGLPSSIEKTISKAK 594

RESULT 2

Q95M34 ID Q95M34 PRELIMINARY; PRT; 337 AA.

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AC Q95W34;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE IMMUNOGLOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
DE (FRAGMENT).
GN IGHCL1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Wagner B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B.; Overesch G.; Sheoran A.; Holmes M.; Richards C.;
RA Leibold W.; Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199;105-119(1998).
DR EMBL; AJ300675; CAC44624.1; -.
FT NON_TER 1
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 78.0%; Score 458; DB 6; Length 337;
Best Local Similarity 73.6%; Pred. No. 1.3e-42;
Matches 81; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDILMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 119 APELGGGSPVFIAPPNPKDILMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 178

QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 179 PKEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 228

RESULT 3
Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 51.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 67.6%; Score 397; DB 11; Length 473;
Best Local Similarity 65.5%; Pred. No. 1.1e-35;
Matches 72; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDILMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 257 APNLEGGSPVFIAPPNPKDILMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 316

QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 317 THREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 366
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RESULT 4
Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G.; Yu X.; Ekramoddoullah A.K.M.; Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; Ig_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 67.5%; Score 396; DB 11; Length 437;
Best Local Similarity 67.6%; Pred. No. 1.3e-35;
Matches 69; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 9 SVFLFPKPKDILMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYNS 68
Db 229 SVFIAPPKPKDILMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYNS 288

QY 69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 289 TFRSVSELPIMHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 330

RESULT 5
Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 2.
```

```
DR SMART: SM00407: IGcl: 1.
DR SMART: SM00406: IGV: 1.
DR SMART: SM00410: IG_like: 1.
DR PROSITE: PS00290: IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BEC30783 CRC64;

Query Match          67.5%; Score 396; DB 11; Length 463;
Best Local Similarity 67.6%; Pred. No. 1.4e-35;
Matches 69; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 9 SVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVNS 68
DB 255 SVFLPPKPKDVLTLTKPKVTCVVVDISKDDPEVQFSWFVDVDEVHTAQTQPREEQFNS 314
QY 69 TVYVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIKSKAK 110
DB 315 TFRSVSELPIMHQDLNGKEFKRCVNSAFAPIEKTISKTK 356

RESULT 6
QY9D8L4
ID QY9D8L4 PRELIMINARY; PRT; 473 AA.
AC QY9D8L4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 181006009RIK PROTEIN.
GN IGH-1 OR 181006009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK007918: BAB25349.1; -
DR HSP: P01842; 7FAB.
DR MGD: MGI:96443; Igh-1.
DR InterPro: IPR003599; Igh-1.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig: 2.
DR SMART: SM00407; IGcl: 3.
DR SMART: SM00406; IGV: 1.
DR SMART: SM00410; IG_like: 1.
DR PROSITE: PS00290: IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
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Query Match          67.1%; Score 394; DB 11; Length 473;
Best Local Similarity 64.5%; Pred. No. 2.4e-35;
Matches 71; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 257 APDLGGSPVFIFPPKIKDVLMLISLSPWTCVVVDVSEDDPDVQISWFWNNVEVHTAQIQ 316
QY 61 PREEQVNSYRVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIKSKAK 110
DB 317 THREDYNSTLRVVSALPIQHQMWSGKEFKCKVNNRNLSPLEKTIKPKR 366

RESULT 7
QY9L31
ID QY9L31 PRELIMINARY; PRT; 468 AA.
AC QY9L31;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 181006009RIK PROTEIN.
GN IGH-1 OR 181006009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC003878: AAH03878.1; -
DR HSP: P01842; 7FAB.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig: 4.
DR SMART: SM00409; IG: 2.
DR SMART: SM00407; IGcl: 3.
DR SMART: SM00406; IGV: 1.
DR SMART: SM00410; IG_like: 1.
DR PROSITE: PS00290: IG_MHC; UNKNOWN_1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match          65.1%; Score 382; DB 11; Length 468;
Best Local Similarity 63.6%; Pred. No. 5.2e-34;
Matches 70; Conservative 18; Mismatches 22; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 252 APNLLGGSPVFIFPPKIKDVLMLISLSPWTCVVVDVSEDDPDVQISWFWNNVEVHTAQIQ 311
QY 61 PREEQVNSYRVSVLTVLHQLDNLNGKEYCKVSNKGLPSSIEKTIKSKAK 110
DB 312 THREDYNSTLRVVSALPIQHQMWSGKEFKCKVNNRNLSPLEKTIKPKR 361

RESULT 8
QY9L25
ID QY9L25 PRELIMINARY; PRT; 473 AA.
AC QY9L25;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 181006009RIK PROTEIN.
GN IGH-1 OR 181006009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
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RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -;
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003600; Ig.like.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 65.1%; Score 382; DB 11; Length 473;
Best Local Similarity 63.6%; Pred. No. 5.2e-34;
Matches 70; Conservative 18; Mismatches 22; Indels 0; Gaps 0;
QY 1 APPVAGGSPVFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 257 APNLLGSPSVFPPPKIKDKVLMISLSPMTVCVVVDVSEDDPDVQISWVNNVEVLTAQTQ 316
QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 317 THREDYNSTLRVVSALPQHQDWMSGKFKCKVNNKALPAPIERTISKPK 366

RESULT 9
Q9BSZ1 ID Q9BSZ1 PRELIMINARY; PRT; 375 AA.
AC Q9BSZ1;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL 41.3 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH, LYMPHOMA;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004476; AAH04476.1; -;
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003600; Ig.like.
DR InterPro; IPR003006; Ig.MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 375 AA; 41314 MW; BIA0A0998F473619 CRC64;

Query Match 23.5%; Score 138; DB 4; Length 375;
Best Local Similarity 28.7%; Pred. No. 4.5e-07;
Matches 29; Conservative 25; Mismatches 45; Indels 2; Gaps 2;
QY 10 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69
Db 146 VFAIPPS-FASIFLTKSTKLTCLVTDLTID-SVTISWTRONGEAVKTHNISHPNAT 203
QY 70 YRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 204 FSAVGEASICEDDMNSGRFTCTVTHTDLPSPKQTSRPK 244

RESULT 10
Q9BQB8 ID Q9BQB8 PRELIMINARY; PRT; 597 AA.
AC Q9BQB8;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RHABDOMYOSARCOMA;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -;
DR EMBL; BC001872; AAH01872.1; -;
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003600; Ig.like.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 23.5%; Score 138; DB 4; Length 597;
Best Local Similarity 28.7%; Pred. No. 8.1e-07;
Matches 29; Conservative 25; Mismatches 45; Indels 2; Gaps 2;
QY 10 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69
Db 368 VFAIPPS-FASIFLTKSTKLTCLVTDLTID-SVTISWTRONGEAVKTHNISHPNAT 425
QY 70 YRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Db 426 FSAVGEASICEDDMNSGRFTCTVTHTDLPSPKQTSRPK 466

RESULT 11
Q9BU10 ID Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL 65.3 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH, LYMPHOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -;
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003599; Ig.

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC017356; AAH17356.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 618 AA: 67758 MW: 96DBD4C7C96E0A6 CRC64:

	Query Match	23.5%	Score 138;	DB 4;	Length 618;
	Best Local Similarity	28.7%	Pred. No. 8.4e-07;		
	Matches	29;	Conservative	25;	Mismatches 45; Indels 2; Gaps 2;
QY	10	VFLPPPKFDLMLSRPEVTCVVVDSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYNST	69		
Db	368	VFAIPPS-FA5IFLTKTKLTLTDLTYD-SVTISWTRQNGEAVKHTNISEHPNAT	425		
QY	70	YRVYSVLTVLHQDNLNGKEYCKVKSNKGLPSSIEKTI5AK	110		
Db	426	TSVAGEASICEDDWNNSGRFTCTVTHDLP5LKQITSRPK	466		

Search completed: June 21, 2002, 08:59:30
Job time: 1629 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 08:36:05 ; Search time 224.82 Seconds
(without alignments)
54.346 Million cell updates/sec

Title: US-09-674-857-3
Perfect score: 587
Sequence: 1 APPVAGPSVFLPPRPKDT.....CKVSNKGLPSSIEKTIISKAK 110

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	576	98.1	110	21	AA1980
2	570.5	97.2	109	21	AA1981
3	562	95.7	468	21	AA1982
4	562	95.7	488	21	AA1983
5	562	95.7	497	21	AA1984
6	562	95.7	525	21	AA1985
7	562	95.7	711	20	AA1986
8	558	95.1	251	20	AA1987
9	558	95.1	251	21	AA1988
10	558	95.1	251	21	AA1989
11	558	95.1	559	22	AA1990

12	558	95.1	594	22	AAU04062	Human IL-20RA/immu
13	558	95.1	594	22	AA1985274	Human IL-20RA-Ig 9
14	557	94.9	110	13	AA19827680	Human immunoglobul
15	557	94.9	110	14	AA1981684	Undefined ORE2 enc
16	557	94.9	116	20	AA1982621	Human IgG1 Fc gamma
17	557	94.9	212	16	AA1987023	Immunoglobulin G1
18	557	94.9	212	17	AA1987264	Human immunoglobul
19	557	94.9	212	17	AA1987264	Human IgG1 Fc regi
20	557	94.9	212	19	AA1987354	Human immunoglobul
21	557	94.9	212	20	AA1987354	IgG1 Fc protein us
22	557	94.9	212	20	AA1987354	Human IgG1 Fc prot
23	557	94.9	212	21	AA1987354	Human IgG1 Fc regi
24	557	94.9	212	21	AA1987354	Human immunoglobul
25	557	94.9	212	21	AA1987354	Human immunoglobul
26	557	94.9	212	21	AA1987354	FC region of human
27	557	94.9	212	22	AA1987354	FC region of human
28	557	94.9	212	22	AA1987354	Human immunoglobul
29	557	94.9	218	21	AA1987354	Native IgG Fc regi
30	557	94.9	218	21	AA1987354	Native IgG Fc regi
31	557	94.9	218	22	AA1987354	Human IgG Fc 1 all
32	557	94.9	218	22	AA1987354	Human IgG Fc 1 all
33	557	94.9	218	22	AA1987354	Human IgG1 non-A F
34	557	94.9	218	22	AA1987354	Human IgG1 A allot
35	557	94.9	224	8	AA1987354	Sequence of human
36	557	94.9	224	9	AA1987354	Immunoglobulin G F
37	557	94.9	228	21	AA1987354	Human IgG1 Fc prot
38	557	94.9	228	21	AA1987354	Human IgG1 Fc chai
39	557	94.9	228	22	AA1987354	Human IgG1 Fc regi
40	557	94.9	232	18	AA1987354	Human IgG1 hinge/F
41	557	94.9	232	21	AA1987354	Human IgG1 hinge/F
42	557	94.9	232	21	AA1987354	Human immunoglobul
43	557	94.9	232	21	AA1987354	Human immunoglobul
44	557	94.9	232	21	AA1987354	Human immunoglobul
45	557	94.9	232	22	AA1987354	Human partial IgG1

ALIGNMENTS

RESULT 1
AA1987354
ID AA1987354 standard; protein; 110 AA.
XX AC AA1987354
XX AC
DT 17-FEB-2000 (first entry)
DE Mutated CH2 sequence G1deltaaac.
XX
XX
XX
KW Binding molecule: CH2 sequence; complement dependent lysis; Fc gammaRIIb;
KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
KW alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
KW autoimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
KW neonatal alloimmune thrombocytopenia; Goodpasture disease; therapy;
KW sickle cell anaemia; coronary artery occlusion.
XX
XX Synthetic.
XX
XX WO1987354-2A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-GB01441.
XX
XX 08-MAY-1998; 98GB-0009951.
XX
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
XX Armour KL, Clark MR, Williamson LM;
XX

KW immune disease; multiple sclerosis; Crohn's disease; skin
 KW disorders; inflammation; neoplasia; dermatitis; monoclonal
 KW antibody; diabody; scfv; multivalent; ruminant.
 XX
 OS Synthetic.
 OS Mus musculus.

XX Key Location/Qualifiers
 XX Peptide 1..20
 FT /note= "D9D10 light chain signal peptide"
 FT Domain 21..137
 FT /note= "Humanised heavy chain variable domain of
 FT D9D10"
 FT Domain 138..467
 FT /note= "Human IgG1 heavy chain constant domain"
 FT Misc-difference 468
 FT /note= "Leu added by cloning strategy"

XX WO9909055-A2.
 XX
 XX 25-FEB-1999.
 XX
 XX 14-AUG-1998; 98WO-EP05165.
 XX
 XX 18-JUN-1998; 98EP-0870139.
 PR
 PR 18-AUG-1997; 97EP-0870122.
 XX
 XX (INNO-) INNOGENETICS NV.

XX Buyse M, Sablon E;
 PI
 XX
 XX WPI: 1999-180969/15.
 DR
 DR N-PSDB; AAX08631.

PT New engineered antibodies which bind and neutralise interferon-gamma
 PT - useful for prevention and treatment of septic shock, cachexia,
 PT immune diseases and skin disorders
 XX
 XX Disclosure; Fig 9; 134pp; English.

XX New antibodies which bind and neutralise interferon-gamma (IFN
 gamma) can be used as a medicant, for preventing or treating
 CC septic shock, cachexia, immune diseases including multiple sclerosis
 CC and Crohn's disease and skin disorders including bullous,
 CC inflammatory and neoplastic dermatoses. The antibody is selected
 CC from a single chain antibody (scfv), a chimeric antibody or diabody
 CC comprising the humanised variable domain of the monoclonal mouse
 CC anti-IFN gamma antibody D9D10; a multivalent antibody; or a ruminant
 CC antibody. The antibodies are also useful for determining IFN
 CC gamma levels in a sample. Two fusion cDNA genes encoding heavy and
 CC light chain fusion proteins of the humanised D9D10 antibody were
 CC constructed. The light chain comprised cDNA encoding the mouse D9D10
 CC leader sequence, the humanised D9D10 light chain and a human
 CC immunoglobulin kappa light chain constant region. The heavy chain
 CC comprised cDNA encoding the mouse D9D10 light chain leader sequence
 CC followed by the humanised D9D10 heavy chain variable domain and a
 CC human IgG1 heavy chain constant domain in which the C1q-complement
 CC binding site had been mutated. Four overlapping synthetic
 CC oligonucleotides (AAX08585-88) were used to construct the D9D10 light
 CC chain leader sequence. This was then subsequently amplified using two
 CC primers (AAX08589, AAX08590) to generate PCR-V fragment. The humanised
 CC heavy chain variable domain was amplified from pGEM-T-VH using two
 CC primers (AAX08591, AAX08592) to generate PCR-VI fragment. The two
 CC fragments had a base pair overlap and were fused together using
 CC primers (AAX08593, AAX08594) and then cloned into pGEM-T to give
 CC pGEMldrVHh. The human heavy chain constant domain was amplified
 CC with two primers (AAX08595, AAX08596) and cloned into pGEM-T to give
 CC pGEM-TCh. Two separate PCR amplifications were then performed
 CC using pGEM-T-Ch as a template. The primers used were AAX08598, AAX08599
 CC to generate PCR-VII fragment and AAX08597, AAX08600 to generate PCR-IX
 CC fragment. These were then overlapped and fused using primers AAX08599,
 CC AAX08600 and the resulting PCR-X fragment inserted into pGEMldrVHh to
 CC generate the complete heavy chain fusion DNA in a vector designated

CC pGEMhD9D10H. For a description of the construction of the light chain
 CC fusion cDNA see GENESEQ records AAX08573-X08584.
 XX
 SQ Sequence 468 AA;

Query Match 95.7%; Score 562; DB 20; Length 468;
 Best Local Similarity 95.5%; Pred. No. 5.6e-50;
 Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 APVAGGSPVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNARTK 60
 II : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 251 apellggpsvflppkpkdtlmisrtpevtcvcvvdvshedpevkfnkyvdgvevhnaktk 310
 QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAK 110
 || : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 311 preeqynstyrvvsvltvlhqdwlngkeykckvsnkalpasiektiskak 360

RESULT 4
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 ID AAY97175 standard; Protein: 488 AA.
 XX
 XX AC AAY97175;
 XX
 XX 04-DEC-2000 (first entry)
 XX
 XX Human FGF-RI Extracellular domain-Ig Fc fusion protein 6.
 DE
 KW FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1;
 KW immunoglobulin; G1; oligomerization domain; Fc region; fusion protein;
 KW inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary;
 KW ophthalmological; anti-proliferative.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= FGF-RI_signal_peptide
 FT Domain 22..257
 FT /label= FGF-RI_extracellular_domain
 FT /note= "The Ig I segment and acid box are deleted"
 FT Domain 59..111
 FT /label= Ig_II_segment
 FT Domain 157..222
 FT /label= Ig_III_segment
 FT Region 258..488
 FT /label= Human_IgG1_Fc_region
 FT /note= "Contains hinge region and domains CH2 and CH3"
 FT Misc-difference 276
 FT /label= L276E
 FT /note= "This mutation decreases the affinity of the Fc
 FT portion for Fc receptors"
 FT Misc-difference 376
 FT /label= P376S
 FT /note= "this mutation decreases the affinity of the Fc
 FT portion for complement"
 XX
 XX WO200046380-A2.
 XX
 XX 10-AUG-2000.
 XX
 XX 07-FEB-2000; 2000WO-US03166.
 XX
 XX 08-FEB-1999; 99US-0119002.
 XX
 XX (CHIR) CHIRON CORP.
 XX
 XX Kavanaugh WM, Ballinger M;
 XX WPI: 2000-514961/46.
 DR
 DR N-PSDB; AAX52132.
 XX

PT New polypeptide comprising a fibroblast growth factor receptor
 PT extracellular domain fused to a heterologous oligomerization domain for
 PT treating FGF-, angiogenesis-, or FGF receptor-mediated disorders
 XX
 PS Claim 14; Page 68-69; 70pp; English.
 XX
 CC Novel fusion protein constructs comprise a fibroblast growth factor (FGF)
 CC receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin
 CC (Ig) I segment fused to a heterologous oligomerization domain that
 CC comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4
 CC region, or light chain of an immunoglobulin molecule, or a peptide with a
 CC leucine zipper motif. The Ig I segment is not necessary for binding of
 CC acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the
 CC affinity for aFGF and heparin, protects the core of the molecule from
 CC proteolysis, and abrogates the heparin requirement for aFGF binding. The
 CC new fusion polypeptides are better FGF inhibitors than FGF-R monomer
 CC proteins. The FGF-R-Ig Fc fusion dimers are active as FGF antagonists at
 CC subnanomolar concentrations and were 20-fold more potent than the FGF-R
 CC monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The
 CC fusion constructs are useful to treat FGF-, angiogenesis-, or
 CC FGF-R-mediated disorders, such as tumorigenesis (e.g. bladder, breast,
 CC lung, rectal, testis and cervical tumours), neovascularization (e.g.
 CC diabetic retinopathy, neovascular glaucoma, wound healing and corneal
 CC scarring) and hyper-proliferation of vascular smooth muscle cells (e.g.
 CC postangioplasty and postatherectomy restenosis).
 XX
 SQ Sequence 488 AA;

Query Match 95.7%; Score 562; DB 21; Length 488;
 Best Local Similarity 95.5%; Pred. No. 5.9e-50;
 Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db II : |||||
 272 apeleggpsvflfpkpkdtlmisrtpevtcvvvdshedpevkfnwydgvvevhnatk 331
 QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
 Db |||||
 332 preeqynstyrvvsvltvlhqdwlngkeykckvsnkalpasiektiskak 381

RESULT 5
 AAY97174
 ID AAY97174 standard; Protein; 497 AA.
 XX
 AC AAY97174;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 XX Human FGF-RI Extracellular domain-Ig Fc fusion protein 5.

XX FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1;
 KW immunoglobulin; G1; oligomerization domain; Fc region; fusion protein;
 KW inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary;
 KW ophthalmological; anti-proliferative.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= FGF-RI_signal_peptide
 FT Domain 22..257
 FT /label= FGF-RI_extracellular_domain
 FT /note= "The Ig I segment and acid box are deleted"
 FT Domain 59..111
 FT /label= Ig_II_segment
 FT Domain 157..222
 FT /label= Ig_III_segment
 FT Peptide 258..265
 FT /label= Linker
 FT Region 266..497
 FT /label= Human_IgG1_Fc_region

FT Misc-difference 285 /note= "Contains hinge region and domains CH2 and CH3"
 FT /label= L285E
 FT /note= "This mutation decreases the affinity of the Fc
 FT portion for Fc receptors"
 FT Misc-difference 385 /label= P385S
 FT /note= "This mutation decreases the affinity of the Fc
 FT portion for complement"
 XX
 PN W0200046380-A2.
 XX 10-AUG-2000.
 XX
 XX 07-FEB-2000; 2000WO-US03166.
 XX
 XX 08-FEB-1999; 99US-0119002.
 XX (CHIR) CHIRON CORP.
 PA Kavanaugh WM, Ballinger M;
 PI WPI; 2000-514961/46.
 DR N-PSDB; AAA52131.
 XX
 XX New polypeptide comprising a fibroblast growth factor receptor
 PT extracellular domain fused to a heterologous oligomerization domain for
 PT treating FGF-, angiogenesis-, or FGF receptor-mediated disorders
 PT
 PS Claim 14; Page 65-66; 70pp; English.

XX Novel fusion protein constructs comprise a fibroblast growth factor (FGF)
 CC receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin
 CC (Ig) I segment fused to a heterologous oligomerization domain that
 CC comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4
 CC region, or light chain of an immunoglobulin molecule, or a peptide with a
 CC leucine zipper motif. The Ig I segment is not necessary for binding of
 CC acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the
 CC affinity for aFGF and heparin, protects the core of the molecule from
 CC proteolysis, and abrogates the heparin requirement for aFGF binding. The
 CC new fusion polypeptides are better FGF inhibitors than FGF-R monomer
 CC proteins. The FGF-R-Ig Fc fusion dimers are active as FGF antagonists at
 CC subnanomolar concentrations and were 20-fold more potent than the FGF-R
 CC monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The
 CC fusion constructs are useful to treat FGF-, angiogenesis-, or
 CC FGF-R-mediated disorders, such as tumorigenesis (e.g. bladder, breast,
 CC lung, rectal, testis and cervical tumours), neovascularization (e.g.
 CC diabetic retinopathy, neovascular glaucoma, wound healing and corneal
 CC scarring) and hyper-proliferation of vascular smooth muscle cells (e.g.
 CC postangioplasty and postatherectomy restenosis).
 XX
 SQ Sequence 497 AA;

Query Match 95.7%; Score 562; DB 21; Length 497;
 Best Local Similarity 95.5%; Pred. No. 6.1e-50;
 Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db II : |||||
 281 apeleggpsvflfpkpkdtlmisrtpevtcvvvdshedpevkfnwydgvvevhnatk 340
 QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
 Db |||||
 341 preeqynstyrvvsvltvlhqdwlngkeykckvsnkalpasiektiskak 390

RESULT 6
 AAY97173
 ID AAY97173 standard; Protein; 525 AA.
 XX
 AC AAY97173;
 XX

DT 04-DEC-2000 (first entry)

DE Human FGF-RI Extracellular domain-Ig Fc fusion protein 4.

XX FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1;

XX immunoglobulin; G1; oligomerization domain; Fc region; fusion protein;

KW inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary;

KW ophthalmological; anti-proliferative.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..21

FT /label= FGF-RI_signal_peptide

FT Domain 22..285

FT /label= FGF-RI_extracellular_domain

FT /note= "Ig I segment is deleted"

FT Domain 37..44

FT /label= Acid_box_segment

FT Domain 87..139

FT /label= Ig_II_segment

FT Misc-difference 313

FT /label= L313E

FT /note= "The mutation decreases the affinity of the Fc

FT portion for Fc receptors"

FT Misc-difference 409

FT /label= P409S

FT /note= "The mutation decreases the affinity of the Fc

FT portion for complement"

FT Domain 445..250

FT /label= Ig_III_segment

FT Peptide 286..293

FT /label= Linker

FT Region 294..525

FT /label= Human_IgG1_Fc_region

FT /note= "Contains hinge region and domains CH2 and CH3"

XX WO200046380-A2.

XX 10-AUG-2000.

XX 07-FEB-2000; 2000WO-US03166.

XX 08-FEB-1999; 99US-0119002.

XX (CHIR) CHIRON CORP.

XX Kavanaugh WM, Ballinger M;

XX WPI; 2000-514961/46.

XX N-PSDB; AAA52130.

XX New polypeptide comprising a fibroblast growth factor receptor

XX extracellular domain fused to a heterologous oligomerization domain for

XX treating FGF-, angiogenesis-, or FGF receptor-mediated disorders

XX Claim 14; Page 61-62; 70pp; English.

XX Novel fusion protein constructs comprise a fibroblast growth factor (FGF)

XX receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin

XX (Ig) I segment fused to a heterologous oligomerization domain that

XX comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4

XX region, or light chain of an immunoglobulin molecule, or a peptide with a

XX leucine zipper motif. The Ig I segment is not necessary for binding of

XX acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the

XX affinity for aFGF and heparin, protects the core of the molecule from

XX proteolysis, and abrogates the heparin requirement for aFGF binding. The

XX new fusion polypeptides are better FGF inhibitors than FGF-R monomer

XX proteins. The FGF-R-Ig Fc fusion dimers are active as FGF antagonists at

XX subnanomolar concentrations and were 20-fold more potent than the FGF-R

XX monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The

XX fusion constructs are useful to treat FGF-, angiogenesis-, or

XX FGF-R-mediated disorders, such as tumorigenesis (e.g. bladder, breast,

CC lung, rectal, testis and cervical tumours), neovascularization (e.g.

CC diabetic retinopathy, neovascular glaucoma, wound healing and corneal

CC scarring) and hyper-proliferation of vascular smooth muscle cells (e.g.

CC postangioplasty and postatherectomy restenosis).

XX Sequence 525 AA;

SQ

Query Match 95.7%; Score 562; DB 21; Length 525;

Best Local Similarity 95.5%; Pred. No. 6.5e-50;

Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNATK 60

Db 309 apeleggpsvflppkpkdtlmsrtpevtcvvvdvshedpevkfnkyvdgvevhnatk 368

QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAK 110

Db 369 preeqynstyrvvsvltvlhqdwlngkeyckvsnkalpasiektiskak 418

RESULT 7

AAW85692

ID AAW85692 standard; Protein; 711 AA.

XX AC AAW85692;

XX 12-AUG-1999 (first entry)

XX MoTabII fusion protein.

XX Antibody; humanised; variable region; heavy chain; light chain;

KW interferon gamma; IFN; treatment; prevention; septic shock; cachexia;

KW immune disease; multiple sclerosis; Crohn's disease; skin

KW disorders; inflammation; neoplasia; dermatitis; monoclonal

KW antibody; diadbody; scfv; multivalent; ruminant.

XX Synthetic.

OS

XX Key Location/Qualifiers

FT Peptide 1..20

FT /label= Mouse_D9D10_light_chain_signal_peptide

FT Domain 21..137

FT /note= "Humanised heavy chain variable domain of

FT D9D10"

FT Domain 138..467

FT /note= "Human IgG1 heavy chain constant domain"

FT Misc-difference 468

FT /note= "Leu added by cloning strategy"

FT Region 469..472

FT /label= Gly(3)Ser_linker

FT Domain 473..711

FT /label= Humanised_D9D10_ScFv

XX WO9909055-A2.

XX 25-FEB-1999.

XX 14-AUG-1998; 98WO-EP05165.

XX 18-JUN-1998; 98EP-0870139.

XX 18-AUG-1997; 97EP-0870122.

XX (INNO-) INNOGENETICS NV.

XX Buyse M, Sablon E;

XX WPI; 1999-180969/15.

XX N-PSDB; AAW85692.

XX New engineered antibodies which bind and neutralise interferon-gamma

XX PT - useful for prevention and treatment of septic shock, cachexia,

XX immune diseases and skin disorders

```

XX PS Disclosure; Fig 20; 134pp; English.
XX CC
XX CC New antibodies which bind and neutralise interferon-gamma (IFN
XX CC gamma) can be used as a medicant, for preventing or treating
XX CC septic shock, cachexia, immune diseases including multiple sclerosis
XX CC and Crohn's disease and skin disorders including bullous,
XX CC inflammatory and neoplastic dermatoses. The antibody is selected
XX CC from a single chain antibody (scFv), a chimeric antibody or diabody
XX CC comprising the humanised variable domain of the monoclonal mouse
XX CC anti-IFN gamma antibody D9D10; a multivalent antibody; or a ruminant
XX CC gamma levels in a sample.
XX CC
XX SQ Sequence 711 AA;

Query Match 95.7%; Score 562; DB 20; Length 711;
Best Local Similarity 95.5%; Pred. No. 9.4e-50;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 251 apelliggspsvflfppkpkdtlmisrtpevtcvvvdshedpevkfnwvydgvvghnaktk 310
QY 61 PREEQYNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 311 preeqynstyrvvsvltvhlqdwlngkeykckvsnkalpasiectiskak 360

RESULT 8
RAY05688
ID AAY05688 standard; Protein; 251 AA.
AC AAY05688;
XX
XX 19-JUL-1999 (first entry)
XX DE Modified human IgG Fc sequence.
XX DE
XX KW ZTNFR-6; tumour necrosis factor receptor-6; human; IgG1; Fc region;
XX KW cell maturation; bone cell regulation; mutant.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 38
XX FT /note= "Leu in native sequence"
XX FT Misc-difference 39
XX FT /note= "Leu in native sequence"
XX FT Misc-difference 41
XX FT /note= "Gly in native sequence"
XX FT Misc-difference 134
XX FT /note= "Ala in native sequence"
XX FT Misc-difference 135
XX FT /note= "Pro in native sequence"
XX PN WO9911790-A1.
XX
XX PD 11-MAR-1999.
XX
XX PF 03-SEP-1998; 98WO-US18364.
XX
XX PR 04-SEP-1997; 97US-0923725.
XX PR 04-SEP-1997; 97US-0057608.
XX
XX PA (ZYMO ) ZYMOGENETICS INC.
XX
XX PI Farrah TM, Gross JA, Matthews SM;
XX
XX WPI; 1999-205190/17.
XX DR N-PSDB; AAX25272.

```

```

XX PT New secreted or membrane bound tumor necrosis factor receptor
XX PS ZTNFR-6 - useful for detecting a genetic abnormality in a patient
XX CC
XX CC Example 4; Page 138-139; 145pp; English.
XX CC
XX CC The present sequence represents a modified human IgG1 Fc region in
XX CC which the FcγRI binding site has been mutated from Leu-Leu-Gly-Gly
XX CC to Ala-Glu-Glu-Ala in order to reduce FcγRI binding, and residues
XX CC Ala-134 and Pro-135 have been altered to Ser-134 and Ser-135 to
XX CC reduce complement C1q binding and/or complement fixation. The
XX CC mutations were introduced into the native Fc DNA sequence by
XX CC PCR-mediated mutagenesis (see also AAX25272). The construct was
XX CC utilised in the preparation of ZTNFR-6-Ig fusion vectors. Soluble
XX CC ZTNFR-6 (see AAY05679) was expressed in BHK 570 mammalian cells and
XX CC also in baculovirus-infected Spodoptera frugiperda Sf9 insect
XX CC cells. ZTNFR-6 is a novel human tumour necrosis factor receptor.
XX CC ZTNFR-6 polypeptides are useful for promoting cellular maturation
XX CC and bone cell regulation.
XX SQ Sequence 251 AA;

Query Match 95.1%; Score 558; DB 20; Length 251;
Best Local Similarity 95.5%; Pred. No. 6.9e-50;
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 35 apeaegapsvflfppkpkdtlmisrtpevtcvvvdshedpevkfnwvydgvvghnaktk 94
QY 61 PREEQYNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
DB 95 preeqynstyrvvsvltvhlqdwlngkeykckvsnkalpssiectiskak 144

RESULT 9
AAW97756
ID AAW97756 standard; Protein; 251 AA.
XX
XX AC AAW97756;
XX
XX DT 21-MAY-1999 (first entry)
XX
XX DE Modified human IgG1 Fc region.
XX
XX KW ZTNFR-5; tumour necrosis factor receptor; TNFR; human;
XX KW cell maturation; bone cell regulation; IgG1; immunoglobulin;
XX KW fusion protein; mutant.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PN WO9904001-A1.
XX
XX PD 28-JAN-1999.
XX
XX PF 21-JUL-1998; 98WO-US15072.
XX
XX PR 21-JUL-1997; 97US-0053203.
XX
XX PA (ZYMO ) ZYMOGENETICS INC.
XX
XX PI Farrah TM;
XX
XX WPI; 1999-132245/11.
XX DR N-PSDB; AAX07232.
XX
XX PT Novel tumour necrosis factor receptor ZTNFR5 - useful for
XX PT regulating maturation of TNF-ligand bearing cells
XX PS Example 3; Page 90-92; 109pp; English.
XX

```


PT treating inflammatory diseases such as psoriasis -

PS Claim 8; Page 110-112; 119pp; English.

XX The invention relates to an interleukin 20 (IL-20) soluble receptor

XX comprising two polypeptide subunits IL-20RA (formerly known as Zcytor7)

CC and IL-20RB (formerly known as DIRS1). The two subunits are preferably

CC linked together. In one embodiment, one subunit is fused to the constant

CC region of the light chain of an immunoglobulin, and the other subunit is

CC fused to constant region of the heavy chain of an immunoglobulin. The

CC light chain and the heavy chain are connected via a disulphide bond.

CC The soluble receptor can be used to down-regulate IL-20 and thus treat

CC inflammatory diseases such as psoriasis, inflammatory lung injury such

CC as asthma or bronchitis, adult respiratory disease (ARD), septic shock,

CC multiple organ failure, bacterial pneumonia, eczema, atopic and contact

CC dermatitis, and inflammatory bowel disease such as ulcerative colitis and

CC Crohn's disease. The present sequence represents the extracellular domain

CC fragment of a fusion protein containing the extracellular domain of

CC IL-20RA fused to a mutated human immunoglobulin gamma 1 constant region.

XX

SQ Sequence 559 AA;

Query Match 95.1%; Score 558; DB 22; Length 559;

Best Local Similarity 95.5%; Pred. No. 1.8e-49;

Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGGVSFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 60

DB 343 apegagpsvflfpkpkdmlsrtpetvcvvdvshedpevkfnwvdgvevhnatk 402

QY 61 PREQYNSTYRVVSVLTVLDHQLNGKEYCKVSNKGLPSSIEKTSKAK 110

DB 403 preeqynstyrsvsvltvlhqdwlngkeyckvsnkalpssiektiskak 452

RESULT 12

AAU04062

ID AAU04062 standard; Protein; 594 AA.

XX AAU04062;

XX 23-OCT-2001 (first entry)

XX Human IL-20RA/immunoglobulin kappa heavy chain fusion protein.

XX Human; interleukin-20 receptor A; IL-20RA; antagonist; psoriasis; eczema;

KW dermatitis; adult respiratory disease; asthma; bronchitis; pneumonia;

KW multiple organ failure; inflammatory lung injury; septic shock;

KW bacterial pneumonia; inflammatory bowel disease; rheumatoid arthritis;

KW ulcerative colitis; Crohn's disease; immunoglobulin kappa heavy chain;

KW tissue plasminogen activator; tpa.

XX Synthetic.

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FX Peptide 1..35

FT /label= Signal_peptide

FT Protein 36..594

FT Domain /label= Mature_fusion_protein

FT /label= Extracellular_domain

FT Peptide 250..264

FT /label= Linker_peptide

FT Protein 265..594

FT /label= Immunoglobulin_heavy_chain

XX WO200146261-A1.

XX 28-JUN-2001.

XX 22-DEC-2000; 2000WO-US35305.

XX 23-DEC-1999; 99US-0470898.

PR 22-JUN-2000; 2000US-0213341.

XX (ZYMO) ZYMOGENETICS INC.

PA Thompson P, Foster DC, Wenfeng X, Madden KL, Kelly JD;

PI Sprecher CA, Blumberg H, Eagan MA, Jaspers SR, Chandrasekher JA;

PI Novak JB;

XX WPI; 2001-418045/44.

DR N-PSDB; AAS07649.

XX Treating interleukin-20 induced inflammation in a mammal, such as adult

PT respiratory disease, eczema, psoriasis, contact dermatitis, multiple

PT organ failure and septic shock, involves administering IL-20 antagonist

XX

PS Example 5; Page 75-76; 117pp; English.

XX The sequence represents the Human interleukin-20 receptor A, IL-20RA/

CC immunoglobulin kappa heavy chain fusion protein, consisting of a

CC signal peptide from tissue plasminogen activator, tpa, amino

CC acids 30-243 of IL-20RA (extracellular domain) and human immunoglobulin

CC kappa heavy chain. The invention relates to treating a mammal afflicted

CC with a disease in which an interleukin-20 (IL-20) polypeptide plays a

CC role, involves administering antagonist of IL-20 polypeptide to the

CC individual. The method is useful for treating psoriasis, eczema, atopic

CC dermatitis, contact dermatitis, adult respiratory disease, asthma,

CC bronchitis and pneumonia and is also useful for treating multiple organ

CC failure, inflammatory lung injury, septic shock, bacterial pneumonia,

CC inflammatory bowel disease, rheumatoid arthritis, ulcerative colitis

CC and Crohn's disease.

XX

SQ Sequence 594 AA;

Query Match 95.1%; Score 558; DB 22; Length 594;

Best Local Similarity 95.5%; Pred. No. 2e-49;

Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 APPVAGGVSFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 60

DB 378 apegagpsvflfpkpkdmlsrtpetvcvvdvshedpevkfnwvdgvevhnatk 437

QY 61 PREQYNSTYRVVSVLTVLDHQLNGKEYCKVSNKGLPSSIEKTSKAK 110

DB 438 preeqynstyrsvsvltvlhqdwlngkeyckvsnkalpssiektiskak 487

RESULT 13

AA85274

ID AAB85274 standard; Protein; 594 AA.

XX AAB85274;

XX 07-SEP-2001 (first entry)

XX Human IL-20RA-Ig gamma 1 constant region fusion protein.

DE Interleukin 20; IL-20; IL-20RA; Zcytor7; IL-20RB; DIRS1; immunoglobulin;

XX antiinflammatory; antipsoriatic; antiasthmatic; antibacterial; human;

KW dermatological; antiulcer; antagonist.

XX Homo sapiens.

XX WO200146232-A2.

XX 28-JUN-2001.

XX 22-DEC-2000; 2000WO-US35307.

XX 23-DEC-1999; 99US-0471774.

PR 22-JUN-2000; 2000US-0213416.
XX (ZYMO) ZYMOGENETICS INC.
XX Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA, Brandt CS;
PI Rixon MW, Presnell SR, Fox BA;
XX WPI; 2001-398320/42.
DR N-PSDB; AAH22821.
XX
PT Isolated interleukin 20 soluble receptor comprising two polypeptide
PT subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus
PT treating inflammatory diseases such as psoriasis -
XX Claim 8; Page 81-82; 119pp; English.
XX The invention relates to an interleukin 20 (IL-20) soluble receptor
CC comprising two polypeptide subunits IL-20RA (formerly known as ZcytoR7)
CC and IL-20RB (formerly known as DIRS1). The two subunits are preferably
CC linked together. In one embodiment, one subunit is fused to the constant
CC region of the light chain of an immunoglobulin, and the other subunit is
CC fused to constant region of the heavy chain of an immunoglobulin. The
CC light chain and the heavy chain are connected via a disulphide bond.
CC The soluble receptor can be used to down-regulate IL-20 and thus treat
CC inflammatory diseases such as psoriasis, inflammatory lung injury such
CC as asthma or bronchitis, adult respiratory disease (ARD), septic shock,
CC multiple organ failure, bacterial pneumonia, eczema, atopic and contact
CC dermatitis, and inflammatory bowel disease such as ulcerative colitis and
CC Crohn's disease. The present sequence represents DNA sequence of a
CC construct containing the extracellular domain of IL-20RA fused to a
CC mutated human immunoglobulin gamma 1 constant region.
XX
XX Sequence 594 AA;
XX
Query Match 95.1%; Score 558; DB 22; Length 594;
Best Local Similarity 95.5%; Pred. No. 2e-49;
Matches 105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 APPVAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 378 apegagpsvflfpkpkdtlmisrtpevtcvvvdvshedpevkfnwydvgevhnaakt 437
QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 438 preeqnstyrvvsvltvlhqdwlngkeykckvsnkalpssiektiskak 487
RESULT 14
AAR27680
ID AAR27680 standard; Protein; 110 AA.
AC AAR27680;
XX
XX 10-MAR-1993 (first entry)
XX Human immunoglobulin IgG1 CH2 region.
XX Isoallotype; IgG1 G1m(1,2,17); anti-allotype response;
KW humanised Ab.
XX Homo sapiens.
XX WO9216562-A.
XX 01-OCT-1992.
XX 12-MAR-1992; 92WO-GB00445.
XX 12-MAR-1991; 91GB-0005245.
XX (LYNX-) LYNNVALE LTD.
XX

PI Clark MR;
XX WPI; 1992-349162/42.
XX Humanised antibodies having modified allotypic determinant -
PT useful for matching allotypes in therapy with decreased
PT likelihood of causing undesirable immune responses
XX Disclosure; Fig 4c; 57pp; English.
XX In humans, IgG1 may exist as either of two allotypes at site 1, 2
CC or 17. The inventor's propose eliminating these allotypes by
CC amino acid changes to agree with the sequences of IgG2, IgG3 and
CC IgG4. None of the allotype sites (1, 2 and 17) are located within
CC the CH2 domain. New "isoallotypes" should be suitable for therapeutic
CC use in all patients. See AAR27678-R27681.
XX
XX Sequence 110 AA;
XX
Query Match 94.9%; Score 557; DB 13; Length 110;
Best Local Similarity 94.5%; Pred. No. 3.2e-50;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 APPVAGPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 1 apeilggpsvflfpkpkdtlmisrtpevtcvvvdvshedpevkfnwydvgevhnaakt 60
QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAK 110
Db 61 preeqnstyrvvsvltvlhqdwlngkeykckvsnkalpssiektiskak 110
RESULT 15
AAR41684
ID AAR41684 standard; Protein; 110 AA.
XX
XX AAR41684;
XX
XX 20-OCT-1993 (first entry)
XX Undefined ORF2 encoded by pAH4602.
XX Polymerase chain reaction; primer: PCR; amplify; murine; heavy;
KW light; chain; variable; constant; region; anti-human; transferrin;
KW receptor; antibody; brain; capillary; endothelial cell; conjugate;
KW neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke;
KW epilepsy; Parkinsons disease; Alzheimers disease.
XX
XX Synthetic.
XX WO9310819-A.
XX 10-JUN-1993.
XX 24-NOV-1992; 92WO-US10206.
XX 26-NOV-1991; 91US-0800458.
XX (ALKE-) ALKERMES INC.
XX Friden PM;
XX WPI; 1993-196742/24.
DR N-PSDB; AAQ43844.
XX
XX Antibody conjugates specific for transferrin receptor - used
PT for diagnosis and treatment of cancer, AIDS and neurological
PT disorders
XX Disclosure; Fig 11K; 151pp; English.
XX The sequences given in AAR41682-85 are encoded by the expression vector,
XX

CC PAH4602. This vector contains open reading frames encoding the heavy
CC chain variable region (VH) of the antibody 128.1, an ampicillin
CC resistance gene and a histidine (histidinol) selection marker.
CC Transcription of the VH gene is from the VH promoter of the murine
CC 27.44 gene. The vector also includes a heavy chain immunoglobulin
CC enhancer and the human gamma constant region (CH). The VH region of
CC PAH4274. This was achieved by polymerase chain reaction and cloned into plasmid
CC with EcoRV and NheI. The VH gene was inserted in-frame with the human
CC gamma CH region CH at the 3' end of the VH-J region by means of a NheI
CC site. 128.1 is an anti-human transferrin receptor antibody which binds
CC to the transferrin receptor on brain capillary endothelial cells. This
CC antibody may be used in a conjugate in which it is linked to a neuro-
CC pharmaceutical or diagnostic agent. The conjugate may be used to treat
CC or prevent neurological disorders eg. brain tumours, AIDS, stroke,
CC epilepsy, Parkinsons and Alzheimers disease. It may also be used for
CC diagnostic methods.
XX
SQ Sequence 110 AA;

Query Match 94.9%; Score 557; DB 14; Length 110;
Best Local Similarity 94.5%; Pred. No. 3.2e-50;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APPVAGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db ||:|||||
1 apelligpsvflfppkpkdtlmisrtpevtcvtvvdvshedpevkfnwvydgvvhnaktk 60
|||||

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAK 110
Db |||||||
61 preeqynstyrvvsvlvtlqhqlngkeykckvsnkalpapietkiskak 110
|||||

Search completed: June 21, 2002, 08:36:06
Job time: 320 sec

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	586	100.0	330	1	GC1_HUMAN	P01857 homo sapien
2	551	94.0	327	1	GC4_HUMAN	P01861 homo sapien
3	548	93.5	290	1	GC3_HUMAN	P01860 homo sapien
4	534	91.1	326	1	GC2_HUMAN	P01859 homo sapien
5	454	77.5	333	1	GCB_RAT	P20761 rattus norv
6	450	76.8	323	1	GC_RABIT	P01870 coryctolagus
7	447	76.3	329	1	GC2_CAVPO	P01862 cavia porcea
8	434	74.1	329	1	GC3_MOUSE	P22436 mus musculu
9	434	74.1	398	1	GC3_MOUSE	P03987 mus musculu
10	414	70.6	335	1	GCAB_MOUSE	P01864 mus musculu
11	411.5	70.2	324	1	GC1_MOUSE	P01868 mus musculu
12	411.5	70.2	393	1	GC1M_MOUSE	P01869 mus musculu
13	411	70.1	330	1	GCRA_MOUSE	P01863 mus musculu
14	411	70.1	399	1	GCAM_MOUSE	P01865 mus musculu
15	404	68.9	329	1	GCC_RAT	P20762 rattus norv
16	404	68.9	336	1	GCB_MOUSE	P01866 mus musculu
17	404	68.9	405	1	GCBM_MOUSE	P01867 mus musculu
18	389	66.4	326	1	GC1_RAT	P20759 rattus norv
19	354	60.4	322	1	GCA_RAT	P20760 rattus norv
20	164.5	28.1	428	1	EPC_HUMAN	P01854 homo sapien
21	160	27.3	429	1	EPC_RAT	P01855 rattus norv
22	153	26.1	457	1	MUC_SUNMU	P20768 suncus murin
23	144	24.6	421	1	EPC_MOUSE	P06336 mus musculu
24	142	24.2	454	1	MUC_HUMAN	P01871 homo sapien
25	140	23.9	391	1	MUCB_HUMAN	P04220 homo sapien
26	133	22.7	454	1	MUC_MESAU	P06337 mesocricetu
27	133	22.7	455	1	MUC_MOUSE	P01872 mus musculu
28	133	22.7	476	1	MUCM_MOUSE	P01873 mus musculu
29	131	22.4	106	1	KAC_HUMAN	P01834 homo sapien
30	129.5	22.1	299	1	ALC_RABIT	P01879 coryctolagus
31	123.5	21.1	340	1	ALC2_HUMAN	P01877 homo sapien
32	123.5	21.1	353	1	ALC1_GORGO	P20758 gorilla gor
33	123.5	21.1	353	1	ALC1_HUMAN	P01876 homo sapien

RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196(1970).
 RN [7]
 RP DISULFIDE BONDS
 RX MEDLINE-77070267; PubMed-1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE-81208100; PubMed-7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -|- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -|- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35, 116, 198, 269 & 272.
 CC -|- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -|- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198, 267&272.
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 DR EMBL; J00228; AAC82527.1; ALT_INIT.
 DR PIR; A02146; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR MIM; 147100; -
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003600; Ig_Like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; Ig_Like; 1.
 DR SMART; SM00407; IGC1; 2.
 DR PROSITE; PS00290; Ig_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 FT 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT STRAND 123 126
 FT HELIX 130 134

FT TURN 136 137
 FT STRAND 141 148
 FT STRAND 158 162
 FT TURN 163 164
 FT STRAND 165 166
 FT STRAND 175 178
 FT STRAND 183 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 206
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT STRAND 238 240
 FT HELIX 241 242
 FT STRAND 245 256
 FT STRAND 260 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 324
 SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;
 Query Match 100.0%; Score 586; DB 1; Length 330;
 Best Local Similarity 100.0%; Pred. No. 5, 9e-52;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFKNYVDGVGVHNAKTK 60
 Db 114 APELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFKNYVDGVGVHNAKTK 173
 QY 61 PREEOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
 Db 174 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223
 RESULT 2
 ID GC4_HUMAN STANDARD; PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-4 chain C region.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83157104; PubMed=6299662;
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 1:11-18(1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE=70207560; PubMed=4192699;
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 RT constant region of a gamma 4 chain.";
 RL Biochem. J. 117:33-47(1970).
 CC -----
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FT CARBOHYD 140 140 N-LINKED (GLCNAC...),
FT MOD_RES 290 290 REMOVED POST-TRANSLATIONALLY.
FT VARIANT 126 127 QV -> EB (IN ZUC).
FT 128 128 /FTIG=VAR_003890.
FT VARIANT 134 134 P -> L (IN OMM).
FT 135 135 /FTIG=VAR_003891.
FT VARIANT 139 139 F -> Y (IN OMM).
FT 140 140 /FTIG=VAR_003892.
FT VARIANT 182 182 T -> A (IN OMM).
FT 183 183 /FTIG=VAR_003893.
FT VARIANT 227 227 S -> N (IN OMM).
FT 228 228 /FTIG=VAR_003894.
FT VARIANT 227 227 MISSING (IN ZUC).
FT 229 229 /FTIG=VAR_003895.
FT VARIANT 279 279 F -> Y (IN OMM).
FT 280 280 /FTIG=VAR_003896.
SQ SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;

Query Match 93.5%; Score 548; DB 1; Length 290;
Best Local Similarity 91.8%; Pred. No. 3.5e-48;
Matches 101; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPPKDGLMSRTPETVTCVVVDSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 74 APELLGGPSVFLPPPKDGLMSRTPETVTCVVVDSHEDPEVKFNWYVDGVEVHNAKTK 133
QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
DB 134 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 183

RESULT 4
GC2_HUMAN STANDARD; PRT; 326 AA.
ID GC2_HUMAN
AC P01859;
DC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
RT heavy chain constant region genes."
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
RT evolution of a gene family."
RL Cell 29:671-679(1982).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT genes."
RL EMBO J. 1:403-407(1982).
RN [4]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
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RT "The primary structure of a human IgG2 heavy chain: genetic,
RT evolutionary, and functional implications."
RL J. Immunol. 125:1048-1054(1980).
RN [5]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
RT domains of a human IgG2 myeloma protein."
RL Can. J. Biochem. 57:758-767(1979).
RN [6]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
RT immunoglobulin gamma chains."
RL Mol. Immunol. 16:923-925(1979).
RN [7]
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RL Submitted (MAR-1980) to the PIR data bank.
RN [8]
RP SEQUENCE OF 1-121 (DOT).
RX MEDLINE=92525298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
RT immunoglobulins."
RL Eur. J. Biochem. 228:886-893(1995).
RN [9]
RP DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2."
RL Biochem. J. 121:217-225(1971).
RN [10]
RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G."
RL Nature 221:145-148(1969).
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DR EMBL; J00230; AAB59393.1; -.
DR PIR; A02148; G2HU.
DR HSP; P01857; 1FC1.
DR MIM; 147110; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
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FT DISULFID 246 304 AT OR NEAR THE COMPLEMENT-BINDING SITE.
FT SITE 156 156 REMOVED POST-TRANSLATIONALLY (PROBABLY).
FT MOD_RES 326 326 S -> A (IN MYELOMA PROTEINS TIL & ZIE).
FT VARIANT 60 60 /FTIG=VAR_003889.
FT CONFLICT 109 109 C -> S (IN REF. 3).
SQ SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;

Query Match 91.1%; Score 534; DB 1; Length 326;
Best Local Similarity 92.5%; Pred. No. 1e-46;
Matches 98; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 5 LGGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 64
Db 114 VAGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 173
QY 65 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
Db 174 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAK 219

RESULT 5
GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Bruggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG-like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 77.5%; Score 454; DB 1; Length 333;
Best Local Similarity 73.4%; Pred. No. 1.2e-38;
Matches 80; Conservative 19; Mismatches 10; Indels 0; Gaps 0;

QY 2 PELLGGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
Db 118 PELLGGPSVFIFFPKPKDILLISQNAKVCVVVDVSEEPDVFQFSFVNVEVHTAQTP 177
QY 62 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
Db 178 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKPK 226

RESULT 6

GC_RABIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-1 haplotype.";
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G.";
RL Biochem. J. 116:249-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (In) Kiland J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell, Stockholm (1967).
CC -!- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER, 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15 MARKERS AND REF.5 THE E15 MARKER.
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CC -----
CC EMBL; M16426; AAA31289.1; -.
DR PIR; A02161; GHRB.
DR HSSP; P01857; IFCL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).

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FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 76.8%; Score 450; DB 1; Length 323;
Best Local Similarity 75.2%; Pred. No. 3e-38;
Matches 82; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 2 PELLGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKP 61
Db 108 PELLGSPVFIFFPKPKDTLMISRTPEVTCVVVDVSDQDPEVQFTWYINNEQVTRAPPL 167

QY 62 REQYNSTVRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 110
Db 168 REQQFNSTIRVSTLPIHQDWLNGRGEKCKVHNKALPAPIEKTISKAR 216

RESULT 7
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RX MEDLINE=71058471; PubMed=5538606;
RA Birstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
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antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP MEDLINE=71058474; PubMed=4922544;
RX Oliveira B., Lamm M.E.;
RA "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RT Biochemistry 10:26-31(1971).
CC -!- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IgC1; 2.
DR PROSITE; PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 16 16 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 28 79 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202 N-LINKED (GLCNAC. .).
FT CARBOHYD 178 178
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 76.3%; Score 447; DB 1; Length 329;
Best Local Similarity 76.1%; Pred. No. 6.2e-38;
Matches 83; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 2 PELLGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKP 61
Db 113 PELLGSPVFIFFPKPKDTLMISRTPEVTCVVVDVSDQDPEVQFTWYINNEQVTRAPPL 172

QY 62 REQYNSTVRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 110
Db 173 RVEQYNTTFRVESVLPIHQDWLNGRGEKCKVHNKALPAPIEKTISKTK 221

RESULT 8
GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
CC -----
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CC
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DR EMBL: J00451; -- NOT_ANNOTATED_CDS.
DR PIR: B02156; G3MSC.
DR HSSP: P01857; IFCL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam: PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 74.1%; Score 434; DB 1; Length 329;
Best Local Similarity 72.9%; Pred. No. 1.3e-36;
Matches 78; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 4 LLGGSVLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 63
DB 116 ILGGSVFIFPPKDALMISLTPTKVCVVVDVSEDDPDVHVSWFVDNKEVHTAQTQPRE 175

QY 64 EYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETISKAK 110
DB 176 AQYNSTFRVVSALPIQHQDMRGKEFKCKVNNKALPAPIETISKPK 222

RESULT 9
GC3M_MOUSE
ID GC3M_MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=8401483; PubMed=6314258;
RA Konaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00451; AAB59655.1; -
DR EMBL: P01526; CAA24767.1; ALT_SEQ.
DR PIR: A02155; G3MSM.
DR HSSP: P01857; IFCL.
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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam: PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 74.1%; Score 434; DB 1; Length 398;
Best Local Similarity 72.9%; Pred. No. 1.6e-36;
Matches 78; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 4 LLGGSVLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 63
DB 116 ILGGSVFIFPPKDALMISLTPTKVCVVVDVSEDDPDVHVSWFVDNKEVHTAQTQPRE 175

QY 64 EYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETISKAK 110
DB 176 AQYNSTFRVVSALPIQHQDMRGKEFKCKVNNKALPAPIETISKPK 222

RESULT 10
GCAB_MOUSE
ID GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT IgG2aa and IgG2ab alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain Fc regions of IgA and IgG1 allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -1- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
CC -----
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DR EMBL; J00479; -, NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IG_C1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 70.6%; Score 414; DB 1; Length 335;
Best Local Similarity 67.3%; Pred. No. 1.4e-34;
Matches 74; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
DB 119 APDLGGPSVFIFPPKIKDLVMSLSPMVTCVVVDVSEDDPDVQISWFEVNVVHTAQTK 178
QY 61 PREQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIETKTSKAK 110
DB 179 THREDYNSTLRVYSLPQHODWMSGKEFKCKVNNRALPSPIETKTSKPR 228

RESULT 11
GC1_MOUSE STANDARD; PRT; 324 AA.
ID GC1_MOUSE 98 110
AC P01868; 111 217
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RT Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
RT cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salser W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
RT heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=78242288; PubMed=98524;
RA Adeugbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
RT murine myeloma gamma chain.";
RL J. Biol. Chem. 253:6068-6075(1978).
RN [5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;

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RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
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CC -----
DR EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR EMBL; V00793; CAA24175.1; -
DR EMBL; V00793; CAA24176.1; -
DR PIR; A02159; GLMS.
DR HSSP; P01842; 7FAB.
DR GLYCSUITEDB; P01868; -.
DR MGI; 96446; Igh-4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IG_C1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97
FT DOMAIN 98 110
FT DOMAIN 111 217
FT DOMAIN 218 324
FT DISULFID 27 82
FT DISULFID 102 102
FT DISULFID 104 104
FT DISULFID 107 107
FT DISULFID 109 109
FT DISULFID 138 198
FT CARBOHYD 174 174
FT DISULFID 244 302
FT MOD_RES 324 324
FT CONFLICT 276 276
FT CONFLICT 278 278
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;

Query Match 70.2%; Score 411.5; DB 1; Length 324;
Best Local Similarity 67.9%; Pred. No. 2.3e-34;
Matches 74; Conservative 19; Mismatches 13; Indels 3; Gaps 1;

QY 2 PELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
DB 112 PEV---SSVFIFPPKPKDKVLTITLTPKVCVVVDISKDDPEVQFVDFVDDVEVHTAQTP 168
QY 62 REEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIETKTSKAK 110
DB 169 REEQNSTFRSVSELPINHQDWLNGKEFKCRVNSAFAFPAPIETKTSKTK 217

RESULT 12
GC1M_MOUSE STANDARD; PRT; 393 AA.
ID GC1M_MOUSE 324 393
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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CC -----
DR EMBL; V00798; CAA24178.1; -
DR PIR; A02152; G2MSA.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 REMOVED POST-TRANSLATIONALLY.
FT SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 70.1%; Score 411; DB 1; Length 330;
Best Local Similarity 68.2%; Pred. No. 2.7e-34;
Matches 75; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 1 APPELLGSPVFLPPPKDKTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATK 60
DB 114 APNLLGGPSVFIFPPPKIKDVLMSLSPIVTCVVDVSEDDPDVQISFWNNVEVHTAQ 173

QY 61 PREEQYNSTYRVSVLTVLHQDLNKGKEYCKVSKNKPAPIETKTSKAK 110
DB 174 THREDYNSTLRVVSALPIQHQDMSGKEFKCKVNNKDLPAPIERTISKPK 223

RESULT 14
GCAM_MOUSE STANDARD; PRT; 399 AA.
AC P01865;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
SEGMENT OF MU CHAINS.
CC -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
THE A ALLELE.
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CC -----
DR EMBL; J00471; AAB59661.1; ALT_INIT.
DR PIR; A02154; G2MSAM.
DR HSSP; P01857; 1FC1.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
transmembrane; Alternative splicing.
FT NON_TER 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT TRANSMEM 346 363
FT DOMAIN 364 399
FT DOMAIN CYTOPLASMIC (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;

Query Match 70.1%; Score 411; DB 1; Length 399;
Best Local Similarity 68.2%; Pred. No. 3.3e-34;
Matches 75; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 1 APPELLGSPVFLPPPKDKTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATK 60
DB 114 APNLLGGPSVFIFPPPKIKDVLMSLSPIVTCVVDVSEDDPDVQISFWNNVEVHTAQ 173

QY 61 PREEQYNSTYRVSVLTVLHQDLNKGKEYCKVSKNKPAPIETKTSKAK 110
DB 174 THREDYNSTLRVVSALPIQHQDMSGKEFKCKVNNKDLPAPIERTISKPK 223

RESULT 15
GCC_RAT STANDARD; PRT; 329 AA.
ID GCC_RAT
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Bruggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
CC -----
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DR HSP: P01857; 1FC1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00410; Ig_like; 1.
DR SMART: SM00407; IGCL; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 68.9%; Score 404; DB 1; Length 329;
Best Local Similarity 67.9%; Pred. No. 1.4e-33;
Matches 72; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

QY 5 LGGSPVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 64
Db 117 LGRPSVFIFPPKPKDILMITLTPKVCVVVDVSEEDPDVQFSWFDVNRVYFTAQTQPHEE 176

QY 65 QYNSTRVRSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
Db 177 QLNGTRVRSVLTVLHQDWMSGKEFKCKVNNKDLPSPIEKTISKPR 222

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Search completed: June 21, 2002, 09:00:24
Job time: 1448 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 08:59:30 ; Search time 176.89 Seconds
(without alignments)
107.578 Million cell updates/sec

Title: US-09-674-857-4
Perfect score: 586
Sequence: 1 APELLGGPSVFLPPPKDPT.....CKVSNKALPAPIETISKAK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTREMBL_19.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_phage.*
- 11: sp_plant.*
- 12: sp_rodent.*
- 13: sp_virus.*
- 14: sp_vertebrate.*
- 15: sp_unclassified.*
- 16: sp_rvirus.*
- 17: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	586	100.0	701	4 Q96PQ8	Q96pq8 homo sapien
2	483	82.4	337	6 Q95M34	Q95m34 equus cabal
3	414	70.6	473	11 Q9D8L4	Q9d8l4 mus musculu
4	411.5	70.2	437	11 Q9R1A4	Q9r1a4 mus musculu
5	411.5	70.2	463	11 Q9RLC4	Q9rlc4 mus musculu
6	407	69.5	468	11 Q99L31	Q99l31 mus musculu
7	407	69.5	473	11 Q99L25	Q99l25 mus musculu
8	404	68.9	473	11 Q91Z05	Q91z05 mus musculu
9	142	24.2	375	4 Q9BS21	Q9bsz1 homo sapien
10	142	24.2	597	4 Q9BQ88	Q9bq88 homo sapien
11	142	24.2	597	4 Q9BU10	Q9bu10 homo sapien
12	142	24.2	597	4 Q9GBB9	Q9gbb9 homo sapien
13	142	24.2	613	4 Q96EY0	Q96ey0 homo sapien
14	142	24.2	614	4 Q96GA6	Q96ga6 homo sapien
15	142	24.2	618	4 Q96AA6	Q96aa6 homo sapien
16	130.5	22.3	684	13 Q90544	Q90544 ginglymosto

17	123.5	21.1	384	4 Q9UP60	Q9up60 homo sapien
18	123.5	21.1	416	4 Q9NPP6	Q9npp6 homo sapien
19	123.5	21.1	494	4 Q96K68	Q96k68 homo sapien
20	123.5	21.1	496	4 Q96KX8	Q96kx8 homo sapien
21	123.5	21.1	496	4 Q96DK0	Q96dk0 homo sapien
22	119.5	20.4	500	4 Q9BRV0	Q9brv0 homo sapien
23	113.5	19.4	486	11 Q91Z07	Q91z07 mus musculu
24	113.5	19.4	487	11 Q99KA4	Q99ka4 mus musculu
25	112.5	19.2	130	11 Q9D8W4	Q9d8w4 mus musculu
26	112.5	19.2	233	11 Q91V32	Q91v32 m adult mal
27	112.5	19.2	479	11 Q99M22	Q99m22 mus musculu
28	112.5	19.2	484	11 Q99LA6	Q99la6 mus musculu
29	112	19.1	211	11 Q91XL0	Q91xl0 mus musculu
30	111.5	19.0	479	11 Q91WP5	Q91wp5 mus musculu
31	111.5	19.0	481	11 Q91WT3	Q91wt3 mus musculu
32	111.5	19.0	481	11 Q91WT1	Q91wt1 mus musculu
33	111.5	19.0	482	11 Q91X92	Q91x92 mus musculu
34	111.5	19.0	488	11 Q91WR1	Q91wr1 mus musculu
35	110.5	18.9	426	11 Q9DCD9	Q9acd9 mus musculu
36	110.5	18.9	480	11 Q91XE1	Q91xe1 mus musculu
37	110	18.8	233	11 Q91WS9	Q91ws9 mus musculu
38	110	18.8	234	11 Q91WF8	Q91wf8 mus musculu
39	110	18.8	235	11 Q91W12	Q91w12 mus musculu
40	110	18.8	238	11 Q99M37	Q99m37 mus musculu
41	108	18.4	214	11 Q9R1A5	Q9r1a5 mus musculu
42	107.5	18.3	235	11 Q99M11	Q99m11 mus musculu
43	103.5	17.7	233	4 Q96I69	Q96i69 homo sapien
44	103.5	17.7	236	4 Q96E61	Q96e61 homo sapien
45	101	17.2	1215	5 Q9V787	Q9v787 drosophila

ALIGNMENTS

RESULT 1

Q96PQ8	PRELIMINARY;	PRT;	701 AA.
AC Q96PQ8:			
DT 01-DEC-2001 (Tremblrel. 19, Created)			
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=21477448; PubMed=11593034;			
RA Hu Z., Garen A.;			
RA "Targeting tissue factor on tumor vascular endothelial cells and tumor			
RT cells for immunotherapy in mouse models of prostatic cancer.";			
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).			
DR EMBL; AF272774; AAK58686.1; -.			
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;			

Query Match 100.0%; Score 586; DB 4; Length 701;
Best Local Similarity 100.0%; Pred. No. 1.8e-56;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1	APELLGGPSVFLPPPKDPTLMISRTPEVTCVVVYVSHEDPEVKFNWYDGVGVHNAKTK 60		
Db 485	APELLGGPSVFLPPPKDPTLMISRTPEVTCVVVYVSHEDPEVKFNWYDGVGVHNAKTK 544		

QY 61	PREEOYNSYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAK 110		
Db 545	PREEQINSTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAK 594		

RESULT 2

Q95M34	PRELIMINARY;	PRT;	337 AA.
ID Q95M34			

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AC Q95M34;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE IMMUNOGLOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
DE (FRAGMENT).
GN IGHCL1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Wagner B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199;105-119(1998).
DR EMBL; AJ300675; CAC44624.1; -.
FT NON_TER 1
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 82.4%; Score 483; DB 6; Length 337;
Best Local Similarity 78.2%; Pred. No. 1.9e-45;
Matches 86; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGEVHNKTK 60
DB 119 APELLGGPSVFLPPKPKDTLMITRTPEVTCVVVDVSHEDPEVKFNWYDGVGEVHNKTK 178
QY 61 PREEQNSTYRVSVLTVTHQDNLGNKQYCKVKSNKALPAPIETKISKAK 110
DB 179 PREEQNSTYRVSVSVLRHQDNLGKFKCKVNNQALPQPIERTITKTK 228

RESULT 3
Q9D8L4 ID Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE 1810060009RIK PROTEIN.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gamiya M., Lee N.H.,
RA Guskinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 70.6%; Score 414; DB 11; Length 473;
Best Local Similarity 67.3%; Pred. No. 1.3e-37;
Matches 74; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGEVHNKTK 60
DB 257 ADPLLGGPSVFLPPKPKDVLMSLSPWTCVVVDSEDDPDVQISWFWNNVEVHTAQTK 316
QY 61 PREEQNSTYRVSVLTVTHQDNLGNKQYCKVKSNKALPAPIETKISKAK 110
DB 317 THREDYNSTLRVVSALPQHQDWMGSKFKCKVNNRALPSPTEKTSKPR 366

RESULT 4
Q9R1A4 ID Q9R1A4 PRELIMINARY; PRT; 437 AA.
AC Q9R1A4
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG-like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 70.2%; Score 411.5; DB 11; Length 437;
Best Local Similarity 67.9%; Pred. No. 2.3e-37;
Matches 74; Conservative 19; Mismatches 13; Indels 3; Gaps 1;

QY 2 PELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGEVHNKTKP 61
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AC Q91205;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 51.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
KW EMBL; BC010327; AAH10327.1; -.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match      68.9%; Score 404; DB 11; Length 473;
Best Local Similarity 66.4%; Pred. No. 1.7e-36;
Matches 73; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 1 APELLGGSPVFLFPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTK 60
DB 257 APNLEGGSPVFLFPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTK 316
QY 61 PREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
DB 317 THREDYNSTIRVVSALPIQHQMWSCKEFCCKVNNKDLSPERTISKIK 366

RESULT 9
Q9BSZ1
ID Q9BSZ1 PRELIMINARY; PRT; 375 AA.
AC Q9BSZ1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 41.3 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
KW EMBL; BC004476; AAH04476.1; -.
SQ SEQUENCE 375 AA; 41314 MW; B1A0A0998F473619 CRC64;

Query Match      24.2%; Score 142; DB 4; Length 375;
Best Local Similarity 28.7%; Pred. No. 1.5e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 10 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQYNST 59
DB 146 VFAIPPS-FASIFLTKSKTLCLVTLDTLTYD-SVTISWTRQNGEAVKTHNTISESHPNAT 203
QY 70 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
DB 204 FSAVGEASICEDDWSNGERTCTVTHTDLPSPKQTISRPK 244

AC Q9BQB8 PRELIMINARY; PRT; 597 AA.
AC Q9BQB8;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
KW EMBL; BC001872; AAH01872.1; -.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match      24.2%; Score 142; DB 4; Length 597;
Best Local Similarity 28.7%; Pred. No. 2.7e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 10 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQYNST 69
DB 368 VFAIPPS-FASIFLTKSKTLCLVTLDTLTYD-SVTISWTRQNGEAVKTHNTISESHPNAT 425
QY 70 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
DB 426 FSAVGEASICEDDWSNGERTCTVTHTDLPSPKQTISRPK 466

RESULT 11
Q9BU10
ID Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 65.3 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
KW EMBL; BC002963; AAH02963.1; -.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match      24.2%; Score 142; DB 4; Length 597;
Best Local Similarity 28.7%; Pred. No. 2.7e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 10 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQYNST 69
DB 368 VFAIPPS-FASIFLTKSKTLCLVTLDTLTYD-SVTISWTRQNGEAVKTHNTISESHPNAT 425
QY 70 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
DB 426 FSAVGEASICEDDWSNGERTCTVTHTDLPSPKQTISRPK 466
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DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igc1; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA: 65274 MW: 2DAFA8FB7E055851 CRC64;

Query Match 24.2%; Score 142; DB 4; Length 597;
Best Local Similarity 28.7%; Pred. No. 2.7e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 10 VLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYNST 69
|| || : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 368 VFAIPPS-FASIFLTKSTKLTCLVLTLDITYD-SVTISWTRQNGEAVKTHNISESHPNAT 425

QY 70 YRVSVLTVLVHODWLNKGYCKVSKNKPAPIEKTISKAK 110
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 426 FSAVGEASICEDDWSNGERFTCTVTHTDLPSPKQTISRPK 466

RESULT 12
Q96BB9 ID Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE HYPOTHETICAL 65.0 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC015760; AAH15760.1; -.
KW Hypothetical protein.
SQ SEQUENCE 597 AA: 65039 MW: 4FCA3AD8E3E263D9 CRC64;

Query Match 24.2%; Score 142; DB 4; Length 597;
Best Local Similarity 28.7%; Pred. No. 2.7e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 10 VLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYNST 69
|| || : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 368 VFAIPPS-FASIFLTKSTKLTCLVLTLDITYD-SVTISWTRQNGEAVKTHNISESHPNAT 425

QY 70 YRVSVLTVLVHODWLNKGYCKVSKNKPAPIEKTISKAK 110
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 426 FSAVGEASICEDDWSNGERFTCTVTHTDLPSPKQTISRPK 466

RESULT 13
Q96EY0 ID Q96EY0 PRELIMINARY; PRT; 613 AA.
AC Q96EY0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:20337).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH, AND LYMPHOMA;
RA Strausberg R.;
SQ SEQUENCE 613 AA: 67273 MW: 31214203FB8421E7 CRC64;

Query Match 24.2%; Score 142; DB 4; Length 613;
Best Local Similarity 28.7%; Pred. No. 2.8e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 10 VLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYNST 69
|| || : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 363 VFAIPPS-FASIFLTKSTKLTCLVLTLDITYD-SVTISWTRQNGEAVKTHNISESHPNAT 420

QY 70 YRVSVLTVLVHODWLNKGYCKVSKNKPAPIEKTISKAK 110
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 421 FSAVGEASICEDDWSNGERFTCTVTHTDLPSPKQTISRPK 461

RESULT 14
Q96GA6 ID Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
SQ SEQUENCE 614 AA: 67921 MW: 55EF536E77AA9BBB CRC64;

Query Match 24.2%; Score 142; DB 4; Length 614;
Best Local Similarity 28.7%; Pred. No. 2.8e-07;
Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 10 VLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQYNST 69
|| || : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 VFAIPPS-FASIFLTKSTKLTCLVLTLDITYD-SVTISWTRQNGEAVKTHNISESHPNAT 421

QY 70 YRVSVLTVLVHODWLNKGYCKVSKNKPAPIEKTISKAK 110
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 422 FSAVGEASICEDDWSNGERFTCTVTHTDLPSPKQTISRPK 462

RESULT 15
Q96AA6 ID Q96AA6 PRELIMINARY; PRT; 618 AA.
AC Q96AA6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE HYPOTHETICAL 67.8 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH, AND LYMPHOMA;
RA Strausberg R.;
SQ SEQUENCE 618 AA: 67921 MW: 55EF536E77AA9BBB CRC64;
```

RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC017356; AAH17356.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;

Query Match 24.2%; Score 142; DB 4; Length 618;
 Best Local Similarity 28.7%; Pred. No. 2.8e-07;
 Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;
 QY 10 VFLEPPKPKDITLMSRPTVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69
 Db 368 VFAIPPS-FASIFLTKSTKLTCLVTDITYD-SVTISWTRQNGEAVKTHTNISESHPNAT 425
 QY 70 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAK 110
 Db 426 FSAVGEASICEDDWSGERFTCTVTHTDLPSPKQITSRPK 466

Search completed: June 21, 2002, 08:59:31
 Job time: 1630 sec

GenCore version 4.5
 Copyright (c) 1993 - 2000 CompuGen Ltd.
 OM protein - protein search, using sw model
 Run on: June 21, 2002, 08:36:06 ; Search time 224.82 Seconds
 (without alignments)
 54.346 Million cell updates/sec

Title: US-09-674-857-4
 Perfect score: 586
 Sequence: 1 APELGGPSVFLPPKPKDT.....CKVSNKALPAPIETISKAK 110

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_032802.*
 1: /SIDS1/gcgdata/hold-geneseq/geneqseq-emb1/AA1980.DAT.*
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 3: /SIDS1/gcgdata/hold-geneseq/geneqseq-emb1/AA1982.DAT.*
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 6: /SIDS1/gcgdata/hold-geneseq/geneqseq-emb1/AA1985.DAT.*
 7: /SIDS1/gcgdata/hold-geneseq/geneqseq-emb1/AA1986.DAT.*
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 12: /SIDS1/gcgdata/hold-geneseq/geneqseq-emb1/AA1991.DAT.*
 13: /SIDS1/gcgdata/hold-geneseq/geneqseq-emb1/AA1992.DAT.*
 14: /SIDS1/gcgdata/hold-geneseq/geneqseq-emb1/AA1993.DAT.*
 15: /SIDS1/gcgdata/hold-geneseq/geneqseq-emb1/AA1994.DAT.*
 16: /SIDS1/gcgdata/hold-geneseq/geneqseq-emb1/AA1995.DAT.*
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 22: /SIDS1/gcgdata/hold-geneseq/geneqseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	586	100.0	110	13	AA27680 Human immunoglobul
2	586	100.0	110	14	AA27680 Undefined ORF2 enc
3	586	100.0	116	20	AA42621 Human IgG1 Fc gamma
4	586	100.0	212	16	AA87023 Immunoglobulin G1
5	586	100.0	212	17	AA87023 Human immunoglobul
6	586	100.0	212	17	AA87023 Human IgG1 Fc regi
7	586	100.0	212	19	AA47354 Human immunoglobul
8	586	100.0	212	20	AA47354 IgG1 Fc protein us
9	586	100.0	212	20	AA47354 Human IgG1 Fc prot
10	586	100.0	212	21	AA47354 Human IgG1 Fc regi
11	586	100.0	212	21	AA47354 Human immunoglobul

SUMMARIES

12	586	100.0	212	21	AA47354 Human immunoglobul
13	586	100.0	212	21	AA47354 Fc region of human
14	586	100.0	212	22	AA62062 Human immunoglobul
15	586	100.0	212	22	AA47354 Native IgG Fc regi
16	586	100.0	218	21	AA870474 Native IgG Fc regi
17	586	100.0	218	21	AA870475 Human IgG Fc 1 all
18	586	100.0	218	22	AA87201 Human IgG Fc 1 all
19	586	100.0	218	22	AA87202 Human IgG1 non-A F
20	586	100.0	218	22	AA87202 Human IgG1 A allot
21	586	100.0	218	22	AA87202 Sequence of human
22	586	100.0	224	8	AA87202 Immunoglobulin G F
23	586	100.0	224	9	AA87202 Human IgG1 Fc prot
24	586	100.0	228	21	AA87202 Human IgG1 Fc chai
25	586	100.0	228	21	AA87202 Human IgG1 Fc regi
26	586	100.0	232	18	AA26232 Human IgG1 hinge/F
27	586	100.0	232	18	AA26232 Human IgG1 hinge/F
28	586	100.0	232	21	AA87202 Human immunoglobul
29	586	100.0	232	21	AA87202 Human immunoglobul
30	586	100.0	232	21	AA87202 Human immunoglobul
31	586	100.0	232	22	AA87202 Human partial IgG1
32	586	100.0	232	22	AA87202 Human IgG1 gamma hi
33	586	100.0	232	22	AA87202 Human immunoglobul
34	586	100.0	233	20	AA87202 Human Fc (IgG1).
35	586	100.0	233	20	AA87202 Amino acid sequenc
36	586	100.0	235	20	AA87202 Human IgG1 Fc regi
37	586	100.0	243	21	AA87202 Fc-MMP inhibitor f
38	586	100.0	247	21	AA87202 Fc-TMP protein seq
39	586	100.0	247	21	AA87202 Fc-TNF-alpha inhib
40	586	100.0	248	21	AA87202 TNF-alpha inhibito
41	586	100.0	248	21	AA87202 Fc-IL-1 antagonist
42	586	100.0	248	21	AA87202 IL-1 antagonist-Fc
43	586	100.0	248	21	AA87202 MMP inhibitor-Fc f
44	586	100.0	250	21	AA87202
45	586	100.0	250	21	AA87202

ALIGNMENTS

RESULT 1	AA27680	standard; Protein; 110 AA.
ID	AA27680	
XX	AA27680	
AC	AA27680	
XX	AA27680	
DT	10-MAR-1993	(first entry)
XX	10-MAR-1993	
DE	Human immunoglobulin IgG1 CH2 region.	
XX	Human immunoglobulin IgG1 CH2 region.	
KW	Isoallotype; IgG1 Glm(1,2,17); anti-allotype response;	
KW	humanised Ab.	
XX	Homo sapiens.	
OS	Homo sapiens.	
PN	WO9216562-A.	
XX	WO9216562-A.	
PD	01-OCT-1992.	
XX	01-OCT-1992.	
PF	12-MAR-1992;	92WO-GB00445.
XX	12-MAR-1992;	92WO-GB00445.
PR	12-MAR-1991;	91GB-0005245.
XX	12-MAR-1991;	91GB-0005245.
PA	(LYNX-) LYNXVALE LTD.	
PI	Clark MR;	
XX	Clark MR;	
DR	WPI; 1992-349162/42.	
XX	WPI; 1992-349162/42.	
PT	Humanised antibodies having modified allotypic determinant -	
PT	useful for matching allotypes in therapy with decreased	
PT	likelihood of causing undesirable immune responses	
XX	Humanised antibodies having modified allotypic determinant -	
PS	Disclosure; Fig 4c; 57pp; English.	

XX In humans, IgG1 may exist as either of two allotypes at site 1, 2
CC or 17. The inventor's propose eliminating these allotypes by
CC amino acid changes to agree with the sequences of IgG2, IgG3 and
CC IgG4. None of the allotype sites (1, 2 and 17) are located within
CC the CH2 domain. New "isoallotypes" should be suitable for therapeutic
CC use in all patients. See AAR27678-R27681.
XX
SQ Sequence 110 AA;

Query Match 100.0%; Score 586; DB 13; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.2e-52;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|||||
DB 1 apelligpsvflfpkpkdtlmisrtpetvctcvvdvshedpevkfnwvdgvevhnaktk 60
|||||

QY 61 PREEQYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAK 110
|||||
DB 61 preeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskak 110
|||||

RESULT 2
AAR41684
ID AAR41684 standard; Protein; 110 AA.
XX
AC AAR41684;
XX
DT 20-OCT-1993 (first entry)
XX
DE Undefined ORF2 encoded by pAH4602.
XX
KW Polymerase chain reaction; primer; PCR; amplify; murine; heavy;
KW light; chain; variable; constant; region; anti-human; transferrin;
KW receptor; antibody; brain; capillary; endothelial cell; conjugate;
KW neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke;
KW epilepsy; Parkinsons disease; Alzheimers disease.
XX
OS Synthetic.
XX
PN WO9310819-A.
XX
PD 10-JUN-1993.
XX
PF 24-NOV-1992; 92WO-US10206.
XX
PR 26-NOV-1991; 91US-0800458.
XX
PA (ALKE-) ALKERMES INC.
XX
PI Friden PM;
XX
DR WPI; 1993-196742/24.
DR N-PSDB; AAQ43844.
XX
PT Antibody conjugates specific for transferrin receptor - used
PT for diagnosis and treatment of cancer, AIDS and neurological
PT disorders
XX
PS Disclosure; Fig 11K; 151pp; English.
XX
CC The sequences given in AAR41682-85 are encoded by the expression vector,
CC pAH4602. This vector contains open reading frames encoding the heavy
CC chain variable region (VH) of the antibody 128.1, an ampicillin
CC resistance gene and a histidine (histidinol) selection marker.
CC Transcription of the VH gene is from the VH promoter of the murine
CC 27.44 gene. The vector also includes a heavy chain immunoglobulin
CC enhancer and the human gamma constant region (CH). The VH region of
CC 128.1 was isolated by polymerase chain reaction and cloned into plasmid
CC pAH4274. This was achieved by digesting the plasmid and the product
CC with EcoRV and NheI. The VH gene was inserted in-frame with the human

CC gammal CH region CH at the 3' end of the VH-J region by means of a NheI
CC site. 128.1 is an anti-human transferrin receptor antibody which binds
CC to the transferrin receptor on brain capillary endothelial cells. This
CC antibody may be used in a conjugate in which it is linked to a neuro-
CC pharmaceutical or diagnostic agent. The conjugate may be used to treat
CC or prevent neurological disorders eg. brain tumours, AIDS, stroke,
CC epilepsy, Parkinsons and Alzheimers disease. It may also be used for
CC diagnostic methods.
XX
SQ Sequence 110 AA;

Query Match 100.0%; Score 586; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.2e-52;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
|||||
DB 1 apelligpsvflfpkpkdtlmisrtpetvctcvvdvshedpevkfnwvdgvevhnaktk 60
|||||

QY 61 PREEQYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAK 110
|||||
DB 61 preeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskak 110
|||||

RESULT 3
AAY42621
ID AAY42621 standard; protein; 116 AA.
XX
AC AAY42621;
XX
DT 10-JAN-2000 (first entry)
XX
DE Human IgG1 Fc gamma2 region.
XX
KW Immunoglobulin E; IgE; antagonist; Fc epsilon RI receptor; human; bds;
KW receptor-binding; binding determinant sequence; anti-IgE antibody;
KW allergic disease.
XX
OS Homo sapiens.
XX
PN US5965709-A.
XX
PD 12-OCT-1999.
XX
PF 21-APR-1994; 94US-0232539.
XX
PR 14-AUG-1991; 91US-0744768.
PR 07-JAN-1994; 94US-0178583.
XX
PA (GETH) GENENTECH INC.
XX
PI Jardieu PM, Presta LG;
XX
DR WPI; 1999-579941/49.
XX
PT Immunoglobulin E variants as peptide antagonists useful for raising and
PT screening anti-immunoglobulin E (IgE) antibodies, in the isolation and
PT purification of Fc epsilon RI receptor and in the treatment of allergic
PT diseases -
XX
PS Example 2; Column 61-62; 37pp; English.
XX
CC The invention provides immunoglobulin E (IgE) antagonists comprising one
CC or more of the Fc epsilon RI receptor-binding determinant sites of human
CC IgE. The antagonists include IgE variants comprising an immunoglobulin
CC template and binding determinant sequences (bds) Cbds, EFBds and the
CC sequence shown in AAY42581. The Cbds (CD loop binding determinant
CC sequence) are selected from the sequences shown in AAY42567-Y42577 and
CC the EFBds (EF loop binding determinant sequence) are selected from
CC sequences shown in AAY42578-Y42580. The variants are useful in raising
CC and screening anti-IgE antibodies, in the isolation and purification of
CC Fc epsilon RI receptor and in the treatment and prophylaxis of allergic


```
Query Match      100.0%; Score 586; DB 17; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGSPSVFLPPPKDFTLMSRTPETVCVVVDVSHEDPEVKFNWYDGVGVHNAKTK 60
   |||||
Db 14 apellgspsvflfppkpkdtlmsrtpetvcvvdvshedpevkfnwydgvvhnaktk 73
   |||||

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
   |||||
Db 74 preeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskak 123

RESULT 6
AAW02305
ID AAW02305 standard; Protein; 212 AA.
XX
AC AAW02305;
XX
DT 05-DEC-1996 (first entry)
XX
DE Human IgG1 Fc region.
XX
KW IgG1; interleukin-17 receptor; IL-17R.
XX
OS Homo sapiens.
XX
PN W09629408-A1.
XX
PD 26-SEP-1996.
XX
PF 21-MAR-1996; 96WO-US04018.
XX
PR 07-AUG-1995; 95US-0538765.
PR 23-MAR-1995; 95US-0410535.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Fanslow WC, Spriggs MK, Yao Z;
XX
DR WPI; 1996-443184/44.
XX
PT DNA encoding interleukin-17 receptor - useful for regulating immune
PT and inflammatory responses, or to suppress graft rejection
PS Example 1; Page 33; 52pp; English.
XX
CC The human IgG1 Fc region (AAW02305) can be used as a fusion partner
CC for interleukin-17 receptor (IL-17R) proteins (see also AAW04184-85),
CC allowing purification of recombinant IL-17R using protein A or
CC protein G affinity chromatography. Fusions between Fc and HVS13
CC (see also AAW02387), a viral homologue of IL-17, and between Fc
CC and murine CTLA8 (AAW02386) were used to identify cells that
CC express the murine IL-17R. Selected murine thymoma EL4 cells
CC were used as a source of murine IL-17R cDNA (AAT33800).
XX
SQ Sequence 212 AA;

Query Match      100.0%; Score 586; DB 17; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGSPSVFLPPPKDFTLMSRTPETVCVVVDVSHEDPEVKFNWYDGVGVHNAKTK 60
   |||||
Db 14 apellgspsvflfppkpkdtlmsrtpetvcvvdvshedpevkfnwydgvvhnaktk 73
   |||||

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
   |||||
Db 74 preeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskak 123

RESULT 7
AAW02305
ID AAW02305 standard; Protein; 212 AA.
XX
AC AAW02305;
XX
DT 05-DEC-1996 (first entry)
XX
DE Human IgG1 Fc region.
XX
KW IgG1; interleukin-17 receptor; IL-17R.
XX
OS Homo sapiens.
XX
PN W09629408-A1.
XX
PD 26-SEP-1996.
XX
PF 21-MAR-1996; 96WO-US04018.
XX
PR 07-AUG-1995; 95US-0538765.
PR 23-MAR-1995; 95US-0410535.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Fanslow WC, Spriggs MK, Yao Z;
XX
DR WPI; 1996-443184/44.
XX
PT DNA encoding interleukin-17 receptor - useful for regulating immune
PT and inflammatory responses, or to suppress graft rejection
PS Example 1; Page 33; 52pp; English.
XX
CC The human IgG1 Fc region (AAW02305) can be used as a fusion partner
CC for interleukin-17 receptor (IL-17R) proteins (see also AAW04184-85),
CC allowing purification of recombinant IL-17R using protein A or
CC protein G affinity chromatography. Fusions between Fc and HVS13
CC (see also AAW02387), a viral homologue of IL-17, and between Fc
CC and murine CTLA8 (AAW02386) were used to identify cells that
CC express the murine IL-17R. Selected murine thymoma EL4 cells
CC were used as a source of murine IL-17R cDNA (AAT33800).
XX
SQ Sequence 212 AA;
```

```
AAW47354
ID AAW47354 standard; protein; 212 AA.
XX
AC AAW47354;
XX
DT 01-JUN-1998 (first entry)
XX
DE Human immunoglobulin G1 Fc fragment.
XX
KW BZLF2; beta-chain; major histocompatibility complex; MHC;
KW class II; antigen; prevention; treatment; autoimmune disease;
KW transplant rejection; allergy; asthma; super-antigen; IgG1;
KW Epstein-Barr virus; human; immunoglobulin G1; Fc fragment.
XX
OS Homo sapiens.
XX
PN US5726286-A.
XX
PD 10-MAR-1998.
XX
PF 28-APR-1995; 95US-0430633.
XX
PR 28-APR-1995; 95US-0430633.
PR 28-APR-1994; 94US-0235397.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Alderson M, Armitage RJ, Cohen JI, Comeau MR, Farrah TM;
PI Hutt-Fletcher LM, Spriggs MK;
XX
DR WPI; 1998-192827/17.
XX
PT Epstein-Barr virus protein - binds to major histocompatibility
PT complex class II beta chain, useful for treating, e.g. auto-immune
PT diseases or transplant rejection
XX
PS Example 1; Columns 31-32; 25pp; English.
XX
CC The present sequence was used in the preparation of a synthetic
CC construct containing the Epstein-Barr virus (EBV) BZLF2 protein,
CC which is capable of binding a beta-chain of a major
CC histocompatibility complex (MHC) class II antigen.
CC The protein can be used to inhibit antigen-specific antibody
CC formation, peripheral blood mononuclear cell proliferation and
CC cytotoxic T-cell responses, e.g. in the prevention or treatment of
CC autoimmune diseases, transplant rejection, allergies or asthma,
CC and as a super-antigen.
XX
SQ Sequence 212 AA;

Query Match      100.0%; Score 586; DB 19; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGSPSVFLPPPKDFTLMSRTPETVCVVVDVSHEDPEVKFNWYDGVGVHNAKTK 60
   |||||
Db 14 apellgspsvflfppkpkdtlmsrtpetvcvvdvshedpevkfnwydgvvhnaktk 73
   |||||

QY 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
   |||||
Db 74 preeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskak 123

RESULT 8
AAW23637
ID AAY23637 standard; protein; 212 AA.
XX
AC AAY23637;
XX
DT 06-SEP-1999 (first entry)
XX
DE IgG1 Fc protein used to make BZLF2 fusion proteins.
```

XX B2LF2 protein; beta chain; blood mononuclear mononuclear cell;
 KW Class II major histocompatibility complex antigen; proliferation;
 KW cytotoxic T cell response; antigen specific response; asthma;
 KW autoimmune disease; transplant rejection.
 XX Homo sapiens.
 OS US5925734-A.
 XX 20-JUL-1999.
 XX 24-SEP-1997; 97US-0936854.
 XX 28-APR-1995; 95US-0430633.
 PR 28-APR-1994; 94US-0235397.
 PR 24-SEP-1997; 97US-0936854.
 XX (IMMV) IMMUNEX CORP.
 PA Alderson M, Armitage RJ, Cohen JI, Comeau MR, Farrah TM;
 PI Hutt-Fletcher LM, Spriggs MK;
 XX WPI; 1999-418295/35.
 XX Epstein-Barr virus B2LF2 proteins
 PT Claim 2; Column 31-32; 25pp; English.
 XX The present sequence represents a protein used to create fusion proteins
 CC with the Epstein-Barr virus B2LF2 proteins of the invention. The B2LF2
 CC protein is capable of binding to a beta chain of a Class II major
 CC histocompatibility complex antigen to inhibit an antigen-specific
 CC response. B2LF2 is useful for inhibiting antigen-specific antibody
 CC formation, the proliferation of blood mononuclear mononuclear cells,
 CC and cytotoxic T cell responses. B2LF2 is also useful for inhibiting
 CC undesirable antigen specific responses, e.g. in the treatment or
 CC prevention of asthma; for preventing or treating autoimmune disease;
 CC and for preventing tissue or organ transplant rejection.
 XX Sequence 212 AA;
 SQ Query Match 100.0%; Score 586; DB 20; Length 212;
 Best Local Similarity 100.0%; Pred. No. 1.2e-51;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APELLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 14 apellgspsvflpppkdptlmisrtpevtcvvvdvshedpevkfnwvydgvevhnatk 73
 QY 61 PREEQNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIETISKAK 110
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 74 preeqnstyrvvsvltvlhqdwlngkeyckvsnkalpapietiskak 123
 RESULT 9
 AAW92411
 ID AAW92411 standard; Protein; 212 AA.
 XX
 AC AAW92411;
 XX 21-APR-1999 (first entry)
 DT Human IgG1 Fc protein fragment.
 XX IL-17R; human; interleukin-17 receptor; immunoregulator; inhibitor;
 XX T cell proliferation; T cell activation; organ; graft; rejection;
 KW autoimmune disease; allergy; asthma; treatment; inflammatory disease;
 KW B cell proliferation; immunoglobulin secretion; immunogen; IgG1; Fc.
 XX Homo sapiens.
 OS
 XX

PN US5869286-A.
 XX 09-FEB-1999.
 XX 21-MAR-1996; 96US-0620694.
 XX 21-MAR-1996; 96US-0620694.
 PR 23-MAR-1995; 95US-0410535.
 PR 07-AUG-1995; 95US-0538765.
 XX (IMMV) IMMUNEX CORP.
 XX Fanslow WC, Spriggs MK, Yao Z;
 PI WPI; 1999-152766/13.
 DR Isolated interleukin-17 receptor DNA - used to develop products for
 PT treating e.g. organ or graft rejection, autoimmune disease, allergy,
 PT asthma or inflammatory disease
 XX Example 1; Column 31-32; 25pp; English.
 XX This sequence represents a human IgG1 Fc fragment which is used in the
 CC construction of a fusion protein with human interleukin-17 receptor
 CC (IL-17R). IL-17R polypeptides have immunoregulatory activity. They can be
 CC used for inhibiting T cell proliferation, or for inhibiting T cell
 CC activation. In particular they can be used for preventing or treating
 CC organ or graft rejection, autoimmune disease, allergy or asthma. They can
 CC also be used for the prevention or treatment of inflammatory disease in
 CC which activated T cells play a role or for inhibiting B cell
 CC proliferation or immunoglobulin secretion. The IL-17 polypeptides can
 CC also be used as immunogens, reagents in in vitro assays, or as binding
 CC agents for affinity purification procedures.
 XX Sequence 212 AA;
 SQ Query Match 100.0%; Score 586; DB 20; Length 212;
 Best Local Similarity 100.0%; Pred. No. 1.2e-51;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APELLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 14 apellgspsvflpppkdptlmisrtpevtcvvvdvshedpevkfnwvydgvevhnatk 73
 QY 61 PREEQNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIETISKAK 110
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 74 preeqnstyrvvsvltvlhqdwlngkeyckvsnkalpapietiskak 123
 RESULT 10
 AAY99937
 ID AAY99937 standard; Protein; 212 AA.
 XX
 AC AAY99937;
 XX 10-JAN-2001 (first entry)
 DT Human IgG1 Fc region.
 XX IL-17R; CTLA-8; interleukin 17; Herpesvirus saimiri; HVS 13;
 KW human; antibody; immune suppression.
 XX Homo sapiens.
 OS US6072037-A.
 XX 06-JUN-2000.
 XX 12-FEB-1998; 98US-0022696.
 PR 21-MAR-1996; 96US-0620694.
 PR 23-MAR-1995; 95US-0410535.
 XX

PR 07-AUG-1995; 95US-0538765.
XX (IMMV) IMMUNEX CORP.
XX Fanslow WC, Spriggs MK, Yao Z;
XX WPI; 2000-411206/35.
XX
XX Antibodies immunoreactive with interleukin-17 receptor protein useful
PT in interfering with receptor binding to CTLA-8, as components of
PT diagnostic or research assays or in affinity purification of the
PT receptor -
XX
XX Disclosure; Column 31-32; 25pp; English.
XX
XX The present invention relates to a novel receptor that binds Interleukin
CC 17 (IL-17, also known as CTLA-8) and a Herpesvirus saimiri homolog,
CC HSV13. The receptor is a type I transmembrane protein which is referred
CC to as IL-17R. Murine thymoma EL4 cells were found to express a
CC receptor for IL-17. An EL4 mammalian expression library was screened
CC and a cDNA encoding the receptor was identified (see AAA61238). The cDNA
CC was used to isolate DNA encoding human IL-17R by cross species
CC hybridisation. The human IL-17R cDNA and protein are described in
CC AAA61240 and AAY9941. The present sequence is a human IgG1 Fc region
CC that may be used with IL-17R to make a fusion protein. Soluble forms of
CC the receptor may be used to regulate immune responses, for example to
CC suppress rejection of organ grafts. Antibodies to IL-17R consisting of
CC amino acids 1-322 of murine IL-17R or 1-320 of human IL-17R may be
CC useful as components of diagnostic or research assays. Such antibodies
CC may also be used in affinity purification of the receptor.
XX
XX Sequence 212 AA;
SQ

Query Match 100.0%; Score 586; DB 21; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 14 APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
QY 61 PREEQNSYRYVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 110
Db 74 PREEQNSTYRYVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 123

RESULT 11
AAY97182
ID AAY97182 standard; Protein; 212 AA.
XX
XX AAY97182;
XX
XX 04-DEC-2000 (first entry)
XX Human immunoglobulin G1 Fc region.
DE
XX IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
KW HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KW anti-asthmatic; immunoglobulin G1; Fc region.
XX
XX Homo sapiens.
OS
XX US6096305-A.
PN
XX 01-AUG-2000.
PD
XX 11-FEB-1998; 98US-0022253.
PF
XX 21-MAR-1996; 96US-0620694.
PR
XX 23-MAR-1995; 95US-0410535.
PR
XX 07-AUG-1995; 95US-0538765.
XX

PA (IMMV) IMMUNEX CORP.
XX Fanslow WC, Spriggs MK, Yao Z;
XX WPI; 2000-523862/47.
XX
XX Suppressing rejection of a grafted syngeneic or allogeneic organ or
PT tissue in a graft recipient for organ transplantation involves
PT transfecting the organ or tissue with DNA encoding soluble
PT interleukin-17R receptor
XX
XX Example 1; Column 31-32; 27pp; English.
XX
XX A novel interleukin-17 receptor (IL-17R) was identified by screening a
CC cDNA library from T cell thymoma EL4 cells, which were identified as
CC binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
CC region and soluble IL-17 (CTLA-8) protein or a homologous
CC Herpesvirus saimiri (HSV) protein, designated HSV13. Suppressing
CC rejection of a grafted syngeneic or allogeneic organ or tissue in a graft
CC recipient involves transfecting the organ or tissue to be transplanted
CC with DNA encoding soluble IL-17R, so that expression of IL-17R by the
CC engrafted organ or tissue results in suppression of rejection. Soluble
CC IL-17R fragments comprise residues 1-322 of the murine IL-17R, residues
CC 1-320 of the human IL-17R, and fragments of the extracellular domain
CC that bind IL-17. The method is useful for regulating an immunoresponse,
CC for suppressing rejection of grafted organs or tissues in the recipient
CC and for treating or preventing diseases like allergy, asthma and
CC autoimmune diseases.
XX
XX Sequence 212 AA;
SQ

Query Match 100.0%; Score 586; DB 21; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
Db 14 APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
QY 61 PREEQNSYRYVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 110
Db 74 PREEQNSTYRYVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 123

RESULT 12
AAY97250
ID AAY97250 standard; Protein; 212 AA.
XX
XX AAY97250;
XX
XX 04-DEC-2000 (first entry)
XX Human immunoglobulin G1 Fc region.
DE
XX IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
KW HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
KW anti-asthmatic; immunoglobulin G1; Fc region.
XX
XX Homo sapiens.
OS
XX US6100235-A.
PN
XX 08-AUG-2000.
PD
XX 11-FEB-1998; 98US-0022260.
PF
XX 21-MAR-1996; 96US-0620694.
PR
XX 23-MAR-1995; 95US-0410535.
PR
XX 07-AUG-1995; 95US-0538765.
XX
XX (IMMV) IMMUNEX CORP.
XX

PI Fanslow WC, Spriggs MK, Yao Z;
 XX WPI; 2000-548298/50.
 XX
 XX Regulating, treating or preventing immune or inflammatory response in a
 PT mammal, especially organ or graft rejection, allergy or asthma,
 PT comprises administering interleukin-17 receptors
 XX
 XX Example 1; Column 31-32; 26pp; English.
 XX
 CC A novel interleukin-17 receptor (IL-17R) was identified by screening a
 CC cDNA library from T cell thymoma EL4 cells, which were identified as
 CC binding fusion proteins comprising human immunoglobulin G1 (IgG1) Fc
 CC region and soluble IL-17 (CTLA-8) protein or a homologous
 CC Herpesvirus saimiri (HSV) protein, designated HSV13. Regulating an
 CC immune or inflammatory response in a mammal comprises administering
 CC soluble IL-17R. Soluble IL-17R fragments comprise residues 1-322 of the
 CC murine IL-17R, residues 1-320 of the human IL-17R, and fragments of the
 CC extracellular domain that bind IL-17. The method is useful for regulating
 CC an immunoresponse, for treating or preventing diseases like allergy,
 CC asthma and autoimmune diseases, and for suppressing rejection of grafted
 CC organs or tissues in the recipient.
 XX
 XX Sequence 212 AA;

Query Match 100.0%; Score 586; DB 21; Length 212;
 Best Local Similarity 100.0%; Pred. No. 1.2e-51;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db 14 apellggpsvfllppkpkdtlmisrtpevtcvvvdvshedpevkfnwvydgvevhnaktk 73

QY 61 PREEQNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKALPAPIETKTSKAK 110
 Db 74 preeqnstyrvvsvltvhlqgdwlngkeykckvsnkalpapietktskak 123

RESULT 13
 AAB03809
 ID AAB03809 standard; Protein; 212 AA.
 XX
 AC AAB03809;
 XX
 DT 13-OCT-2000 (first entry)
 XX
 DE Fc region of human immunoglobulin G1.
 XX
 KW Interleukin-17 receptor; IL-17R; CTLA8; antiinflammatory; antiallergic;
 KW immunosuppressive; organ rejection; graft rejection; autoimmune disease;
 KW allergy; asthma; IgG1; immunoglobulin G1; human.
 XX
 OS Homo sapiens.
 XX
 XX US6072033-A.
 XX
 XX 06-JUN-2000.
 XX
 XX 11-FEB-1998; 98US-0022255.
 XX
 XX 21-MAR-1996; 96US-0620694.
 XX 23-MAR-1995; 95US-0410535.
 XX 07-AUG-1995; 95US-0538765.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX
 XX Fanslow WC, Spriggs MK, Yao Z;
 XX WPI; 2000-411205/35.
 XX
 XX Interleukin-17 receptor protein useful for regulating immune functions
 PT and for preventing or treating organ or graft rejection, autoimmune

PT disease, allergy or asthma in human -
 XX Example 1; Column 31-32; 26pp; English.
 XX
 XX This invention relates to an isolated and purified interleukin-17
 CC receptor (IL-17R). A soluble IL-17 protein (CTLA8) and a herpesvirus
 CC siamiri (HVS13) open reading frame (homologous to CTLA8) were expressed
 CC as fusion proteins comprising an immunoglobulin Fc region, and used to
 CC screen for the expression of the IL-17R. The screening identified the
 CC novel receptor of the invention. IL-17R is a type I transmembrane
 CC protein that exhibits antiinflammatory, immunosuppressive, antiasthmatic
 CC and antiallergic activities, and is an inhibitor of T cell proliferation
 CC and activation. IL-17R can be used to regulate immune functions, and is
 CC useful for preventing or treating organ or graft rejection, autoimmune
 CC disease, allergy or asthma. The present sequence represents the Fc region
 CC of human immunoglobulin G1 (IgG1). This fragment of IgG1 forms part of
 CC the IL-17 fusion protein used to identify IL-17R.
 XX
 XX Sequence 212 AA;

Query Match 100.0%; Score 586; DB 21; Length 212;
 Best Local Similarity 100.0%; Pred. No. 1.2e-51;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
 Db 14 apellggpsvfllppkpkdtlmisrtpevtcvvvdvshedpevkfnwvydgvevhnaktk 73

QY 61 PREEQNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKALPAPIETKTSKAK 110
 Db 74 preeqnstyrvvsvltvhlqgdwlngkeykckvsnkalpapietktskak 123

RESULT 14
 AAB62062
 ID AAB62062 standard; Protein; 212 AA.
 XX
 AC AAB62062;
 XX
 DT 29-MAY-2001 (first entry)
 XX
 DE Fc region of human immunoglobulin IgG1.
 XX
 KW CTLA-8; interleukin-17; IL-17; IL-17 receptor; IL-17R; human; IgG1;
 KW immunosuppressive; antiallergic; antiasthmatic; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 XX US6197525-B1.
 XX
 XX 06-MAR-2001.
 XX
 XX 11-FEB-1998; 98US-0022257.
 XX
 XX 21-MAR-1996; 96US-0620694.
 XX 23-MAR-1995; 95US-0410535.
 XX 07-AUG-1995; 95US-0538765.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX
 XX Yao Z, Spriggs MK, Fanslow WC;
 XX WPI; 2001-234480/24.
 XX
 XX New assay kits for detecting interleukin-17 (IL-17), IL-17 receptors
 PT and (antagonists or mimetics of) the interaction between IL-17 and
 PT IL-17 receptor, useful for treating autoimmune diseases -
 XX
 XX Example 1; Columns 31-32; 26pp; English.
 XX
 CC The invention is directed towards assays for detection of interleukin-17
 CC (IL-17), IL-17 receptor (IL-17R), and (antagonists or mimetics of) the

CC interaction between IL-17 and IL-17R. The assay kit comprises an IL-17R
 CC protein and a detecting reagent. The method is useful for inhibiting
 CC binding of IL-17 to cells expressing IL-17R. IL-17 receptors are also
 CC useful for preventing or treating organ or graft rejection, autoimmune
 CC diseases, allergy, asthma and inflammatory diseases in which activated
 CC T-cells play an important role. The present sequence represents Fc
 CC region of human immunoglobulin IgG1, used for constructing a murine
 CC CTLA-8/Fc fusion protein.
 XX
 SQ Sequence 212 AA;

Query Match 100.0%; Score 586; DB 22; Length 212;
 Best Local Similarity 100.0%; Pred. No. 1.2e-51;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPPKPKDTLMISRPETCVVVDVSHEDPEVKFNWYDGVGVHNAKTK 60
 |||||
 Db 14 apellggpsvflfppkpkdtlmisrtpetcvvvdvshedpevkfnwydgvgevhnaaktk 73
 |||||

QY 61 PREEQYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAK 110
 |||||
 Db 74 preeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiaktiskak 123
 |||||

RESULT 15
 AAY72750
 ID AAY72750 standard; Protein; 212 AA.
 XX
 AC AAY72750;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Human immunoglobulin IgG1 Fc region.
 XX
 KW Human; Interleukin-17 receptor; IL-17R; immunosuppressive; antiallergic;
 KW antiasthmatic; antiinflammatory; graft rejection; autoimmune disease;
 KW inflammatory disease; allergy; CTLA-8; immunogen; immunoglobulin G; IgG1;
 KW asthma.
 XX
 OS Homo sapiens.
 XX
 PN US6191104-B1.
 XX
 PD 20-FEB-2001.
 XX
 PF 11-FEB-1998; 98US-0022259.
 XX
 PR 21-MAR-1996; 96US-0620694.
 PR 23-MAR-1995; 95US-0410535.
 PR 07-AUG-1995; 95US-0538765.
 XX
 PA (IMV) IMMUNEX CORP.
 XX
 PI Spriggs MK, Fanslow WC;
 XX
 DR WPI; 2001-217901/22.
 XX
 PT Suppressing rejection of grafted organ or tissue in graft recipient,
 PT involves administering to recipient a composition comprising
 PT interleukin 17 receptor protein -
 XX
 PS Example 1; Column 31-32; 26pp; English.
 XX
 CC The present sequence is the Fc region of human immunoglobulin IgG1
 CC which is used for constructing fusion protein with Interleukin-17
 CC receptor (IL-17R).
 CC The invention relates to Interleukin-17 receptors (IL-17R),
 CC Interleukin-17 and their corresponding nucleic acid molecules. IL-17R is
 CC a Type I transmembrane protein which is used for regulating the immune
 CC response. The invention is useful for suppressing rejection of a grafted
 CC organ or tissue in a graft recipient. Soluble IL-17 (CTLA-8) receptors
 CC are useful for preventing or treating organ or graft rejection,

CC autoimmune disease, allergy, asthma, and inflammatory disease in which
 CC activated T-cells play a role. Soluble IL-17 fusion proteins are used to
 CC screen cells for the expression of IL-17 receptor. Derivatives of IL-17R
 CC are also used as immunogens, reagents in in vitro assays, or as binding
 CC agents for affinity purification procedures.
 XX
 SQ Sequence 212 AA;

Query Match 100.0%; Score 586; DB 22; Length 212;
 Best Local Similarity 100.0%; Pred. No. 1.2e-51;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPPKPKDTLMISRPETCVVVDVSHEDPEVKFNWYDGVGVHNAKTK 60
 |||||
 Db 14 apellggpsvflfppkpkdtlmisrtpetcvvvdvshedpevkfnwydgvgevhnaaktk 73
 |||||

QY 61 PREEQYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAK 110
 |||||
 Db 74 preeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiaktiskak 123
 |||||

Search completed: June 21, 2002, 08:36:07
 Job time: 321 sec

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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:37:53 ; Search time 102.05 Seconds

(without alignments)
102.633 Million cell updates/sec

Title: US-09-674-857-5

Perfect score: 583

Sequence: 1 APPVAGPSVFLFPKPKDTL.....CKVSNKGLPAPIETKTK 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	583	100.0	326	1 G2HU	Ig gamma-2 chain C
2	540	92.6	377	2 A60764	Ig gamma-2 chain C
3	540	92.6	377	2 A23511	Ig gamma-3 chain C
4	537	92.1	234	2 PT0207	Ig gamma chain C r
5	535	91.8	255	4 S31866	Ig gamma-1 chain C
6	535	91.8	330	1 GHU	Ig gamma-1 chain C
7	535	91.8	374	2 S69339	Ig heavy chain v r
8	528	90.6	327	1 G4HU	Ig gamma-4 chain C
9	527	90.4	289	1 G3HUWI	Ig gamma-3 heavy c
10	468	80.3	328	2 I47160	Ig gamma 2b chain
11	468	80.3	328	2 I47159	Ig gamma 2a chain
12	463	79.4	277	2 I47162	Ig gamma 4 chain c
13	452	77.5	328	2 I47161	Ig gamma 3 chain c
14	452	77.5	328	2 I47158	Ig gamma 1 chain c
15	440	75.5	470	2 S22080	Ig heavy chain pre
16	436	74.8	308	2 C30554	Ig heavy chain C r
17	436	74.8	329	2 G2GP	Ig gamma-2 chain C
18	436	74.8	472	2 S31459	Ig gamma-1 chain -
19	429	73.6	323	1 GHRB	Ig gamma chain C r
20	428	73.4	333	2 PS0018	Ig gamma-2b chain
21	421.5	72.3	329	1 G3MSC	Ig gamma-3 chain C
22	421.5	72.3	398	1 G3MSM	Ig gamma-3 chain C
23	421	72.2	324	1 G1MS	Ig gamma-1 chain C
24	421	72.2	393	1 G1MSM	Ig gamma-1 chain C
25	421	72.2	444	2 PC4436	monoclonal antibod
26	412	70.7	327	2 S06511	Ig gamma-2 chain C
27	405	69.5	329	2 S00847	Ig gamma-2c chain
28	389	66.7	326	2 PS0017	Ig gamma-1 chain C
29	389	66.7	330	1 G2MSA	Ig gamma-2a chain

30	389	66.7	399	1 G2MSAM	Ig gamma-2a chain
31	389	66.7	469	2 S37483	Ig gamma-2a chain
32	388	66.6	335	1 G2MSAB	Ig gamma-2a chain
33	388	66.6	405	1 G2MSBM	Ig gamma-2b chain
34	388	66.6	474	1 G2MS11	Ig gamma-2b chain
35	380	65.2	475	2 S01321	Ig gamma-2b chain
36	379	65.0	446	2 S40295	Ig gamma-2a chain
37	353	60.5	322	2 PS0019	Ig gamma-2a chain
38	321	55.1	112	2 B30503	Ig gamma-2a chain
39	277	47.5	88	2 A30503	Ig gamma-2b chain
40	265	45.5	180	2 I46732	Ig gamma heavy cha
41	183	31.4	152	2 S14236	Ig gamma-1 chain C
42	171.5	29.4	426	2 I36948	Ig epsilon-chain -
43	170.5	29.2	428	1 EHHU	Ig epsilon chain C
44	161	27.6	549	2 S04845	Ig heavy chain pre
45	154	26.4	429	1 EHRT	Ig epsilon chain C

ALIGNMENTS

RESULT 1
G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain
A:Reference number: A93906; MUID:82197621
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: GB:J00230; GB:J02759; PIDN:CAB58438.1; PID:g5066056
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, an
A:Reference number: A92809; MUID:81007873
A:Contents: myeloma protein Til
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of
A:Reference number: A90752; MUID:80001357
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 1
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A:Reference number: A93132; MUID:80114419
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation: Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amid
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500
A:Contents: annotation; myeloma protein Sa, disulfide bonds

R:Frangione, B.; Milstein, C.; Pink, J.R.L.
 Nature 221, 145-148, 1969
 A:Title: Structural studies of immunoglobulin G.
 A:Reference number: A93157; MUID:69064124
 A:Contents: annotation; Sa, disulfide bonds
 C:Genetics:

A:Gene: GDB:IGHG2
 A:Cross-references: GDB:119338; OMIM:147110
 A:Map position: 14q32.33-14q32.33
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IM1>
 F:133-202/Domain: immunoglobulin homology <IM2>
 F:239-306/Domain: immunoglobulin homology <IM3>
 F:14/Disulfide bonds: interchain (to light chain) #status experimental
 F:27-83,140-200,246-304/Disulfide bonds: #status experimental
 F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 583; DB 1; Length 326;
 Best Local Similarity 100.0%; Pred. No. 1.8e-51;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNATKTP 60

Db 111 APPVAGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNATKTP 170

QY 61 REQFNSTFRVSVLTIVHODWLNKGKEYCKVSNKGLPAPIETISKT 109

Db 171 REQFNSTFRVSVLTIVHODWLNKGKEYCKVSNKGLPAPIETISKT 219

RESULT 2
 A60764
 Ig gamma-3 chain C region, form LAT - human
 C:Species: Homo sapiens (man)
 C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
 C:Accession: A60764
 R:Huck, S.; Lefranc, G.; Lefranc, M.P.
 Immunogenetics 30, 250-257, 1989
 A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
 A:Reference number: A60764; MUID:90007613
 A:Accession: A60764
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-377 <HUC>
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 540; DB 2; Length 377;
 Best Local Similarity 94.3%; Pred. No. 4.8e-47;
 Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNATKTP 63

Db 165 LGGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNATKTP 224

QY 64 QFNSTFRVSVLTIVHODWLNKGKEYCKVSNKGLPAPIETISKT 109

Db 225 QYNSTFRVSVLTIVHODWLNKGKEYCKVSNKGLPAPIETISKT 270

RESULT 3
 A23511
 Ig gamma*3 chain C region (allotype G3m(b)) - human
 C:Species: Homo sapiens (man)
 C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
 C:Accession: A23511

R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
 Nucleic Acids Res. 14, 1779-1789, 1986
 A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:
 A:Reference number: A23511; MUID:86148507
 A:Accession: A23511
 A:Molecule type: DNA
 A:Residues: 1-377 <HUC>
 A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
 C:Genetics:

A:Gene: GDB:IGHG3
 A:Cross-references: GDB:119339; OMIM:147120
 A:Map position: 14q32.33-14q32.33
 A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 540; DB 2; Length 377;
 Best Local Similarity 94.3%; Pred. No. 4.8e-47;
 Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNATKTP 63

Db 165 LGGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNATKTP 224

QY 64 QFNSTFRVSVLTIVHODWLNKGKEYCKVSNKGLPAPIETISKT 109

Db 225 QYNSTFRVSVLTIVHODWLNKGKEYCKVSNKGLPAPIETISKT 270

RESULT 4
 PT0207
 Ig gamma chain C region - chimpanzee
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
 C:Accession: PT0207
 R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
 Mol. Immunol. 28, 319-322, 1991
 A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
 A:Reference number: PT0207; MUID:91287716
 A:Accession: PT0207
 A:Molecule type: mRNA
 A:Residues: 1-234 <EHR>
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 92.1%; Score 537; DB 2; Length 234;
 Best Local Similarity 88.6%; Pred. No. 5.5e-47;
 Matches 101; Conservative 4; Mismatches 3; Indels 6; Gaps 1;

QY 2 PPVA-----GPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 55

Db 21 PCAAPELGGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 80

QY 56 AKTKPREQFNSTFRVSVLTIVHODWLNKGKEYCKVSNKGLPAPIETISKT 109

Db 81 AKTKPREQFNSTFRVSVLTIVHODWLNKGKEYCKVSNKGLPAPIETISKT 134

RESULT 5
 S31866
 Ig gamma-1 chain C region - synthetic
 C:Species: synthetic
 A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
 C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
 C:Accession: S31866
 R:Filpula, D.
 submitted to the EMBL Data Library, February 1993
 A:Description: Screening method for protein-protein interactions of cloned gene products
 A:Reference number: S31866

A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FIL>
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 91.8%; Score 535; DB 4; Length 255;
Best Local Similarity 87.7%; Pred. No. 9.8e-47;
Matches 100; Conservative 5; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 55
|| : |||||
DB 35 PGPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 94
|||
QY 56 AKTKPREQFNSTFRVSVLTVHQDLNGKEYCKVSKNKGLPAPLEKTSKTK 109
|||
DB 95 AKTKPREQFNSTFRVSVLTVHQDLNGKEYCKVSKNKGLPAPLEKTSKAK 148
|||

RESULT 6
GHHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
A:Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.
A:Reference number: A93433; MUID:82274238
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <CELL>
A:Cross-references: EMBL:213770
A:Note: This sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers,
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAP>
A:Cross-references: EMBL:213770
R:Fukunishi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113/235-330 <TAK>
A:Cross-references: EMBL:213770
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A:Reference number: A90563; MUID:71064024
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-135 <CUN>
A:Note: this sequence has the Gln(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
A:Reference number: A90564; MUID:71064025
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
A:Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein N1
igen Primaerstruktur.
A:Reference number: A91668; MUID:77070269
A:Contents: myeloma protein Nile
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E',
A:Note: this sequence has the Gln(17) and Gln(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <
A:Note: this sequence has the Gln(3) and Gln(non-1) markers
R:Galli, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul
A:Reference number: A90565; MUID:71064027
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunog
endamide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
C:Introns: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C
Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83, 144-204, 250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109, 112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 91.8%; Score 535; DB 1; Length 330;
Best Local Similarity 87.7%; Pred. No. 1.3e-46;
Matches 100; Conservative 5; Mismatches 3; Indels 6; Gaps 1;

QY 2 PP-----VAGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 55
|| : |||||
DB 110 PGPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 169
|||
QY 56 AKTKPREQFNSTFRVSVLTVHQDLNGKEYCKVSKNKGLPAPLEKTSKTK 109
|||
DB 170 AKTKPREQFNSTFRVSVLTVHQDLNGKEYCKVSKNKGLPAPLEKTSKAK 223
|||

RESULT 7
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
A:Accession: S69339; S72664
R:Khamilchi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>

A:Cross-references: EMBL:X81695
R:Khamlichi, A.A.
Submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140,'C',142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 91.8%; Score 535; DB 2; Length 374;
Best Local Similarity 87.7%; Pred. No. 1.5e-46;
Matches 100; Conservative 5; Mismatches 3; Indels 3; Gaps 1;

QY 2 PP-----VAGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 55
II : |||||
DB 154 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 213
QY 56 AKTKPREQFNSTFRVSVLTIVVHODWLNKKEYCKVSNKGLPAPIETKTSKTK 109
II : |||||
DB 214 AKTKPREQFNSTFRVSVLTIVVHODWLNKKEYCKVSNKGLPAPIETKTSKTK 267

RESULT 8
G4HU

Ig gamma-4 chain C region - human
C:Species: Homo sapiens (nan)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C:Accession: A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104
A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant
A:Reference number: A90249; MUID:70207560
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30;81-326 <PIN>
C:Genetics:

A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.6%; Score 528; DB 1; Length 327;
Best Local Similarity 92.5%; Pred. No. 6.7e-46;
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNKTKPREE 63
II : |||||
DB 115 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNKTKPREE 174

QY 64 QFNSTFRVSVLTIVVHODWLNKKEYCKVSNKGLPAPIETKTSKTK 109
II : |||||
DB 175 QFNSTFRVSVLTIVVHODWLNKKEYCKVSNKGLPAPIETKTSKTK 220

RESULT 9
G3HUWI

Ig gamma-3 heavy chain disease proteins - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C:Accession: A90442; A92219; A90198; A93915; A02149
R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 hea
A:Reference number: A90442; MUID:81021548
A:Contents: heavy chain disease protein Wis
A:Accession: A90442
A:Molecule type: protein
A:Residues: 1-289 <FRA>
A:Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch
A:Note: this protein lacks most of the V region and all of the CH1 region. Residue 12
A:Note: the sequence of residues 42-76 was taken from the reference that follows
R:Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977

A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplicat
A:Reference number: A92219; MUID:77118561
A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protei
A:Accession: A92219
A:Molecule type: protein
A:Residues: 12-97 <MIC>
A:Note: the hinge region in gamma-3 chains is about four times as long as in other ga
idue segment (12-28)
A:Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form in
R:Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of t
A:Reference number: A90198; MUID:77021516
A:Contents: heavy chain disease protein Zuc, partial sequence corresponding to residu
A:Accession: A90198
A:Molecule type: protein
A:Residues: 59-125,'EB',128-226,228-289 <MOL>
A:Note: this protein lacks most of the V region, all of the CH1 region, and part of t
R:Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood,
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A:Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deleti
A:Reference number: A93915; MUID:82247835
A:Contents: heavy chain disease protein Omn
A:Accession: A93915

A:Molecule type: mRNA
A:Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-
A:Note: a carboxyl-terminal lys is removed posttranslationally
A:Note: this sequence may represent an allelic form or another gamma chain subclass
C:Comment: The heavy chain disease protein Wis is shown.

C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F:203-270/Domain: immunoglobulin homology <IMX>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 90.4%; Score 527; DB 1; Length 289;
Best Local Similarity 91.5%; Pred. No. 7.3e-46;
Matches 97; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNKTKPREE 63
II : |||||
DB 78 LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNKTKPREQ 137

QY 64 QFNSTFRVSVLTIVVHODWLNKKEYCKVSNKGLPAPIETKTSKTK 109

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Db 138 QFNSTFRVSVLTVLHQNDLQNGKEYCKVSNKALPAPIETISKTK 183
|||||
RESULT 10
I47160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845
A:Accession: I47160
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C:Genetics:
A:Gene: IgG2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 468; DB 2; Length 328;
Best Local Similarity 80.8%; Pred. No. 8.1e-40;
Matches 84; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 6 GPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEQF 65
|||||
Db 116 GPSVFIFFPKPKDTLMISRTPTQVTCVVDVSOENPEVQFSWYVDGVEVHTAQTTPKREEQF 175
|||||

QY 66 NSTFRVSVLTVVHODWLNKGYCKVSNKGLPAPIETISKTK 109
|||||
Db 176 NSTYRVSVLPIQHODWLNKGFCKVKNKDLPAPIETRIISKAK 219
|||||

RESULT 11
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C:Genetics:
A:Gene: IgG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 468; DB 2; Length 328;
Best Local Similarity 80.8%; Pred. No. 8.1e-40;
Matches 84; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 6 GPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEQF 65
|||||
Db 116 GPSVFIFFPKPKDTLMISRTPTQVTCVVDVSOENPEVQFSWYVDGVEVHTAQTTPKREEQF 175
|||||

QY 66 NSTFRVSVLTVVHODWLNKGYCKVSNKGLPAPIETISKTK 109
|||||
Db 176 NSTYRVSVLPIQHODWLNKGFCKVKNKDLPAPIETRIISKAK 219
|||||

RESULT 12
```

```

I47162
Ig gamma 4 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47162
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845
A:Accession: I47162
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C:Genetics:
A:Gene: IgG4
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 463; DB 2; Length 277;
Best Local Similarity 79.8%; Pred. No. 2.1e-39;
Matches 83; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 6 GPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEQF 65
|||||
Db 65 GPSAFIFPPKPKDTLMISRTPKVTCVVDVSOENPEVQFSWYVDGVEVHTAQTTPKREEQF 124
|||||

QY 66 NSTFRVSVLTVVHODWLNKGYCKVSNKGLPAPIETISKTK 109
|||||
Db 125 NSTYRVSVLPIQHODWLNKGFCKVKNKDLPAPIETRIISKAK 168
|||||

RESULT 13
I47161
Ig gamma 3 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47161
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845
A:Accession: I47161
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128
C:Genetics:
A:Gene: IgG3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 452; DB 2; Length 328;
Best Local Similarity 79.8%; Pred. No. 3.4e-38;
Matches 83; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREE 63
Db 114 VAGPSVFIFFPKPKDTLMISQIPEVTCVVDVSKAEAEVQFSWYVDGVEVHTAETPKEE 173
|||||

QY 64 QFNSTFRVSVLTVVHODWLNKGYCKVSNKGLPAPIETISKTK 107
|||||
Db 174 QFNSTYRVSVLPIQHODWLNKGFCKVKNVNDLPAPIETRIISK 217
|||||

RESULT 14
I47158
Ig gamma 1 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47158
```

R:Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a

A:Reference number: I47158; MUID:95015845

A:Accession: I47158

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-328 <NAC>

A:Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122

C:Genetics:

A:Gene: IgG1

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:133-202/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 77.5%; Score 452; DB 2; Length 328;

Matches 83; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63

Db 114 VAGPSVFIFPPPKDKLTLSQTPETCVVVDVSKHAIEQFSWYVDGVEVHTAETRPKEE 173

QY 64 QFNSTFRVSVLTVTVHQDLNGKEYCKVSNKGLPAPIEKTISK 107

Db 174 QFNSTYRVSVLPIQHQDLNGKEYCKVSNKGLPAPIEKTISK 217

RESULT 15

S22080

Ig heavy chain precursor (B/MT 4A.17, H5, A5) - bovine

N:Alternate names: Ig gamma-1 chain C region (clone 8.10)

C:Species: Bos primigenius taurus (cattle)

C:Date: 06-Jan-1995 #sequence-revision 06-Jan-1995 #text-change 23-Jul-1999

C:Accession: S22080; S06610; A31303

R:Sanders, P. G.

submitted to the EMBL Data Library, November 1991

A:Reference number: S22080

A:Accession: S22080

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-470 <SAN>

A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440

R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.

Mol. Immunol. 26, 841-850, 1989

A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma

A:Reference number: S06610; MUID:90097956

A:Accession: S06610

A:Molecule type: DNA

A:Residues: 142-470 <SYM>

A:Cross-references: EMBL:X16701

A:Note: the sequence was determined from the germline gene

C:Genetics:

A:Gene: Ig CH gamma-1

A:Introns: 98/1, 111/1, 221/1

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein

F:161-225/Domain: immunoglobulin homology <IMM>

F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 75.5%; Score 440; DB 2; Length 470;

Matches 81; Conservative 12; Mismatches 15; Indels 2; Gaps 1;

QY 2 PP--VAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTK 59

Db 252 PPELPGGPSVFIFPPPKDKLTLSGTPETCVVVDVGHDDPEVKFSWFDVDDVEVNTATTK 311

QY 60 PREEQFNSTFRVSVLTVTVHQDLNGKEYCKVSNKGLPAPIEKTISKTK 109

Db 312 PREEQFNSTYRVSVLRIQHQDWTGGKFKCKVHNEGLPAPIVTRTISRTK 361

Search completed: June 21, 2002, 08:37:54

Job time: 428 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 08:36:04 ; Search time 224.82 Seconds
(without alignments)
53.852 Million cell updates/sec

Title: US-09-674-857-2
Perfect score: 580
Sequence: 1 APPVAGPSVFLPPKPKDTL.....CKVSNKGLPSSIEKTIKTK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	98.6	109	AA1980	Undefined ORF2 enc
2	572	98.6	109	AA1981	Mutated CH2 sequen
3	572	98.6	217	AA1982	Amino acid sequenc
4	572	98.6	217	AA1983	Human IgG2. Homo
5	572	98.6	217	AA1984	Human IgG2 FC regi
6	572	98.6	326	AA1985	Human immunoglobul
7	572	98.6	381	AA1986	Human IL-2/Ig fusi
8	572	98.6	432	AA1987	CD4-gamma2 chimeri
9	572	98.6	432	AA1988	CD4-gamma 2 chim
10	572	98.6	432	AA1989	Human CD4-gamma 2
11	572	98.6	432	AA1990	Human CD4-gamma2 c

12	572	98.6	432	AA1991	CD4-gamma2 chimeri
13	572	98.6	442	AA1992	Human IgG2 chain C
14	572	98.6	443	AA1993	The heavy chain of
15	572	98.6	451	AA1994	Humanised 323/A3 (
16	572	98.6	461	AA1995	The heavy chain of
17	572	98.6	462	AA1996	Human immunoglobul
18	572	98.6	463	AA1997	The heavy chain of
19	572	98.6	463	AA1998	The heavy chain of
20	572	98.6	463	AA1999	The heavy chain of
21	572	98.6	463	AA2000	The heavy chain of
22	572	98.6	464	AA2001	The heavy chain of
23	572	98.6	464	AA2002	The heavy chain of
24	572	98.6	530	AA2003	CD4-IgG2 chimeric
25	572	98.6	530	AA2004	CD4-IgG2 chimeric
26	572	98.6	530	AA2005	Human CD4-IgG2 chl
27	572	98.6	530	AA2006	CD4-IgG2 chimeric
28	572	98.6	530	AA2007	Heavy chain of ful
29	569	98.1	450	AA2008	Human IgG2 huh52 h
30	569	98.1	450	AA2009	CD4-IgG2 chimeric
31	569	98.1	552	AA2010	PH52-8.0 humanised
32	566	97.6	463	AA2011	The heavy chain of
33	563	97.1	643	AA2012	A33 chimeric recep
34	563	97.1	643	AA2013	233G2G237A2 chim
35	562	96.9	109	AA2014	Mutated-CH2 sequen
36	562	96.9	326	AA2015	Heavy chain consta
37	561	96.7	462	AA2016	2A2 (Chimeric) hum
38	561	96.7	462	AA2017	2A2 (Chimeric) hum
39	561	96.7	463	AA2018	3F4 (Chimeric) hum
40	561	96.7	463	AA2019	3F4 (Chimeric) hum
41	540	93.2	110	AA2020	Mutated CH2 sequen
42	539	92.9	447	AA2021	TF8-5G9 CDR-grafte
43	536	92.4	109	AA2022	OKT3 monoclonal an
44	536	92.4	110	AA2023	Undefined ORF2 enc
45	536	92.4	218	AA2024	Amino acid sequenc

ALIGNMENTS

RESULT 1
AA1980
ID AA1980 standard; Protein; 109 AA.
XX
AC
AA1980;
XX
DT 20-OCT-1993 (first entry)
XX
DE Undefined ORF2 encoded by plasmid pAH4625.
XX
KW Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625;
KW heavy; light; chain; variable; constant; region; anti-human; pAH4807;
KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
KW endothelial cell; conjugate; neuropharmacological; gamma-3; gamma-4;
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
KW Parkinsons disease; Alzheimers disease; Sp2/0 cell.
XX
OS Synthetic.
XX
PN WO9310819-A.
XX
PD 10-JUN-1993.
XX
PF 24-NOV-1992; 92WO-US10206.
XX
PR 26-NOV-1991; 91US-0800458.
XX
PA (ALKE-) ALKERMES INC.
XX
PI Friden PW;
XX
DR WPI; 1993-196742/24.
DR N-PSDB; AAQ43846.
XX

PT Antibody conjugates specific for transferrin receptor - used
 PT for diagnosis and treatment of cancer, AIDS and neurological
 PT disorders

XX Disclosure; Fig 17J; 151pp; English.

XX The sequences given in ARA41707-09 are encoded by the expression vector
 CC PAH4625. This vector represents the cloning of the human gamma
 CC isotype, gamma-2, with the variable region of the murine monoclonal
 CC antibody 128.1. This plasmid encodes a chimeric monoclonal antibody
 CC in which the heavy chain (VH) is derived from a murine source and the
 CC sequences encoding CH1, CH2 and CH3 are derived from a human source.
 CC This vector, in combination with the chimeric light chain vector,
 CC PAG4611 (see also AAQ43845), was transfected into SP2/0 cells and clones
 CC were isolated. 128.1 is an anti-human transferrin receptor antibody
 CC which binds to the transferrin receptor on brain capillary endothelial
 CC cells. This antibody may be used in a conjugate in which it is linked
 CC to a neuropharmaceutical or diagnostic agent. The conjugate may be
 CC used to treat or prevent neurological disorders eg. brain tumours,
 CC AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may
 CC also be used for diagnostic methods.

XX Sequence 109 AA;

Query Match 98.6%; Score 572; DB 14; Length 109;
 Best Local Similarity 98.2%; Pred. No. 1e-51;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYDGVVHNATKTP 60
 Db 1 appvagsvflfpkpkdtlmisrtpetvctcvvdshdpevqfnwydvghvhnatktp 60

QY 61 REEQFNSTFRVSVLTVVHODWLNKGYCKVSNKGLPSSIEKTISKTK 109
 Db 61 reeqfnstfrvsvltvvhqdwlngkyckvsnkglpapiektisktk 109

RESULT 2

ID AAY54997 standard; protein; 109 AA.

XX AAY54997;

DT 17-FEB-2000 (first entry)

DE Mutated CH2 sequence G2delta.

XX Binding molecule; CH2 sequence; complement dependent lysis; Fc gammaRIIb;
 KW cell-mediated destruction; human; immunoglobulin G; IgG heavy chain;
 KW B cell activation; mast cell degranulation; phagocytosis; vasculitis;
 KW Crohn's disease; graft-vs-host disease; organ transplant rejection;
 KW bone-marrow transplant rejection; autoimmune disease; asthma; allergy;
 KW autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease;
 KW autoallimmune thrombocytopenia; arthritis; erythroblastosis foetalis;
 KW neonatal alloimmune thrombocytopenia; Goodpastures disease; therapy;
 KW sickle cell anaemia; coronary artery occlusion.

XX Synthetic.

XX WO9558572-A1.

PN 18-NOV-1999.

PD 07-MAY-1999; 99WO-GB01441.

XX 08-MAY-1998; 98GB-0009951.

XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX Arm&ur KL, Clark MR, Williamson IM;

PI WPI; 2000-039075/03.

DR

XX

PT Immunoglobulin-derived binding molecules that do not activate
 PT complement or trigger cytotoxic activities and maintaining desirable
 PT immunoglobulin properties -

XX Claim 12; Fig 17; 81pp; English.

XX

XX This sequence represents the mutated CH2 molecule G2delta, and is a
 CC binding molecule of the invention. The recombinant binding molecule
 CC is capable of binding a target molecule without triggering complement
 CC dependent lysis, or the cell-mediated destruction of the target
 CC comprises: (a) a binding domain capable of binding a target molecule; and
 CC (b) an effector domain that is homologous to all or part of a constant
 CC domain of a human immunoglobulin G (IgG) heavy chain. The binding
 CC molecule is used to bind a target molecule (especially Fc gammaRIIb
 CC causing inhibition of B cell activation, mast cell degranulation or
 CC phagocytosis). The binding molecule can be used to prevent or inhibit the
 CC binding of a second binding molecule, e.g. an antibody, to the target
 CC molecule. The binding molecule is useful for the treatment of
 CC graft-vs-host disease, organ transplant rejection, bone-marrow transplant
 CC rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia,
 CC autoallimmune thrombocytopenia and arthritis), alloimmunity
 CC (e.g. foetal/neonatal alloimmune thrombocytopenia, asthma and allergy),
 CC chronic or acute inflammatory diseases (e.g. Crohn's, HDN
 CC (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and
 CC coronary artery occlusion). The binding molecules do not activate
 CC complement or trigger cytotoxic activities through Fc gammaR and desirable
 CC IgG properties have been retained. The polypeptides do not contain
 CC non-human amino acids, and are therefore likely to have reduced
 CC immunogenicity. Further, they still bind Protein A, which is consistent
 CC with being able to cross the human placenta through interaction with FcRn
 CC (neonatal Fc receptor).

XX Sequence 109 AA;

Query Match 98.6%; Score 572; DB 21; Length 109;
 Best Local Similarity 99.1%; Pred. No. 1e-51;
 Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYDGVVHNATKTP 60

Db 1 appvagsvflfpkpkdtlmisrtpetvctcvvdshdpevqfnwydvghvhnatktp 60

QY 61 REEQFNSTFRVSVLTVVHODWLNKGYCKVSNKGLPSSIEKTISKTK 109

Db 61 reeqfnstfrvsvltvvhqdwlngkyckvsnkglpapiektisktk 109

RESULT 3

AAB07476

ID AAB07476 standard; protein; 217 AA.

XX AAB07476;

XX 20-OCT-2000 (first entry)

XX Amino acid sequence of native IgG Fc region humIgG2.

XX IgG antibody; light chain; Fc region; effector function; cancer;
 KW allergy; asthma; IFA-I-mediated disorder; tumour; cancer.

XX Homo sapiens.

XX WO200042072-A2.

XX 20-JUL-2000.

XX 14-JAN-2000; 2000WO-US00973.

XX 15-JAN-1999; 99US-0116023.

XX (GETH) GENENTECH INC.

Sequence 217 AA:

RESULT

(GETH) GENENTECH INC.

This invention relates to non-naturally occurring peptide ligands which bind to the human ErbB2 gene product ErbB2 (also known as HER2). Peptides represented in AAB76350 - AAB76420 and AAB76432 - AAB76509 are examples of the ErbB2 binding ligands of the invention. Sequences AAB76421 - AAB76431 represent antibody FC amino acid sequences used in the isolation of the peptides of the invention. The peptides compete for

CC binding ErbB2 with naturally occurring ligands, and may be used to treat
 CC disorders characterized by over expression of HER2/ErbB2 such as cancers,
 CC diseases of the nervous system, musculature and epithelia, e.g. nervous
 CC system damage resulting from trauma, surgery, strokes, ischaemia,
 CC infection, metabolic disorders, nutritional deficiency or toxic agents.
 CC In particular the synthetic peptide ligands may be used to treat
 CC Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis,
 CC Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease
 CC and neuropathy associated with diabetes.
 XX Sequence 217 AA;

Query Match 98.6%; Score 572; DB 22; Length 217;
 Best Local Similarity 98.2%; Pred. No. 2.4e-51;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 APPVAGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTKP 60
 Db 2 appvagsvflfpkpkdtlmisrtpevtcvvvdvshedpevqfnwvdygvevhnaktkp 61
 QY 61 REEQFNSTRFVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
 Db 62 reeqfnstrfvsvltvvhqdnlngkeyckvsnkglpapiextisktk 110

RESULT 6
 AA02643
 ID AA02643 standard; Protein; 326 AA.
 XX
 AC AA02643;
 XX
 DT 06-AUG-2001 (first entry)
 XX
 DE Human immunoglobulin G2 constant region mature protein.
 XX
 KW Human; erythropoietin; EPO; antianaemic; nephrotrophic; anti-HIV;
 KW vaccine; haemostatic; immunoglobulin G2; IgG2; EPO deficient disease;
 KW anaemia; renal failure; Human Immunodeficiency Virus; HIV;
 KW haematopoietic growth factor.
 XX
 OS Homo sapiens.
 XX
 PN WO200136489-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-EPI0843.
 XX
 PR 12-NOV-1999; 99US-0164855.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Hartmann A, Brandt S, Rieke E, Sobel C, Lo K, Way JC, Gillies S;
 XX
 DR WPI; 2001-367563/38.
 XX
 PT Novel modified erythropoietin forms such as fusion proteins, comprising
 PT Fc portion of an immunoglobulin molecule and a target molecule having
 PT the biological activity of erythropoietin forms
 XX
 PS Example 1; Page 24; 58pp; English.
 XX

CC The present sequence is human immunoglobulin G2 (IgG2) constant region
 CC mature protein. IgG2 forms a fusion protein with human erythropoietin
 CC (EPO). EPO has improved biological activity and an extended serum half
 CC life greater than 20 hours. The present invention relates to modified
 CC EPO forms such as fusion proteins comprising a Fc portion of an
 CC immunoglobulin (Ig) molecule and an EPO molecule (Fc-EPO). The Fc portion
 CC is fused covalently through its C-terminus directly or indirectly to the
 CC EPO molecule, and where the Fc portion as well as EPO portion may be
 CC modified or mutated. The invention also relates to non-fused EPO
 CC molecules which have a pattern of cysteines or disulphide bonding which

CC is distinct from human or animal EPO. Pharmaceutical compositions
 CC containing EPO are useful in the treatment of EPO deficient diseases such
 CC as anaemia, renal failure, HIV infection, blood loss and chronic disease
 CC that can be treated with haematopoietic growth factor.
 XX Sequence 326 AA;

Query Match 98.6%; Score 572; DB 22; Length 326;
 Best Local Similarity 98.2%; Pred. No. 3.9e-51;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 APPVAGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTKP 60
 Db 111 appvagsvflfpkpkdtlmisrtpevtcvvvdvshedpevqfnwvdygvevhnaktkp 170
 QY 61 REEQFNSTRFVSVLTVVHQDNLNGKEYCKVSNKGLPSSIEKTIKTK 109
 Db 171 reeqfnstrfvsvltvvhqdnlngkeyckvsnkglpapiextisktk 219

RESULT 7
 AA06895
 ID AA06895 standard; Protein; 381 AA.
 XX
 AC AA06895;
 XX
 DT 01-JUL-1999 (first entry)
 XX
 DE Human IL-2/Ig fusion protein.
 XX
 KW Fusion protein; vaccine; cytokine; immunoglobulin; autoimmune disease;
 KW infectious disease; inflammatory disease; neoplastic disease; cancer;
 KW immunologic disease; immune response; malaria; tuberculosis; hepatitis;
 KW AIDS; influenza; interleukin; IL-2; Ig; human.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Protein 1..153
 FT /note= "interleukin-2 (IL-2)"
 FT 154..381
 FT /note= "immunoglobulin G"
 XX
 PN WO9916466-A2.
 XX
 PD 08-APR-1999.
 XX
 PF 29-SEP-1998; 98WO-US20321.
 XX
 PR 12-DEC-1997; 97US-0990180.
 PR 29-SEP-1997; 97US-0060338.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX
 PI Barouch DH, Letvin NL;
 XX
 DR WPI; 1999-254931/21.
 DR N-PSDB; AAX34598.
 XX
 PT New vaccine compositions
 XX
 PS Claim 16; Fig 10A-E; 66pp; English.

CC The invention relates to vaccine compositions comprising a vaccine and a
 CC timed-release formulation of a cytokine or cytokine/immunoglobulin fusion
 CC protein or plasmid. The formulation or device releases the cytokine
 CC protein or plasmid at one or more temporal points subsequent to vaccine
 CC administration. The vaccines can be used for treating an autoimmune
 CC disease, an infectious disease, an inflammatory disease, a neoplastic
 CC disease, or an immunologic disease in an individual. The vaccines can be
 CC used to elicit immune responses against diseases such as AIDS, malaria,
 CC tuberculosis, hepatitis C, hepatitis B, cancer or influenza. The methods

CC can provide for enhancement of one or more immunologic parameters such as
 CC an antibody response, a cellular proliferative response as well as
 CC cytotoxic T-lymphocyte levels. In addition the Ig can increase the
 CC circulating half life of the cytokine. The present sequence represents
 CC a human interleukin-2 (IL-2)/Ig fusion protein.

XX
 SQ Sequence 381 AA;

Query Match 98.6%; Score 572; DB 20; Length 381;
 Best Local Similarity 98.2%; Pred. No. 4.7e-51;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDKDILMSRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTKP 60
 |||||
 Db 166 appvagsvflppkpkdklmsrtpevtcvcvvdvshedpevfqfnwydvgevhnaaktkp 225

QY 61 REQFNSTFRVSVLVVHVDLWNGKEYCKVSNKGLPSSIEKTIKTK 109
 |||||

Db 226 reeqfnstfrvsvlvvhqdwlngkeyckvsnkglpapiektisktk 274

RESULT 8

AAR26782
 ID AAR26782 standard; Protein; 432 AA.

XX AC AAR26782;

XX DT 06-FEB-1993 (first entry)

XX DE CD4-gamma2 chimeric heavy chain homodimer.

XX KW homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;
 KW chimeric; increased serum half life; HIV infection; AIDS; ss.

XX OS Homo sapiens chimeric.

XX FH Key Location/Qualifiers

FT Domain 1..216

FT /label= CD4

FT Domain 217..325

FT /label= CH2

FT Domain 326..433

FT /label= CH3

XX W09213947-A.

XX 20-AUG-1992.

XX 10-FEB-1992; 92WO-US01143.

XX 08-FEB-1991; 91US-0653684.

XX (PROG-) PROGENICS PHARM INC.

XX Beaudry GA, Maddon PJ;

XX WPI; 1992-300034/36.

XX N-PSDB; AAQ28088.

XX CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for
 PT treatment, prevention and diagnosis of HIV infection

XX Claim 2; Fig 3; 90pp; English.

XX This sequence represents a CD4-gamma2 chimeric heavy chain homodimer.
 CC It was produced by expression of the coding mutagenised cDNA
 CC (produced as described in AAQ28088) in Dnfr-CHO cells. The protein is
 CC efficiently assembled intracellularly and effectively secreted from
 CC mammalian cells pref. CHO, COS, or myeloma cells as a homodimer,
 CC enabling high recovery and purification from the medium of cells
 CC expressing it. It possesses increased serum half-life and has increased
 CC avidity for HIV cf. heavy chain dimers. It can inhibit HIV infection of

CC CD4+ cells and block the spread of HIV infection within a patient.
 CC Attachment to a detectable marker makes it useful in an assay for HIV
 CC or HIV infection, and it can also be linked to toxins, eg Diphtheria,
 CC Pseudomonas exotoxin A (domains I or II) or the deglycosylated A-chain
 CC of ricin.

XX SQ Sequence 432 AA;

Query Match 98.6%; Score 572; DB 13; Length 432;
 Best Local Similarity 98.2%; Pred. No. 5.5e-51;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDKDILMSRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTKP 60
 |||||
 Db 217 appvagsvflppkpkdklmsrtpevtcvcvvdvshedpevfqfnwydvgevhnaaktkp 276

QY 61 REQFNSTFRVSVLVVHVDLWNGKEYCKVSNKGLPSSIEKTIKTK 109
 |||||

Db 277 reeqfnstfrvsvlvvhqdwlngkeyckvsnkglpapiektisktk 325

RESULT 9

AAR46678
 ID AAR46678 standard; Protein; 432 AA.

XX AC AAR46678;

XX DT 08-AUG-1994 (first entry)

XX DE CD4-gamma 2 chimeric heavy chain.

XX KW CD4; gamma; heavy chain; chimeric; chimaeric; immunconjugate; HIV;
 KW human immunodeficiency virus; radionuclide; toxin; therapy;
 KW treatment; imaging; detection; targeting.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 1..204

FT /label= CD4 Region.

FT Region 205..216

FT /label= Hinge Region.

FT Region 217..325

FT /label= CH2 Region.

FT Region 326..432

FT /label= CH3 Region.

XX W09403191-A.

XX 17-FEB-1994.

XX 06-AUG-1993; 93WO-US07422.

XX 07-AUG-1992; 92US-0927931.

XX (PROG-) PROGENICS PHARM INC.

XX Allaway GP, Maddon PJ;

XX WPI; 1994-065392/08.

XX N-PSDB; AAQ57750.

XX Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2
 PT immunoconjugates - used to kill HIV-infected cells and to image
 PT and stage HIV infection

XX Disclosure; Figure 3; 142pp; English.

XX A CD4-gamma 2 chimeric heavy chain homodimer is linked to a non-
 CC peptidyl toxin or a gamma radiation-emitting radionuclide of low to
 CC moderate cytotoxicity. The resulting immunoconjugate comprising the
 CC toxin can be used to kill HIV infected cells and to treat HIV

CC infected subjects to reduce the population of HIV infected cells.
CC It can also be used to reduce the likelihood of infection. The
CC immunoconjugate comprising the radionuclide can be used to image HIV
CC infected tissue, to calculate the stage of HIV infection or the
CC efficacy of an anti-HIV treatment using the imaging technique and
CC for determining the prognosis of an HIV infected subject.
XX
SQ Sequence 432 AA;

Query Match 98.6%; Score 572; DB 15; Length 432;
Best Local Similarity 98.2%; Pred. No. 5.5e-51;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
Db 217 appvagsvflfppkpkdtlmisrtpevtcvvvdvshedpevqfnwvydgvvghnaktkp 276
|||||
QY 61 REEQFNSTFRVSVLTWVHODWLNKGYCKVSNKGLPSSIEKTIKTK 109
Db 277 reeqfnstfrvsvltwvhodwlngkyckvsnkglpaplektisktk 325
|||||

RESULT 10
AAY85079
ID AAY85079 standard; Protein; 432 AA.
XX AAY85079;
AC AAY85079;
XX
XX 19-JUN-2000 (first entry)
XX Human CD4-gamma 2 chimeric heavy chain homodimer amino acid sequence.
XX
XX CD4-gamma 2 chimeric heavy chain homodimer; immunoconjugate: treatment;
KW cytotoxic radionuclide; cell surface glycoprotein; prevent; infection;
KW cellular immune response interaction mediator; HIV interaction;
KW staging; prognosis; envelope glycoprotein burden; human.
XX
XX Homo sapiens.
XX
XX US6034223-A.
XX
XX 07-MAR-2000.
XX
XX 07-JUN-1995; 95US-0477460.
XX
XX 07-AUG-1992; 92US-0927931.
PR 06-AUG-1993; 93WO-US07422.
PR 03-FEB-1995; 95US-0379516.
XX
XX (PROG-) PROGENICS PHARM INC.
XX
XX Allaway GP, Maddon PJ;
XX
XX WPI; 2000-269502/23.
DR N-PSDB; AAZ98855.
XX
XX New immunoconjugate, used to treat, prevent or image human immune
PT deficiency virus infection, comprises radionuclide attached to
PT heterotetramer of CD4-immunoglobulin chimeras -
XX
XX Disclosure; Fig 3; 58pp; English.
XX
XX This sequence represents the human CD4-gamma 2 chimeric heavy chain
CC homodimer amino acid sequence. The invention relates to an
CC immunoconjugate comprising a cytotoxic radionuclide and a heterotetramer
CC of two heavy chains and two light chains. The cytotoxic radionuclide is
CC linked to either the heavy chains or the light chains, or to all four
CC chains, directly or through a bifunctional chelator. Both heavy chains
CC are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by vector
CC CD4<lg2HC-prcCMV (ATCC 75193) and both light chains are chimeric
CC CD4<lg2HC-prcCMV (ATCC 75193) and both light chains are chimeric
CC CD4<lg2HC-prcCMV (ATCC 75193) and both light chains are chimeric
CC non-polymorphic cell surface glycoprotein that is expressed on the

CC surface of helper T lymphocytes, cells of the monocyte/macrophage lineage
CC and dendritic cells. CD4 associates with major histocompatibility complex
CC (MHC) class II molecules on the surface of antigen presenting cells to
CC mediate efficient cellular immune response interactions. In humans CD4 is
CC the target of interaction with the human immunodeficiency virus HIV. The
CC immunoconjugate is used to kill cells infected with HIV, and for treating
CC or preventing infection. It is also used for imaging HIV-infected tissues
CC (for staging or prognosis of infection, and for assessing efficacy of
CC treatments). The immunoconjugate is also used to determine the HIV
CC envelope glycoprotein burden, once determined, this information is used
CC in the staging and prognosis of HIV infected patients. The
CC immunoconjugate should be active against all strains of HIV (since the
CC CD4-gp120 interaction is essential for infection). The heterotetramers
CC are assembled intracellularly and secreted efficiently from mammalian
CC cells, allowing high recovery and purification from the culture medium.
CC They have longer half-life in serum and greater avidity than heavy chain
CC dimers.
XX
SQ Sequence 432 AA;

Query Match 98.6%; Score 572; DB 21; Length 432;
Best Local Similarity 98.2%; Pred. No. 5.5e-51;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
Db 217 appvagsvflfppkpkdtlmisrtpevtcvvvdvshedpevqfnwvydgvvghnaktkp 276
|||||
QY 61 REEQFNSTFRVSVLTWVHODWLNKGYCKVSNKGLPSSIEKTIKTK 109
Db 277 reeqfnstfrvsvltwvhodwlngkyckvsnkglpaplektisktk 325
|||||

RESULT 11
AAB80883
ID AAB80883 standard; Protein; 432 AA.
XX AAB80883;
XX
XX 29-MAY-2001 (first entry)
XX Human CD4-gamma2 chimeric heavy chain homodimer.
XX
XX Human; Anti-HIV; CD4-IgG2 chimeric heterotetramer;
KW immunoglobulin gamma 2.
XX
XX Homo sapiens.
XX
XX US6187748-B1.
XX
XX 13-FEB-2001.
XX
XX 07-JUN-1995; 95US-0485372.
XX
XX 08-FEB-1991; 91US-0653684.
PR 10-FEB-1992; 92WO-US01143.
PR 08-DEC-1992; 92US-0960440.
XX
XX (PROG-) PROGENICS PHARM INC.
XX
XX Maddon PJ, Beaudry GA;
XX
XX WPI; 2001-264981/27.
DR N-PSDB; AAF77829.
XX
XX Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell,
PT or treating a subject having CD4+ cells infected with HIV involves
PT using CD4-IgG2 chimeric heterotetramer to form a complex with the HIV -
XX
XX Disclosure; Fig 3; 55pp; English.
XX
XX The present invention relates to a method for inhibiting infection of a

XX SQ Sequence 442 AA; Query Match 98.6%; Score 572; DB 22; Length 442; Best Local Similarity 98.2%; Pred. No. 5.7e-51; Mismatches 1; Indels 0; Gaps 0; Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDITLMSRPEVTCVVVDVSHEDPEVFQFNWYGVGVEVHNATKP 60
Db 227 appvagsvflpppkdtlmsrptevtcvvdvshdpevfqfnwgydgvvhnatkcp 286
QY 61 REEQRNSTRFRVSVLTVVHODWLNKGYCKVSNKGLPSSIEKTISKTK 109
Db 287 reeqfnstrfrvsvltvvhqdwlngkyckvsnkglpapiektskck 335

RESULT 14
AA31670
ID AAY31670 standard; Protein; 443 AA.
XX AC AAY31670;
XX 09-NOV-1999 (first entry)
XX Human IgG2 chain C.
XX IgG2; C-gamma-2; antibody; fusion protein; circulating half-life;
KW human; drug delivery.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Misc-difference 1..117 "the identity of these residues is not specified"
FT
XX WO9943713-A1.
XX 02-SEP-1999.
XX 24-FEB-1999; 99WO-US03966.
XX 25-FEB-1998; 98US-0075887.
XX (LEXI-) LEXIGEN PHARM CORP.
XX Gillies SD, Lan Y, Lo K, Wesolowski J;
XX WPI; 1999-527594/44.
XX New antibody-based fusion proteins, used for the delivery of e.g. a cytokine, ligand-binding protein or protein toxin to target cells in vivo
XX Disclosure; Page 32-33; 41pp; English.

XX The present sequence represents the constant region of human IgG isotype 2 (IgG2, C-gamma-2). C-gamma-1 (see AAY31669) and C-gamma-3 (see AAY31671) bind Fc receptors with high affinity, whereas C-gamma-4 (see AAY31672) has 10-fold lower binding affinity and C-gamma-2 does not bind to Fc receptor gamma-1. The invention provides methods for the genetic construction and expression of antibody-based fusion proteins with enhanced circulating half-lives. The fusion proteins lack the ability to bind to immunoglobulin Fc receptors, either as a consequence of the antibody isotype used for protein construction, i.e. a C-gamma-2 constant region (Fc) or a C-gamma-4 Fc receptor, or through directed mutagenesis of antibody isotypes that normally bind Fc receptors, i.e. C-gamma-1 or C-gamma-3. The methods can be used for to increase the circulating half-life of a non-immunoglobulin (Ig) protein such as a cytokine, e.g. tumour necrosis factor (TNF), an interleukin or a lymphokine such as a lymphotoxin or a colony stimulating factor, a

CC ligand-binding protein, e.g. CD4, CTLA-4, TNF receptor or an interleukin receptor, or a protein toxin (claimed). The fusion proteins are used to deliver selectively the second non-Ig protein to a target cell in vivo so that the second non-Ig protein can exert a localised biological effect.

XX SQ Sequence 443 AA; Query Match 98.6%; Score 572; DB 20; Length 443; Best Local Similarity 98.2%; Pred. No. 5.7e-51; Mismatches 1; Indels 0; Gaps 0; Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDITLMSRPEVTCVVVDVSHEDPEVFQFNWYGVGVEVHNATKP 60
Db 228 appvagsvflpppkdtlmsrptevtcvvdvshdpevfqfnwgydgvvhnatkcp 287
QY 61 REEQRNSTRFRVSVLTVVHODWLNKGYCKVSNKGLPSSIEKTISKTK 109
Db 288 reeqfnstrfrvsvltvvhqdwlngkyckvsnkglpapiektskck 336

RESULT 15
AA31670
ID AAY93734 standard; Protein; 451 AA.
XX AC AAY93734;
XX 03-OCT-2000 (first entry)
XX The heavy chain of immunoglobulin clone 11.2.1.
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection; proliferative disorder; cancer; immunodeficient disorder.
XX Homo sapiens.
XX WO200037504-A2.
XX 29-JUN-2000.
XX 23-DEC-1999; 99WO-US030895.
XX 23-DEC-1998; 98US-0113647.
XX (PFIZ) PFIZER INC.
XX (ABGE-) ABGENIX INC.
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG; Corvalan JR;
XX WPI; 2000-442647/38.
XX N-PSDB; AAA46898.
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)-4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders -
XX Claim 2; Fig 22q; 157pp; English.

XX The present sequence represents a heavy chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)-4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a Fc1-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immunodeficient disorders.

SQ Sequence 451 AA;

Query Match 98.6%; Score 572; DB 21; Length 451;
 Best Local Similarity 98.2%; Pred. No. 5.8e-51;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPPKPKDTLMISRTPETVCVVVDYSHEDPEVQFNWYVDGVEVHNAKTKP 60
 Db 236 appvagsvflfppkpkdtlmisrtpetvcvvdvshedpevgfnwydgvevhnaktkp 295
 QY 61 REEQFNSTFRVSVLTVVHODWLNKGKCKVSNKGLPSSIEKTIKTK 109
 Db 296 reeqfnstfrvsvltvvhqdwlngkckvsnkglpapektisktk 344

Search completed: June 21, 2002, 08:36:05
 Job time: 319 sec

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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:37:54 ; Search time 102.05 Seconds
(without alignments)
103.575 Million cell updates/sec

Title: US-09-674-857-6
Perfect score: 585
Sequence: 1 APELLGSPVFLFPKPDKT.....CKVSNKALPAPIETISKT 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	585	100.0	377	2 A60764	Ig gamma-3 chain C
2	585	100.0	377	2 A23511	Ig gamma-3 chain C
3	568	97.1	234	2 PT0207	Ig gamma chain C r
4	568	97.1	255	4 S31866	Ig gamma-1 chain C
5	568	97.1	330	1 GHU	Ig gamma-1 chain C
6	568	97.1	374	2 S69339	Ig heavy chain V r
7	565	96.6	289	1 G3H0W1	Ig gamma-3 heavy c
8	541	92.5	327	1 G4HU	Ig gamma-4 chain C
9	540	92.3	326	1 G2HU	Ig gamma-2 chain C
10	463	79.1	328	2 I47160	Ig gamma 2b chain
11	463	79.1	328	2 I47159	Ig gamma 2a chain
12	460	78.6	333	2 PS0018	Ig gamma-2b chain
13	458	78.3	277	2 I47162	Ig gamma 4 chain C
14	458	78.3	329	1 G2GP	Ig gamma-2 chain C
15	454	77.6	308	2 C30554	Ig heavy chain C r
16	454	77.6	472	2 S31459	Ig gamma-1 chain -
17	450	76.9	323	1 GHRB	Ig gamma chain C r
18	448	76.6	470	2 S22080	Ig heavy chain pre
19	440	75.2	328	2 I47161	Ig gamma 3 chain c
20	440	75.2	328	2 I47158	Ig gamma 1 chain c
21	437	74.7	329	1 G3MSC	Ig gamma-3 chain C
22	437	74.7	398	1 G3MSM	Ig gamma-3 chain C
23	422.5	72.2	324	1 GLMS	Ig gamma-1 chain C
24	422.5	72.2	393	1 GLMSM	Ig gamma-1 chain C
25	422.5	72.2	444	2 PC4436	monoclonal antibod
26	418	71.5	335	1 G2MSAB	Ig gamma-2a chain
27	415	70.9	330	1 G2MSA	Ig gamma-2a chain
28	415	70.9	399	1 G2MSAM	Ig gamma-2a chain
29	415	70.9	469	2 S37483	Ig gamma-2a chain

Ig gamma-2c chain
Ig gamma-2b chain
Ig gamma-2b chain
Ig gamma-2a chain
Ig gamma-2 chain C
Ig gamma-2b chain
Ig gamma-1 chain C
Ig gamma-2a chain
Ig gamma-2b chain
Ig gamma-2b chain
Ig gamma heavy cha
Ig gamma-1 chain C
Ig epsilon chain -
Ig epsilon chain C
Ig heavy chain pre
Ig epsilon chain C

ALIGNMENTS

RESULT 1

A60764

Ig gamma-3 chain C region, form LAT - human

C:Species: Homo sapiens (man)

C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999

C:Accession: A60764

R:Huck, S.; Lefranc, G.; Lefranc, M.P.

Immunogenetics 30, 250-257, 1989

A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conv

A:Reference number: A60764; MUID:90007613

A:Accession: A60764

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-377 <HUC>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 585; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 9.5e-52;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APELLGSPVFLFPKPDKTLMISRTPEVTCVVVDVSHEDPEVFQKWDGVEVHNATK 60

Db 161 APELLGSPVFLFPKPDKTLMISRTPEVTCVVVDVSHEDPEVFQKWDGVEVHNATK 220

QY 61 PREOYNSTRVSVLTVLHODWLNKREYCKVSNKALPAPIETISKT 110

Db 221 PREOYNSTRVSVLTVLHODWLNKREYCKVSNKALPAPIETISKT 270

RESULT 2

A23511

Ig gamma-3 chain C region (allotype G3m(b)) - human

C:Species: Homo sapiens (man)

C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999

C:Accession: A23511

R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.

Nucleic Acids Res. 14, 1779-1789, 1986

A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:

A:Reference number: A23511; MUID:86148507

A:Accession: A23511

A:Molecule type: DNA

A:Residues: 1-377 <HUC>

A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056

C:Genetics:

A:Gene: GDB:IGHG3

A:Cross-references: GDB:119339; OMIM:147120

A:Map position: 14q32.33-14q32.33

A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 585; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 9.5e-52;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFQWYVDGVEVHNAKTK 60
GHHU
Db 161 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFQWYVDGVEVHNAKTK 220
Qy 61 PREQYNSTFRVSVLTVLHODWLNKGKEYCKVSNKALPAPIETISKTK 110
Db 221 PREQYNSTFRVSVLTVLHODWLNKGKEYCKVSNKALPAPIETISKTK 270

RESULT 3
PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
Mol. Immunol. 28, 319-322, 1991
R:Enrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <ERR>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>

Query Match 97.1%; Score 568; DB 2; Length 234;
Best Local Similarity 96.4%; Pred. No. 2.9e-50;
Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFQWYVDGVEVHNAKTK 60
Db 25 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFQWYVDGVEVHNAKTK 84
Qy 61 PREQYNSTFRVSVLTVLHODWLNKGKEYCKVSNKALPAPIETISKTK 110
Db 85 PREQYNSTFRVSVLTVLHODWLNKGKEYCKVSNKALPAPIETISKAK 134

RESULT 4
S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filpula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products.
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FIL>
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

Query Match 97.1%; Score 568; DB 4; Length 255;
Best Local Similarity 96.4%; Pred. No. 3.2e-50;
Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFQWYVDGVEVHNAKTK 60

Db 39 APELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFQWYVDGVEVHNAKTK 98

Qy 61 PREQYNSTFRVSVLTVLHODWLNKGKEYCKVSNKALPAPIETISKTK 110
Db 99 PREQYNSTFRVSVLTVLHODWLNKGKEYCKVSNKALPAPIETISKAK 148

RESULT 5
GHHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C:Accession: A93433; S33861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: EMBL:Z17370
A:Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) marker
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A:Reference number: S33887; MUID:83001943
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:Cross-references: EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A:Reference number: A90563; MUID:71064024
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-135 <CUN>
A:Note: this sequence has the Gln(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A:Reference number: A90564; MUID:71064025
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154, 'Q', 156-165, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2
A:Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein N1
igen Primaerstruktur.
A:Reference number: A91668; MUID:77070269
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E'
A:Note: this sequence has the Gln(17) and Gln(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723

A:Molecule type: protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'W', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A>Note: this sequence has the Gln(3) and Gln(non-1) markers
R:Call, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A:Reference number: A90565; MUID:71064027
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-204,250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 97.1%; Score 568; DB 1; Length 330;
Best Local Similarity 96.4%; Pred. No. 4.3e-50;
Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVQFKWYDGVGVHNAKTK 60
|||||
Db 114 APELLGGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVQFKWYDGVGVHNAKTK 173

QY 61 PREEQNSTYRVSVTLVHQLDMLNGKEYKCKVSNKALPAPIETTSKTK 110
|||||
Db 174 PREEQNSTYRVSVTLVHQLDMLNGKEYKCKVSNKALPAPIETTSKAK 223

RESULT 6
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687
A:Accession: S69339
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamilichi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVQFKWYDGVGVHNAKTK 60
|||||
Db 158 APELLGGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVQFKWYDGVGVHNAKTK 217

QY 61 PREEQNSTYRVSVTLVHQLDMLNGKEYKCKVSNKALPAPIETTSKTK 110
|||||
Db 218 PREEQNSTYRVSVTLVHQLDMLNGKEYKCKVSNKALPAPIETTSKAK 267

RESULT 7
G3HUW1
Ig gamma-3 heavy chain disease proteins - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C:Accession: A90442; A92219; A90198; A93915; A02149
R:Frangione, B.; Rosenwasser, E.; Prellli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 hea
A:Reference number: A90442; MUID:81021548
A:Contents: heavy chain disease protein W1s
A:Accession: A90442
A:Molecule type: protein
A:Residues: 1-289 <FRA>
A>Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch
A>Note: this protein lacks most of the V region and all of the CH1 region. Residue 12
A>Note: the sequence of residues 42-76 was taken from the reference that follows
R:Michaelson, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplicat
A:Reference number: A92219; MUID:77118561
A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protei
A:Accession: A92219
A:Molecule type: protein
A:Residues: 12-97 <MIC>
A>Note: the hinge region in gamma-3 chains is about four times as long as in other ga
idue segment (12-28)
R:Wolfeinstein-Tudel, C.; Frangione, B.; Prellli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of t
A:Reference number: A90198; MUID:77021516
A:Contents: heavy chain disease protein Zuc, partial sequence corresponding to residu
A:Accession: A90198
A:Molecule type: protein
A:Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A>Note: this protein lacks most of the V region, all of the CH1 region, and part of t
R:Alexander, A.; Steinmetz, M.; Bartitault, D.; Frangione, B.; Franklin, E.C.; Hood,
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A:Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deleti
A:Reference number: A93915; MUID:82247835
A:Contents: heavy chain disease protein Omn
A:Accession: A93915
A:Molecule type: mRNA
A:Residues: 12-70, 72-114, 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-
A>Note: a carboxyl-terminal Lys is removed posttranslationally
A>Note: this sequence may represent an allelic form or another gamma chain subclass
C:Comment: The heavy chain disease protein Wis is shown.
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglyutamic acid
F:203-270/Domain: immunoglobulin homology <IM>
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
F:5,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 96.6%; Score 565; DB 1; Length 289;
Best Local Similarity 95.5%; Pred. No. 7.5e-50;
Matches 105; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 APELLGSPVFLPPPKDILMSRTEVTCVVVDVSHEDPEVFQFKWYVDGVEVHNAKTK 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 74 APELLGSPVFLPPPKDILMSRTEVTCVVVDVSHEDPEVFQFKWYVDGVEVHNAKTK 133
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 PREEQNSTFRVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKTK 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 134 PREQFNSTFRVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKTK 183
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
G4HU
Ig gamma-4 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C/Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A/Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A/Reference number: A90933; MUID:83157104
A/Accession: A90933
A/Molecule type: DNA
A/Residues: 1-327 <ELL>
A/Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A/Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant
A/Reference number: A90249; MUID:70207560
A/Accession: A90249
A/Molecule type: protein
A/Residues: 1-30;81-326 <PIN>
C/Genetics:
A/Gene: GDB:IGHG4
A/Cross-references: GDB:119340; OMIM:147130
A/Map position: 14q32.33-14q32.33
A/Introns: 99/1; 111/1; 221/1
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F/20-85/Domain: immunoglobulin homology <IMI>
F/99-110/Region: hinge
F/134-203/Domain: immunoglobulin homology <IM2>
F/240-307/Domain: immunoglobulin homology <IM3>
F/14/Disulfide bonds: interchain (to light chain) #status experimental
F/27-83,141-201,247-305/Disulfide bonds: #status predicted
F/106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F/177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.5%; Score 541; DB 1; Length 327;
Best Local Similarity 91.8%; Pred. No. 2.4e-47;
Matches 101; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 APELLGSPVFLPPPKDILMSRTEVTCVVVDVSHEDPEVFQFKWYVDGVEVHNAKTK 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 111 APELLGSPVFLPPPKDILMSRTEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTK 170
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 PREEQNSTFRVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKTK 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 171 PREQFNSTFRVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKTK 220
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
G2HU
Ig gamma-2 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C/Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A/Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A/Reference number: A93906; MUID:82197621
```

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A/Accession: A93906
A/Molecule type: DNA
A/Residues: 1-326 <ELL>
A/Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A/Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A/Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, an
A/Reference number: A92809; MUID:81007873
A/Contents: myeloma protein Til
A/Accession: A92809
A/Molecule type: protein
A/Residues: 1-19,'Q',21-57,'2',59,'A',61-193,'D',195-325 <WAN>
A/Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A/Title: The amino acid sequences of the three heavy chain constant region domains of
A/Reference number: A90752; MUID:80001357
A/Contents: myeloma protein Zie
A/Accession: A90752
A/Molecule type: protein
A/Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',1
A/Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A/Title: A note on the amino acid sequence of residues 381-391 of human immunoglobuli
A/Reference number: A93132; MUID:80114419
A/Contents: Zie
A/Accession: A93132
A/Molecule type: protein
A/Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A/Reference number: A94591
A/Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A/Note: the revised sequence differs from that shown in having 60-Ala and in the amid
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A/Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A/Reference number: A90253; MUID:72033500
A/Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A/Title: Structural studies of immunoglobulin G.
A/Reference number: A93157; MUID:69064124
A/Contents: annotation; Sa, disulfide bonds
C/Genetics:
A/Gene: GDB:IGHG2
A/Cross-references: GDB:119338; OMIM:147110
A/Map position: 14q32.33-14q32.33
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F/20-85/Domain: immunoglobulin homology <IMI>
F/133-202/Domain: immunoglobulin homology <IM2>
F/239-306/Domain: immunoglobulin homology <IM3>
F/14/Disulfide bonds: interchain (to light chain) #status experimental
F/27-83,140-200,246-304/Disulfide bonds: #status experimental
F/102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F/176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.3%; Score 540; DB 1; Length 326;
Best Local Similarity 94.3%; Pred. No. 3e-47;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 LGGPSVFLPPPKDILMSRTEVTCVVVDVSHEDPEVFQFKWYVDGVEVHNAKTKPREE 64
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 114 VAGPSVFLPPPKDILMSRTEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 173
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 65 QYNSTRVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKTK 110
```

Db 174 QFNSTRVSVLTIVHODWLNKGYCKVSNKGLPAPIETISKT 219
 RESULT 10
 I47160
 Ig gamma 2b chain constant region - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: I47160
 R:Kacskovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
 A:Reference number: I47158; MUID:95015845
 A:Accession: I47160
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-328 <KAC>
 A:Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
 C:Genetics:
 A:Gene: IgG2b
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:133-202/Domain: immunoglobulin homology <IMM>
 Query Match 79.1%; Score 463; DB 2; Length 328;
 Best Local Similarity 79.8%; Pred. No. 2e-39;
 Matches 83; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
 QY 7 GPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQY 66
 DB 116 GPSVFIFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQY 66
 QY 67 NSTFRVSVLTIVHODWLNKGYCKVSNKALPAPIETISKT 110
 DB 176 NSTYRVSVLPIQHODWLNKGYCKVSNKALPAPIETISKT 219
 RESULT 11
 I47159
 Ig gamma 2a chain constant region - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: I47159
 R:Kacskovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
 A:Reference number: I47158; MUID:95015845
 A:Accession: I47159
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-328 <KAC>
 A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
 C:Genetics:
 A:Gene: IgG2a
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:133-202/Domain: immunoglobulin homology <IMM>
 Query Match 79.1%; Score 463; DB 2; Length 328;
 Best Local Similarity 79.8%; Pred. No. 2e-39;
 Matches 83; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
 QY 7 GPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQY 66
 DB 116 GPSVFIFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQY 66
 QY 67 NSTFRVSVLTIVHODWLNKGYCKVSNKALPAPIETISKT 110
 DB 176 NSTYRVSVLPIQHODWLNKGYCKVSNKALPAPIETISKT 219
 RESULT 12

PS0018
 Ig gamma-2b chain C region - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Jul-1999
 C:Accession: PS0018; B25941
 R:Brueggemann, M.
 Gene 74, 473-482, 1988
 A:Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.
 A:Reference number: PS0017; MUID:89232738
 A:Accession: PS0018
 A:Molecule type: DNA
 A:Residues: 1-333 <BRU>
 R:Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.
 Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
 A:Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse anti
 A:Reference number: A25941; MUID:86287397
 A:Accession: B25941
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 227-333 <BR2>
 C:Genetics:
 A:Introns: 96/1; 117/1; 227/1
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:20-82/Domain: immunoglobulin homology <IMM>
 Query Match 78.6%; Score 460; DB 2; Length 333;
 Best Local Similarity 75.2%; Pred. No. 4.1e-39;
 Matches 82; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 QY 2 PELLGSPVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKP 61
 DB 118 PELLGSPVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKP 61
 QY 62 REOYNSTRVSVLTIVHODWLNKGYCKVSNKALPAPIETISKT 110
 DB 178 REOYNSTRVSVLPIQHODWLNKGYCKVSNKALPAPIETISKT 226
 RESULT 13
 I47162
 Ig gamma 4 chain constant region - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: I47162
 R:Kacskovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
 A:Reference number: I47158; MUID:95015845
 A:Accession: I47162
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-277 <KAC>
 A:Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
 C:Genetics:
 A:Gene: IgG4
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:82-151/Domain: immunoglobulin homology <IMM>
 Query Match 78.3%; Score 458; DB 2; Length 277;
 Best Local Similarity 78.8%; Pred. No. 5.3e-39;
 Matches 82; Conservative 12; Mismatches 10; Indels 0; Gaps 0;
 QY 7 GPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQY 66
 DB 65 GPSVFIFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQY 66
 QY 67 NSTFRVSVLTIVHODWLNKGYCKVSNKALPAPIETISKT 110
 DB 125 NSTYRVSVLPIQHODWLNKGYCKVSNKALPAPIETISKT 168

RESULT 14

G2GP
Ig gamma-2 chain C region - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 16-Jul-1999
C:Accession: A94553; A90352; A90359; A90384; A90385; A02151
R:Trischmann, T.M.
submitted to the Atlas, April 1975
A:Reference number: A94553
A:Accession: A94553
A:Molecule type: protein
A:Residues: 1-3 <TRI>
R:Birchstein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
A:Reference number: A90352; MUID:71058471
A:Accession: A90352
A:Molecule type: protein
A:Residues: 4-68 <BIR>
R:Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am
A:Reference number: A90359; MUID:71058486
A:Accession: A90359
A:Molecule type: protein
A:Residues: 69-133:312-329 <TUR>
R:Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90384; MUID:75036072
A:Accession: A90384
A:Molecule type: protein
A:Residues: 134-226 <TRA>
R:Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90385; MUID:75036073
A:Accession: A90385
A:Molecule type: protein
A:Residues: 227-311 <TR2>
R:Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A:Reference number: A90354; MUID:71058474
A:Contents: annotation; disulfide bonds
A:Note: Cys-16 is involved in a heavy-light chain bond
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:21-81/Domain: immunoglobulin homology <IM1>
F:135-204/Domain: immunoglobulin homology <IM2>
F:241-310/Domain: immunoglobulin homology <IM3>
F:28-79/Disulfide bonds: #status experimental
F:142-202/Disulfide bonds: #status experimental
F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:248-308/Disulfide bonds: #status experimental

Query Match 78.3%; Score 458; DB 1; Length 329;
Best Local Similarity 78.9%; Pred. No. 6.5e-39;
Matches 86; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 2 PELLGSPSVLEPPPKDFTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKP 61

DB 113 PENLGGPSVFIIPPCKDFTLMISLTLPRTVCVVVDVSDQDEPEVQFTWFVDNKNVGNATKTP 172

QY 62 REEQNSTFRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKTK 110

DB 173 RVEQYNTFRVESVLPFHQDWTGKKEFKCKVHNEALPAPIVIRTSRTK 221

RESULT 15

C30554
Ig heavy chain C region - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C:Accession: C30554
R:Foley, R.C.; Beh, K.J.
J. Immunol. 142, 708-711, 1989
A:Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A:Reference number: A30554; MUID:89093962
A:Accession: C30554
A:Molecule type: mRNA
A:Status: preliminary; not compared with conceptual translation
A:Residues: 1-308 <FOLE>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:113-182/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 454; DB 2; Length 308;
Best Local Similarity 76.1%; Pred. No. 1.5e-38;
Matches 83; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 2 PELLGSPSVLEPPPKDFTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKP 61

DB 91 PELLGSPSVFIIPPCKDFTLTISGTPEVTCVVVDVQDDPEVQFSWFVDNVEVRTATKTP 150

QY 62 REEQNSTFRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKTK 110

DB 151 REEQNSTFRVSVSALPIHQDWTGKKEFKCKVHNEALPAPIVIRTSRTK 199

Search completed: June 21, 2002, 08:37:54
Job time: 428 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:32:15 ; Search time 77.71 Seconds
(without alignments)
34.575 Million cell updates/sec

Title: US-09-674-857-6
Perfect score: 585
Sequence: 1 APELLGSPVFLFPKPKDT.....CKVSNKALPAPIETISKTK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	585	100.0	377	2	US-08-761-277A-45
2	570	97.4	110	3	US-08-444-644-38
3	570	97.4	110	4	US-08-232-246A-38
4	568	97.1	110	3	US-08-444-644-21
5	568	97.1	110	4	US-08-232-246A-21
6	568	97.1	116	2	US-08-232-539D-55
7	568	97.1	212	1	US-08-430-633-4
8	568	97.1	212	2	US-08-620-694A-4
9	568	97.1	212	2	US-08-936-854-4
10	568	97.1	212	3	US-09-022-255-4
11	568	97.1	212	3	US-09-022-696-4
12	568	97.1	212	3	US-09-022-253-4
13	568	97.1	212	3	US-09-022-260-4
14	568	97.1	212	4	US-09-022-259-4
15	568	97.1	212	4	US-09-022-257-4
16	568	97.1	232	4	US-08-595-043A-50
17	568	97.1	235	4	US-09-131-247-6
18	568	97.1	254	2	US-08-284-391B-33
19	568	97.1	254	4	US-09-218-950-33
20	568	97.1	316	4	US-09-178-869-4
21	568	97.1	331	4	US-09-178-869-2
22	568	97.1	347	1	US-07-940-861-43
23	568	97.1	347	1	US-08-459-512-43
24	568	97.1	347	2	US-08-459-657-43
25	568	97.1	347	2	US-08-460-132-43
26	568	97.1	347	4	US-08-466-465-8
27	568	97.1	347	5	PCr-US92-02050-43

28	568	97.1	360	4	US-09-180-100-11	Sequence 11, Appl
29	568	97.1	371	1	US-08-236-311-7	Sequence 7, Appl
30	568	97.1	371	3	US-08-457-918-7	Sequence 7, Appl
31	568	97.1	376	4	US-09-180-100-22	Sequence 22, Appl
32	568	97.1	387	1	US-08-470-299-4	Sequence 4, Appl
33	568	97.1	388	4	US-09-131-247-16	Sequence 16, Appl
34	568	97.1	389	4	US-09-131-247-14	Sequence 14, Appl
35	568	97.1	396	2	US-08-784-512-3	Sequence 3, Appl
36	568	97.1	396	4	US-09-176-228-3	Sequence 3, Appl
37	568	97.1	424	4	US-09-333-593A-8	Sequence 8, Appl
38	568	97.1	424	5	PCT-US95-03866-12	Sequence 12, Appl
39	568	97.1	424	5	PCT-US95-03866-14	Sequence 14, Appl
40	568	97.1	437	5	PCT-US96-10043-11	Sequence 11, Appl
41	568	97.1	442	5	PCT-US96-10043-9	Sequence 9, Appl
42	568	97.1	446	3	US-08-397-411-7	Sequence 7, Appl
43	568	97.1	449	1	US-08-458-516-13	Sequence 13, Appl
44	568	97.1	449	3	US-08-897-236-23	Sequence 23, Appl
45	568	97.1	449	4	US-09-679-397-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-761-277A-45
; Sequence 45, Application US/08761277A
; Patent No. 5972334
; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
; TITLE OF INVENTION: Leukemia
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,277A
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/644,664
; FILING DATE: 01-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: GENITOPE-02406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-761-277A-45

Query Match 100.0%; Score 585; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.2e-62;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQKWKYVDGVEVHNAKTK 60
|||||

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
APPLICATION DATA:
APPLICATION NUMBER: 07/744758
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-232-539D-55

Query Match 97.1%; Score 568; DB 2; Length 116;

Best Local Similarity 96.4%; Pred. No. 5e-61; Mismatches 2; Indels 0; Gaps 0;

Matches 106; Conservative

QY 1 APELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVVHNAKTK 60

Db 6 APELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVVHNAKTK 65

QY 61 PREQYNSTFRVSVLTVLHODWLNGKEYCKVSNKALPAPIETISKT 110

Db 66 PREQYNSTFRVSVLTVLHODWLNGKEYCKVSNKALPAPIETISKA 115

RESULT 7

US-08-430-633-4

Sequence 4, Application US/08430633

Patent No. 5726286

GENERAL INFORMATION:

APPLICANT: ALDERSON, MARK

APPLICANT: ARMITAGE, RICHARD

APPLICANT: COHEN, JEFFREY

APPLICANT: COMEAU, MICHAEL

APPLICANT: FARRAH, THERESA

APPLICANT: SPRIGGS, MELANIE

TITLE OF INVENTION: Isolated Epstein-Barr Virus B2LF2 proteins

TITLE OF INVENTION: That Bind MHC Class II Beta Chains

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple Operating System 7.1

SOFTWARE: Microsoft Word for Apple, Version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/430,633

FILING DATE: 28-APR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/235,397

FILING DATE: 04/28/94

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Human
IMMEDIATE SOURCE:
CLONE: IgG1 Fc
US-08-430-633-4

Query Match

Best Local Similarity 96.4%; Pred. No. 1.1e-60;

Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVVHNAKTK 60

Db 14 APELLGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVVHNAKTK 73

QY 61 PREQYNSTFRVSVLTVLHODWLNGKEYCKVSNKALPAPIETISKT 110

Db 74 PREQYNSTFRVSVLTVLHODWLNGKEYCKVSNKALPAPIETISKA 123

RESULT 8

US-08-620-694A-4

Sequence 4, Application US/08620694A

Patent No. 5869286

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/620,694A

FILING DATE: 21 MARCH 1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/538,765

FILING DATE: 7 AUGUST 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

```
;
;
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: IgG1 Fc
; US-08-620-694A-4

Query Match          97.1%; Score 568; DB 2; Length 212;
Best Local Similarity 96.4%; Pred. No. 1.1e-60;
Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNATK 60
Db 14 APELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNATK 73
QY 61 PREEQYNSTFRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKTK 110
Db 74 PREEQYNSTFRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAK 123

RESULT 9
US-08-936-854-4
; Sequence 4, Application US/08936854
; Patent No. 5925734
; GENERAL INFORMATION:
; APPLICANT: ALDERSON, MARK
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: COHEN, JEFFREY
; APPLICANT: COMEAU, MICHAEL
; APPLICANT: FARRAH, THERESA
; APPLICANT: SPRIGGS, MELANIE
; TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF2 Proteins
; TITLE OF INVENTION: That Bind MHC Class II Beta Chains
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,633
; FILING DATE: 28-APR-1995
; APPLICATION NUMBER: 08/235,397
; FILING DATE: 04/28/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2612
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids

;
;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: IgG1 Fc
; US-08-936-854-4

Query Match          97.1%; Score 568; DB 2; Length 212;
Best Local Similarity 96.4%; Pred. No. 1.1e-60;
Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 APELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNATK 60
Db 14 APELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNATK 73
QY 61 PREEQYNSTFRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKTK 110
Db 74 PREEQYNSTFRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAK 123

RESULT 10
US-09-022-255-4
; Sequence 4, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
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RESULT 15
US-09-022-257-4
; Sequence 4, Application US/09022257
; Patent No. 6197525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLONE: IgG1 FC
US-09-022-257-4

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Query Match 97.1%; Score 568; DB 4; Length 212;
Best Local Similarity 96.4%; Pred. NO. 1.le-60;
Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 APPELLGGPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKYVYDGVGVHNAKTK 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 14 APPELLGGPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKYVYDGVGVHNAKTK 73
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 PREQYNSTFRVSVTLVLDHDLNGKEYCKVSNKALPAPIEKTISKTK 110
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74 PREQYNSTIRVSVTLVLDHDLNGKEYCKVSNKALPAPIEKTISKAK 123
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Search completed: June 21, 2002, 08:32:15
Job time: 89 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 08:32:15 ; Search time 77.71 Seconds
(without alignments)
34.261 Million cell updates/sec

Title: US-09-674-857-5
Perfect score: 583
Sequence: 1 APPVAGRSVFLPPKPKDFTL.....CKVSNKGLPAPIETISKTK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA: *
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length DB ID	Description	
1	583	100.0	109	3	US-08-444-644-30
2	583	100.0	109	4	US-08-232-246A-30
3	583	100.0	432	3	US-08-477-460B-2
4	583	100.0	432	3	US-08-379-516-2
5	583	100.0	432	4	US-09-329-916-2
6	583	100.0	432	4	US-08-485-372A-2
7	583	100.0	432	4	US-09-409-006A-2
8	583	100.0	432	5	PCT-US93-07422-2
9	583	100.0	530	3	US-08-477-460B-4
10	583	100.0	530	3	US-08-379-516-4
11	583	100.0	530	4	US-09-329-916-4
12	583	100.0	530	4	US-08-485-372A-4
13	583	100.0	530	4	US-09-409-006A-4
14	583	100.0	530	5	PCT-US93-07422-4
15	580	99.5	450	2	US-08-788-800-12
16	580	99.5	469	2	US-07-934-373C-23
17	580	99.5	469	3	US-08-437-642B-23
18	580	99.5	552	5	PCT-US93-07832-23
19	573	98.3	326	2	US-08-656-586-9
20	540	92.6	377	2	US-08-761-277A-45
21	535	91.8	116	2	US-08-232-539D-55
22	535	91.8	212	1	US-08-430-633-4
23	535	91.8	212	2	US-08-620-694A-4
24	535	91.8	212	2	US-08-936-854-4
25	535	91.8	212	3	US-09-022-255-4
26	535	91.8	212	3	US-09-022-696-4
27	535	91.8	212	3	US-09-022-253-4

28 535 91.8 212 3 US-09-022-260-4 Sequence 4, Appli
29 535 91.8 212 4 US-09-022-259-4 Sequence 4, Appli
30 535 91.8 212 4 US-09-022-257-4 Sequence 4, Appli
31 535 91.8 232 2 US-08-595-043A-50 Sequence 50, Appli
32 535 91.8 235 4 US-09-131-247-6 Sequence 6, Appli
33 535 91.8 254 2 US-08-284-391B-33 Sequence 33, Appli
34 535 91.8 254 4 US-09-218-950-33 Sequence 33, Appli
35 535 91.8 331 4 US-09-178-869-2 Sequence 2, Appli
36 535 91.8 347 1 US-07-940-861-43 Sequence 43, Appli
37 535 91.8 347 1 US-08-459-512-43 Sequence 43, Appli
38 535 91.8 347 2 US-08-459-657-43 Sequence 43, Appli
39 535 91.8 347 2 US-08-460-132-43 Sequence 43, Appli
40 535 91.8 347 4 US-08-466-465-8 Sequence 8, Appli
41 535 91.8 347 5 PCT-US92-02050-43 Sequence 43, Appli
42 535 91.8 360 4 US-09-180-100-11 Sequence 11, Appli
43 535 91.8 371 1 US-08-236-311-7 Sequence 7, Appli
44 535 91.8 371 3 US-08-457-918-7 Sequence 7, Appli
45 535 91.8 376 4 US-09-180-100-22 Sequence 22, Appli

ALIGNMENTS

RESULT 1
US-08-444-644-30
; Sequence 30, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Philip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-379-516-2

; Sequence 2, Application US/08379516

; Patent No. 6083478

; GENERAL INFORMATION:

; APPLICANT: Allaway, Graham P.

; APPLICANT: Maddon, Paul J.

; TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2

; TITLE OF INVENTION: Immunoconjugates and Uses Thereof

; FILE REFERENCE: 41215-A-PCT-US

; CURRENT APPLICATION NUMBER: US/08/379,516

; EARLIER FILING DATE: 1996-06-10

; EARLIER FILING DATE: PCT/US93/07422

; EARLIER FILING DATE: 1993-08-06

; EARLIER FILING DATE: 07/927,931

; EARLIER FILING DATE: 1992-08-07

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 2

; LENGTH: 432

; TYPE: PRT

; ORGANISM: Homo sapiens

US-08-379-516-2

Query Match 100.0%; Score 583; DB 3; Length 432;

Best Local Similarity 100.0%; Pred. No. 8.6e-60;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKP 60

Db 217 APPVAGPSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKP 276

QY 61 REQFNSTFRVSVLVVHODWLNKGYCKVSNKGLPAPIETISKT 109

Db 277 REQFNSTFRVSVLVVHODWLNKGYCKVSNKGLPAPIETISKT 325

RESULT 5

US-09-329-916-2

; Sequence 2, Application US/09329916

; Patent No. 6177549

; GENERAL INFORMATION:

; APPLICANT: Progenics Pharmaceuticals, Inc.

; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED

; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/329,916

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/477,460

; FILING DATE: 07-JUN-1995

; APPLICATION NUMBER: US 07/927,931

; FILING DATE: 07-AUG-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 977-9550

; TELEFAX: (212) 977-9809

; TELEX: 422523 COOP UI

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 432 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: homo sapien

; CELL TYPE: lymphocyte

US-09-329-916-2

Query Match 100.0%; Score 583; DB 4; Length 432;

Best Local Similarity 100.0%; Pred. No. 8.6e-60;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKP 60

Db 217 APPVAGPSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKP 276

QY 61 REQFNSTFRVSVLVVHODWLNKGYCKVSNKGLPAPIETISKT 109

Db 277 REQFNSTFRVSVLVVHODWLNKGYCKVSNKGLPAPIETISKT 325

RESULT 6

US-08-485-372A-2

; Sequence 2, Application US/08485372A

; Patent No. 6187748

; GENERAL INFORMATION:

; APPLICANT: Beaudry, Gary A.

; APPLICANT: Maddon, Paul J.

; TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/485,372A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/476,227

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 37690-II-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0525

; TELEX:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 432 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: homo sapien


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Best Local Similarity 100.0%; Pred. No. 1.le-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDFTLMSRTPVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
DB 315 APPVAGPSVFLPPPKDFTLMSRTPVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 374
QY 61 REEQFNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIETISKTK 109
DB 375 REEQFNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIETISKTK 423

RESULT 12
US-08-485-372A-4
; Sequence 4, Application US/08485372A
; Patent No. 6187748
; GENERAL INFORMATION:
; APPLICANT: Beaudry, Gary A.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,372A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,227
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37690-II-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
;
US-08-485-372A-4

Query Match 100.0%; Score 583; DB 4; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.le-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDFTLMSRTPVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
DB 315 APPVAGPSVFLPPPKDFTLMSRTPVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 374
QY 61 REEQFNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIETISKTK 109
DB 375 REEQFNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIETISKTK 423

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RESULT 13
US-09-409-006A-4
; Sequence 4, Application US/09409006A
; Patent No. 6342586
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/409,006A
; FILING DATE: 29-SEP-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
;
US-09-409-006A-4

Query Match 100.0%; Score 583; DB 4; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.le-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKDFTLMSRTPVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
DB 315 APPVAGPSVFLPPPKDFTLMSRTPVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 374
QY 61 REEQFNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIETISKTK 109
DB 375 REEQFNSTFRVSVLTVVHODWLNKGKEYCKVSNKGLPAPIETISKTK 423

RESULT 14
PCT-US93-07422-4
; Sequence 4, Application PC/TUS9307422
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham

```


STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 19930806
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
PCT-US93-07422-4

Query Match 100.0%; Score 583; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.1e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPVAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
|||||
Db 315 APPVAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 374
QY 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTISKTK 109
|||||
Db 375 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTISKTK 423

RESULT 15
US-08-788-800-12
Sequence 12, Application US/08788800
Patent No. 5914112
GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
APPLICANT: Thomas, G. Roger
APPLICANT: Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,800
FILING DATE: 22-Jan-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0987r1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-788-800-12

Query Match 99.5%; Score 580; DB 2; Length 450;
Best Local Similarity 99.1%; Pred. No. 2e-59;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPVAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKP 60
Db 235 APPVAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGMEVHNAKTKP 294
QY 61 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTISKTK 109
Db 295 REEQFNSTFRVSVLTVVHQDNLNGKEYCKVSNKGLPAPIEKTISKTK 343

Search completed: June 21, 2002, 08:32:15
Job time: 89 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 08:36:07 ; Search time 224.82 Seconds
(without alignments)
53.852 Million cell updates/sec

Title: US-09-674-857-5
Perfect score: 583
Sequence: 1 APPVAGSVLFPKPKDNL.....CKVSNKGLPAPIETISKTK 109

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	583	100.0	109	AA1980	Undefined ORF2 enc
2	583	100.0	217	AA1981	Amino acid sequenc
3	583	100.0	217	AA1982	Human IgG2. Homo
4	583	100.0	217	AA1983	Human IgG2 Fc regi
5	583	100.0	326	AA1984	Human immunoglobul
6	583	100.0	381	AA1985	Human IL-2/Ig fusi
7	583	100.0	432	AA1986	CD4-gamma2 chimeri
8	583	100.0	432	AA1987	CD4-gamma2 chimeri
9	583	100.0	432	AA1988	Human CD4-gamma 2
10	583	100.0	432	AA1989	Human CD4-gamma2 c
11	583	100.0	432	AA1990	CD4-gamma2 chimeri

12	583	100.0	442	22	AA1991	Human IgG2 chain C
13	583	100.0	443	20	AA1992	The heavy chain of
14	583	100.0	451	21	AA1993	Human IgG2 chain C
15	583	100.0	461	22	AA1994	Human immunoglobul
16	583	100.0	462	21	AA1995	Human IgG2 chain of
17	583	100.0	463	21	AA1996	The heavy chain of
18	583	100.0	463	21	AA1997	The heavy chain of
19	583	100.0	463	21	AA1998	The heavy chain of
20	583	100.0	463	21	AA1999	The heavy chain of
21	583	100.0	464	21	AA2000	The heavy chain of
22	583	100.0	464	21	AA2001	The heavy chain of
23	583	100.0	530	13	AA2002	CD4-IgG2 chimeric
24	583	100.0	530	21	AA2003	CD4-IgG2 chimeric
25	583	100.0	530	22	AA2004	Human CD4-IgG2 chi
26	583	100.0	530	22	AA2005	CD4-IgG2 chimeric
27	580	99.5	450	18	AA2006	Heavy chain of ful
28	580	99.5	450	20	AA2007	Human IgG2 huH52 h
29	580	99.5	530	15	AA2008	CD4-IgG2 chimeric
30	580	99.5	552	14	AA2009	PH52-8.0 humanised
31	577	99.0	463	21	AA2010	The heavy chain of
32	574	98.5	643	19	AA2011	A33 chimeric recep
33	574	98.5	643	19	AA2012	Z33g2G237Az chimer
34	573	98.3	326	19	AA2013	Heavy chain consta
35	564	96.7	109	21	AA2014	Mutated CH2 sequen
36	554	95.0	109	21	AA2015	Mutated CH2 sequen
37	553	94.9	462	18	AA2016	2A2 (Chimeric) hum
38	553	94.9	462	18	AA2017	2A2 (Chimeric) hum
39	553	94.9	463	18	AA2018	3F4 (Chimeric) hum
40	553	94.9	463	18	AA2019	3F4 (Chimeric) hum
41	543	93.1	218	21	AA2020	Amino acid sequenc
42	543	93.1	218	22	AA2021	Human IgG3. Homo
43	543	93.1	218	22	AA2022	Human IgG3 Fc regi
44	540	92.6	377	18	AA2023	Immunoglobulin C-g
45	540	92.6	494	20	AA2024	Human IgG3 chain C

ALIGNMENTS

RESULT 1
AA1980
ID AA1980 standard; Protein; 109 AA.
XX
AC AA1980;
XX
DT 20-OCT-1993 (first entry)
XX
DE Undefined ORF2 encoded by plasmid pAH4625.
XX
KW Polymerase chain reaction; primer: pAH4625;
KW heavy; light; chain; variable; constant; region; anti-human; pAH4807;
KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;
KW endothelial cell; conjugate; neuropharmacological; gamma-3; gamma-4;
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;
KW Parkinsons disease; Alzheimers disease; SP2/0 cell.
XX
OS Synthetic.
XX
PN WO9310819-A.
XX
PD 10-JUN-1993.
XX
PF 24-NOV-1992; 92WO-US10206.
XX
PR 26-NOV-1991; 91US-0800458.
XX
PA (ALKE-) ALKERMES INC.
XX
PI Friden PM;
XX
DR WPI; 1993-196742/24.
DR N-PSDB; AAQ43846.
XX

PT Antibody conjugates specific for transferrin receptor - used
PT for diagnosis and treatment of cancer, AIDS and neurological
PT disorders

XX Disclosure; Fig 17J; 151pp; English.

XX The sequences given in AAR41707-09 are encoded by the expression vector
CC pAH4625. This vector represents the cloning of the human gamma
CC isotype, gamma-2, with the variable region of the murine monoclonal
CC antibody 128.1. This plasmid encodes a chimeric monoclonal antibody
CC in which the heavy chain (VH) is derived from a murine source and the
CC sequences encoding CH1, CH2 and CH3 are derived from a human source.
CC This vector, in combination with the chimeric light chain vector,
CC pAG4611 (see also AAQ43845), was transfected into Sp2/0 cells and clones
CC were isolated. 128.1 is an anti-human transferrin receptor antibody
CC which binds to the transferrin receptor on brain capillary endothelial
CC cells. This antibody may be used in a conjugate in which it is linked
CC to a neuropharmaceutical or diagnostic agent. The conjugate may be
CC used to treat or prevent neurological disorders eg. brain tumours,
CC AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may
CC also be used for diagnostic methods.

XX Sequence 109 AA;

Query Match 100.0%; Score 583; DB 14; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKTP 60
Db 1 appvagsvflfpkpkdtlmisrtpevtcvvvdvshedpevgfnwvydgvvhnatktp 60

QY 61 REEQFNSTFRVSVLTVVHODWLNKGEYCKVSNKGLPAPIEKTISKTK 109
Db 61 reeqfnstfrvsvltvvhqdwnlgnkgeyckvsnkglpapiectisktk 109

RESULT 2

ID AAB07476
XX AAB07476 standard; protein; 217 AA.

XX AAB07476;

XX 20-OCT-2000 (first entry)

XX Amino acid sequence of native IgG Fc region humIgG2.

XX IgG antibody; light chain; Fc region; effector function; cancer;
XX allergy; asthma; LFA-1-mediated disorder; tumour; cancer.

XX Homo sapiens.

XX WO200042072-A2.

XX 20-JUL-2000.

XX 14-JAN-2000; 2000WO-US00973.

XX 15-JAN-1999; 99US-0116023.

XX (GETH) GENENTECH INC.

XX Presta LG;

XX WPI; 2000-476035/41.

XX New Fc region-containing polypeptides that have altered effector
PT function due to one or more amino acid modifications in the Fc region,
PT useful in the treatment of cancer and allergic conditions such as
PT asthma

XX Disclosure; Fig 22A; 132pp; English.

XX

CC AAB07474-78 represent native IgG Fc regions. The proteins are used to
CC produce Fc region-containing polypeptides that have altered effector
CC function as a consequence of one or more amino acid modifications in
CC the Fc region. The variant polypeptides are useful for treating
CC cancer, allergic conditions such as asthma (with an anti-IgE antibody),
CC and LFA-1-mediated disorders. Where the polypeptide binds the HER2
CC receptor, the disorder preferably is HER2-expressing cancer, e.g. a
CC benign or malignant tumour characterized by overexpression of the
CC HER2 receptor. Such cancers include breast cancer, squamous cell
CC cancer, small-cell lung cancer, non-small cell lung cancer,
CC gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical
CC cancer, ovarian cancer, bladder cancer, hepatoma, colon cancer,
CC colorectal cancer, endometrial carcinoma, salivary gland carcinoma,
CC kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid
CC cancer, hepatic carcinoma and various types of head and neck cancer.

XX Sequence 217 AA;

Query Match 100.0%; Score 583; DB 21; Length 217;
Best Local Similarity 100.0%; Pred. No. 2.4e-51;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKTP 60
Db 2 appvagsvflfpkpkdtlmisrtpevtcvvvdvshedpevgfnwvydgvvhnatktp 61

QY 61 REEQFNSTFRVSVLTVVHODWLNKGEYCKVSNKGLPAPIEKTISKTK 109
Db 62 reeqfnstfrvsvltvvhqdwnlgnkgeyckvsnkglpapiectisktk 110

RESULT 3

ID AAB67203
XX AAB67203 standard; protein; 217 AA.

XX AAB67203;

XX 10-APR-2001 (first entry)

XX Human IgG2.

XX Fusion protein; immunoglobulin; multidimerization domain; ligand.

XX Homo sapiens.

XX WO200102440-A1.

XX 11-JAN-2001.

XX 30-JUN-2000; 2000WO-US18185.

XX 02-JUL-1999; 99US-0142088.

XX (GETH) GENENTECH INC.

XX Dennis MS, Lazarus RA;

XX WPI; 2001-123106/13.

XX Novel fusion polypeptides comprising a peptide ligand domain which
PT functions to target hybrid molecule to target cell, and immunoglobulin
PT constant region multimerization domain

XX Disclosure; Fig 2; 69pp; English.

XX The present invention relates to a fusion protein, comprising a
CC peptide ligand and an immunoglobulin (Ig) constant region
CC multimerization domain (Ib). The hybrid molecules comprising
CC the peptide ligands and their functional derivatives can be used
CC in the same applications as, a peptide ligand can be used. For
CC example the peptide ligand can bind ErbB2. The peptide ligand

QY 1 APPVAGSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVFQNMVYDGVGVHNAKTKP 60
 |||||
 Db 111 appvagsvflfpkpkdtlmisrtpetvctvvvdvshdpevqfnvydgvvhnaktkp 170
 |||||
 QY 61 REQFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPAPIEKTISKTK 109
 |||||
 Db 171 reeqfnstfrvsvltvvhqdwlngkeyckvsnkglpapiektisktk 219
 |||||
 RESULT 6
 AAY06895
 ID AAY06895 standard; Protein; 381 AA.
 AC AAY06895;
 XX
 DT 01-JUL-1999 (first entry)
 XX
 DE Human IL-2/Ig fusion protein.
 XX
 KW Fusion protein; vaccine; cytokine; immunoglobulin; autoimmune disease;
 KW infectious disease; inflammatory disease; neoplastic disease; cancer;
 KW immunologic disease; immune response; malaria; tuberculosis; hepatitis;
 KW AIDS; influenza; interleukin; IL-2; Ig; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..153
 FT Protein /note= "interleukin-2 (IL-2)"
 FT Protein 154..381
 FT Protein /note= "immunoglobulin G"
 XX
 PN W09916466-A2.
 XX
 XX 08-APR-1999.
 XX
 PF 29-SEP-1998; 98NO-US20321.
 XX
 PR 12-DEC-1997; 97US-0990180.
 PR 29-SEP-1997; 97US-0060338.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX
 PI Barouch DH, Letvin NL;
 XX
 XX WPI; 1999-254931/21.
 DR N-PSDB; AAX34598.
 XX
 PT New vaccine compositions
 XX
 PS Claim 16; Fig 10A-E; 66pp; English.
 XX
 CC The invention relates to vaccine compositions comprising a vaccine and a
 CC timed-release formulation of a cytokine or cytokine/immunoglobulin fusion
 CC protein or plasmid. The formulation or device releases the cytokine
 CC protein or plasmid at one or more temporal points subsequent to vaccine
 CC administration. The vaccines can be used for treating an autoimmune
 CC disease, an infectious disease, an inflammatory disease, a neoplastic
 CC disease, or an immunologic disease in an individual. The vaccines can be
 CC used to elicit immune responses against diseases such as AIDS, malaria,
 CC tuberculosis, hepatitis C, hepatitis B, cancer or influenza. The methods
 CC can provide for enhancement of one or more immunologic parameters such as
 CC an antibody response, a cellular proliferative response as well as
 CC cytotoxic T-lymphocyte levels. In addition the Ig can increase the
 CC circulating half life of the cytokine. The present sequence represents
 CC a human interleukin-2 (IL-2)/Ig fusion protein.
 XX
 SQ Sequence 381 AA;

Query Match 100.0%; Score 583; DB 20; Length 381;
 Best Local Similarity 100.0%; Pred. No. 4.6e-51;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APPVAGSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVFQNMVYDGVGVHNAKTKP 60
 |||||
 Db 166 appvagsvflfpkpkdtlmisrtpetvctvvvdvshdpevqfnvydgvvhnaktkp 225
 |||||
 QY 61 REQFNSTFRVSVLTVVHODWLNKGEYKCKVSNKGLPAPIEKTISKTK 109
 |||||
 Db 226 reeqfnstfrvsvltvvhqdwlngkeyckvsnkglpapiektisktk 274
 |||||
 RESULT 7
 AAR26782
 ID AAR26782 standard; Protein; 432 AA.
 AC AAR26782;
 XX
 DT 06-FEB-1993 (first entry)
 XX
 DE CD4-gamma2 chimeric heavy chain homodimer.
 XX
 KW homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;
 KW chimeric; increased serum half life; HIV infection; AIDS; ss.
 XX
 OS Homo sapiens chimeric.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..216
 FT Domain /label= CD4
 FT Domain 217..325
 FT Domain /label= CH2
 FT Domain 326..433
 FT Domain /label= CH3
 XX
 PN W09213947-A.
 XX
 PD 20-AUG-1992.
 XX
 PF 10-FEB-1992; 92WO-US01143.
 XX
 PR 08-FEB-1991; 91US-0653684.
 XX
 PA (PROG-) PROGENICS PHARM INC.
 XX
 PI Beaudry GA, Maddon PJ;
 XX
 XX WPI; 1992-300034/36.
 DR N-PSDB; AAQ28088.
 XX
 PT CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for
 PT treatment, prevention and diagnosis of HIV infection
 XX
 PS Claim 2; Fig 3; 90pp; English.
 XX
 CC This sequence represents a CD4-gamma2 chimeric heavy chain homodimer.
 CC It was produced by expression of the coding mutagenised cDNA
 CC (produced as described in AAQ28088) in Dhfr-CHO cells. The protein is
 CC efficiently assembled intracellularly and effectively secreted from
 CC mammalian cells pref. CHO, COS, or myeloma cells as a homodimer,
 CC enabling high recovery and purification from the medium of cells
 CC expressing it. It possesses increased serum half-life and has increased
 CC avidity for HIV cf. heavy chain dimers. It can inhibit HIV infection of
 CC CD4+ cells and block the spread of HIV infection within a patient.
 CC Attachment to a detectable marker makes it useful in an assay for HIV
 CC or SIV infection, and it can also be linked to toxins, eg Diphtheria,
 CC Pseudomonas exotoxin A (domains I or II) or the deglycosylated A-chain
 CC of ricin.
 XX
 SQ Sequence 432 AA;

Query Match 100.0%; Score 583; DB 13; Length 432;
 Best Local Similarity 100.0%; Pred. No. 5.4e-51;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKPDKDTLMISRTPEVTCVVYVDVSHEDPEVQFNWYDGVGVHNAKTKP 60
 Db 217 appvagsvflfppkpkdtlmisrtpetvctcvvdsvedpvgfnwvsgvevhnaktkp 276

QY 61 REEOFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
 Db 277 reeqninstfrvsvltvvhqdwlngkeyckvsnkglpapiektisktk 325

RESULT 8
 AAR46678
 ID AAR46678 standard; Protein; 432 AA.
 XX AC AAR46678;
 DT 08-AUG-1994 (first entry)
 DE CD4-gamma 2 chimeric heavy chain.
 KW CD4; gamma; heavy chain; chimeric; chimeric; immunoglobulin; HIV;
 KW human immunodeficiency virus; radionuclide; toxin; therapy;
 KW treatment; imaging; detection; targeting.
 XX Homo sapiens.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..204
 FT Region /label= CD4 Region.
 FT Region 205..216
 FT Region /label= Hinge Region.
 FT Region 217..325
 FT Region /label= CH2 Region.
 FT Region 326..432
 FT Region /label= CH3 Region.
 XX WO9403191-A.
 XX 17-FEB-1994.
 XX 06-AUG-1993; 93WO-US07422.
 XX 07-AUG-1992; 92US-0927931.
 XX (PROG-) PROGENICS PHARM INC.
 XX Allaway GP, Maddon PJ;
 XX WPI: 1994-065392/08.
 XX N-PSDB; AAQ57750.
 XX Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2
 XX immunoconjugates - used to kill HIV-infected cells and to image
 XX and stage HIV infection
 XX Disclosure; Figure 3; 142pp; English.
 XX A CD4-gamma 2 chimeric heavy chain homodimer is linked to a non-
 XX peptidyl toxin or a gamma radiation-emitting radionuclide of low to
 XX moderate cytotoxicity. The resulting immunoconjugate comprising the
 XX toxin can be used to kill HIV infected cells and to treat HIV
 XX infected subjects to reduce the population of HIV infected cells.
 XX It can also be used to reduce the likelihood of infection. The
 XX immunoconjugate comprising the radionuclide can be used to image HIV
 XX infected tissue, to calculate the stage of HIV infection or the
 XX efficacy of an anti-HIV treatment using the imaging technique and
 XX for determining the prognosis of an HIV infected subject.
 XX Sequence 432 AA;

Query Match 100.0%; Score 583; DB 15; Length 432;

Best Local Similarity 100.0%; Pred. No. 5.4e-51;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPPKPDKDTLMISRTPEVTCVVYVDVSHEDPEVQFNWYDGVGVHNAKTKP 60
 Db 217 appvagsvflfppkpkdtlmisrtpetvctcvvdsvedpvgfnwvsgvevhnaktkp 276

QY 61 REEOFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
 Db 277 reeqninstfrvsvltvvhqdwlngkeyckvsnkglpapiektisktk 325

RESULT 9
 AAY85079
 ID AAY85079 standard; Protein; 432 AA.
 XX AC AAY85079;
 DT 19-JUN-2000 (first entry)
 DE Human CD4-gamma 2 chimeric heavy chain homodimer amino acid sequence.
 KW CD4-gamma 2 chimeric heavy chain homodimer; immunoconjugate; treatment;
 KW cytotoxic radionuclide; cell surface glycoprotein; prevent; infection;
 KW cellular immune response interaction mediator; HIV interaction;
 KW staging; prognosis; envelope glycoprotein burden; human.
 XX Homo sapiens.
 OS Homo sapiens.
 FH US6034223-A.
 FT 07-MAR-2000.
 XX 07-JUN-1995; 95US-0477460.
 XX 07-AUG-1992; 92US-0927931.
 XX 06-AUG-1993; 93WO-US07422.
 XX 03-FEB-1995; 95US-0379516.
 XX (PROG-) PROGENICS PHARM INC.
 XX Allaway GP, Maddon PJ;
 XX WPI: 2000-269502/23.
 XX N-PSDB; AAZ98855.
 XX New immunoconjugate, used to treat, prevent or image human immune
 XX deficiency virus infection, comprises radionuclide attached to
 XX heterotetramer of CD4-immunoglobulin chimeras
 XX Disclosure; Fig 3; 58pp; English.
 XX This sequence represents the human CD4-gamma 2 chimeric heavy chain
 XX homodimer amino acid sequence. The invention relates to an
 XX immunoconjugate comprising a cytotoxic radionuclide and a heterotetramer
 XX of two heavy chains and two light chains. The cytotoxic radionuclide is
 XX linked to either the heavy chains or the light chains, or to all four
 XX chains, directly or through a bifunctional chelator. Both heavy chains
 XX are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by vector
 XX CD4-IgG2HC-pRCMV (ATCC 75193) and both light chains are chimeric
 XX CD4-kappa chains encoded by vector CD4-kLC-pRCMV (ATCC 75194). CD4 is a
 XX non-polymorphic cell surface glycoprotein that is expressed on the
 XX surface of helper T lymphocytes, cells of the monocyte/macrophage lineage
 XX and dendritic cells. CD4 associates with major histocompatibility complex
 XX (MHC) class II molecules on the surface of antigen presenting cells to
 XX mediate efficient cellular immune response interactions. In humans CD4 is
 XX the target of interaction with the human immunodeficiency virus HIV. The
 XX immunoconjugate is used to kill cells infected with HIV, and for treating
 XX or preventing infection. It is also used for imaging HIV-infected tissues
 XX (for staging or prognosis of infection, and for assessing efficacy of
 XX treatments). The immunoconjugate is also used to determine the HIV
 XX envelope glycoprotein burden, once determined, this information is used
 XX in the staging and prognosis of HIV infected patients. The

CC immunoconjugate should be active against all strains of HIV (since the
 CC CD4-gp120 interaction is essential for infection). The heterotetramers
 CC are assembled intracellularly and secreted efficiently from mammalian
 CC cells, allowing high recovery and purification from the culture medium.
 CC They have longer half-life in serum and greater avidity than heavy chain
 CC dimers.
 XX Sequence 432 AA;
 SQ Query Match 100.0%; Score 583; DB 21; Length 432;
 Best Local Similarity 100.0%; Pred. No. 5.4e-51;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKTP 60
 Db 217 appvagsvflppkpkdtlmisrtpevtcvcvvdvshedpevfqfnwvydgvvhnaktkp 276
 QY 61 REEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIETISKTK 109
 Db 277 reeqfnstfrvsvltvvhqdwlngkeyckvsnkglpapiektisktk 325
 RESULT 10
 AAB80883
 ID AAB80883 standard; Protein; 432 AA.
 XX AC AAB80883;
 XX DT 29-MAY-2001 (first entry)
 XX DE Human CD4-gamma2 chimeric heavy chain homodimer.
 XX KW Human; Anti-HIV; CD4-IgG2 chimeric heterotetramer;
 KW immunoglobulin gamma 2.
 XX OS Homo sapiens.
 XX PN US6187748-B1.
 XX PD 13-FEB-2001.
 XX PF 07-JUN-1995; 95US-0485372.
 XX PR 08-FEB-1991; 91US-0653684.
 PR 10-FEB-1992; 92WO-US01143.
 PR 08-DEC-1992; 92US-0960440.
 XX (PROG-) PROGENICS PHARM INC.
 XX PI Maddon PJ, Beaudry GA;
 DR WPI; 2001-264981/27.
 DR N-PSDB; AAF77829.
 XX Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell,
 PT or treating a subject having CD4+ cells infected with HIV involves
 PT using CD4-IgG2 chimeric heterotetramer to form a complex with the HIV -
 XX N-PSDB; AAF77829.
 PS Disclosure; Fig 3; 55pp; English.
 CC The present invention relates to a method for inhibiting infection of a
 CC CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2
 CC chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of
 CC differentiation 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface
 CC glycoprotein that is expressed primarily on the surface of T cells. In
 CC man, CD4 is the target of interaction with HIV. The heterotetramer has
 CC two heavy and two light chains which are encoded by expression vectors
 CC CD4-IgG2HC-prcCMV (V1) and CD4-kLC-prcCMV (V2), respectively. The method
 CC is used to inhibit infection of a CD4+ cell by a HIV and to prevent CD4+
 CC cells of a subject from becoming infected with HIV. The method is also
 CC useful for treating a subject having CD4+ cells infected with HIV. The
 CC present sequence is human fusion protein: CD4-gamma2 chimeric heavy chain

CC homodimer. This sequence was used in the method of the present invention.
 XX Sequence 432 AA;
 SQ Query Match 100.0%; Score 583; DB 22; Length 432;
 Best Local Similarity 100.0%; Pred. No. 5.4e-51;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNATKTP 60
 Db 217 appvagsvflppkpkdtlmisrtpevtcvcvvdvshedpevfqfnwvydgvvhnaktkp 276
 QY 61 REEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIETISKTK 109
 Db 277 reeqfnstfrvsvltvvhqdwlngkeyckvsnkglpapiektisktk 325
 RESULT 11
 AAB67322
 ID AAB67322 standard; Protein; 432 AA.
 XX AC AAB67322;
 XX DT 23-APR-2001 (first entry)
 XX DE CD4-gamma2 chimeric heavy chain homodimer protien.
 XX KW Immunoconjugate; chelator; chimeric; HIV;
 KW human immunodeficiency virus.
 XX OS Homo sapiens.
 XX PN US6177549-B1.
 XX PD 23-JAN-2001.
 XX PF 10-JUN-1999; 99US-0329916.
 XX PR 07-JUN-1995; 95US-0477460.
 PR 07-AUG-1992; 92US-0927931.
 PR 06-AUG-1993; 93US-0379516.
 PR 06-AUG-1993; 93WO-US07422.
 XX (PROG-) PROGENICS PHARM INC.
 XX PI Maddon PJ, Allaway GP;
 XX WPI; 2001-158582/16.
 XX Immunoconjugate for treating human immunodeficiency virus-infected
 PT subject, consists of cytotoxic radionuclide linked to heterotetramer
 PT comprising two chimeric CD4-IgG2 heavy chains and two chimeric
 PT CD4-kappa light chains -
 XX Disclosure; Fig 3; 43pp; English.
 PS The present invention relates to an immunoconjugate, comprising a
 CC cytotoxic radionuclide linked, directly or via a bifunctional
 CC chelator, to a heterotetramer having two chimeric CD4-IgG2 heavy
 CC chains encoded by an expression vector CD4-IgG2HC-prcCMV and
 CC two chimeric CD4-kappa light chains encoded by an expression vector
 CC CD4-kLC-prcMW. The invention is useful for killing human
 CC immunodeficiency virus (HIV)-infected cells, for the treatment and
 CC prevention of infection with HIV.
 XX Sequence 432 AA;
 SQ Query Match 100.0%; Score 583; DB 22; Length 432;
 Best Local Similarity 100.0%; Pred. No. 5.4e-51;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1' APPVAGPSVFLPPKPKDTLMISRTEPVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 217 appvagsvflppkpkdtlmsrtpevtcvcvvdvshedpevqfnwvydgvvevhnaktkp 276
 QY 61 REEQNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIEKTISKTK 109
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 277 reeqnstfrvsvltvvhqdwlngkeyckvsnkglpapiektisktk 325

RESULT 12
 AAB72230
 ID AAB72230 standard; Protein; 442 AA.
 XX
 AC AAB72230;
 XX
 DT 10-MAY-2001 (first entry)
 XX
 DE Humanised 323/A3 (IgG2cys) antibody heavy chain amino acid sequence.
 XX
 KW Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
 KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
 KW heavy chain.
 XX
 OS Mus sp.
 OS Homo sapiens.
 XX
 PN WO200107082-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 23-JUL-1999; 99WO-EP05271.
 XX
 PR 23-JUL-1999; 99WO-EP05271.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Knick VC, Stimmel JB, Thurmond LM;
 XX
 DR WPI; 2001-182729/18.
 DR N-PSDB; AAF63376.
 XX
 PT Combination for treating cancer (e.g. breast, gastric or prostate
 PT cancers), or in the manufacture of a medicament for anti-cancer
 PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody
 PT with a chemotherapeutic agent -
 XX
 PS Disclosure; Fig 18; 103pp; English.

XX This invention relates to a combination of an anti-Ep-CAM (cyclic
 CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is
 CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
 CC phase or the second growth phase (M) of cell enlargement (G2)/DNA
 CC replication. The antibody exhibits cytostatic activity and is useful in
 CC the manufacture of a medicament for use in anti-cancer therapy,
 CC characterised in that a chemotherapeutic agent, which is capable of
 CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is
 CC co-administered to a patient with an anti-Ep-CAM antibody. The
 CC combination is useful for treating cancer, particularly colorectal
 CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
 CC lung cancer. The present sequence represents the heavy chain of
 CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG2cys) which can be
 CC used in the combination of the invention.
 XX

SQ Sequence 442 AA;
 Query Match 100.0%; Score 583; DB 22; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5.5e-51;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTEPVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 227 appvagsvflppkpkdtlmsrtpevtcvcvvdvshedpevqfnwvydgvvevhnaktkp 286

QY 61 REEQNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIEKTISKTK 109
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 287 reeqnstfrvsvltvvhqdwlngkeyckvsnkglpapiektisktk 335
 RESULT 13
 AAY31670
 ID AAY31670 standard; Protein; 443 AA.
 XX
 AC AAY31670;
 XX
 DT 09-NOV-1999 (first entry)
 XX
 DE Human IgG2 chain C.
 XX
 KW IgG2; C-gamma-2; antibody; fusion protein; circulating half-life;
 KW human; drug delivery.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..117
 FT /note= "the identity of these residues is not
 FT specified"
 XX
 PN WO9943713-A1.
 XX
 PD 02-SEP-1999.
 XX
 PF 24-FEB-1999; 99WO-US03966.
 XX
 PR 25-FEB-1998; 98US-0075887.
 XX
 PA (LEXI-) LEXIGEN PHARM CORP.
 XX
 PI Gillies SD, Lan Y, Lo K, Wesolowski J;
 XX
 DR WPI; 1999-527594/44.
 XX

XX New antibody-based fusion proteins, used for the delivery of e.g. a
 PT cytokine, ligand-binding protein or protein toxin to target cells in
 PT vivo
 XX
 PS Disclosure; Page 32-33; 41pp; English.

XX The present sequence represents the constant region of human IgG
 CC isotype 2 (IgG2, C-gamma-2). C-gamma-1 (see AAY31669) and C-gamma-3
 CC (see AAY31671) bind Fc receptors with high affinity, whereas C-gamma-4
 CC (see AAY31672) has 10-fold lower binding affinity and C-gamma-2 does
 CC not bind to Fc receptor gamma-1. The invention provides methods
 CC for the genetic construction and expression of antibody-based
 CC fusion proteins with enhanced circulating half-lives. The
 CC fusion proteins lack the ability to bind to immunoglobulin Fc
 CC receptors, either as a consequence of the antibody isotype used
 CC for protein construction, i.e. a C-gamma-2 constant region (Fc)
 CC or a C-gamma-4 Fc receptor, or through directed mutagenesis of
 CC antibody isotypes that normally bind Fc receptors, i.e. C-gamma-1
 CC or C-gamma-3. The methods can be used for to increase the
 CC circulating half-life of a non-immunoglobulin (Ig) protein such as
 CC a cytokine, e.g. tumour necrosis factor (TNF), an interleukin or a
 CC lymphokine such as a lymphotoxin or a colony stimulating factor, a
 CC ligand-binding protein, e.g. CD4, CTLA-4, TNF receptor or an
 CC interleukin receptor, or a protein toxin (claimed). The fusion
 CC proteins are used to deliver selectively the second non-Ig protein
 CC to a target cell in vivo so that the second non-Ig protein can
 CC exert a localised biological effect.

SQ Sequence 443 AA;
 Query Match 100.0%; Score 583; DB 20; Length 443;
 Best Local Similarity 100.0%; Pred. No. 5.5e-51;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNMYVDGVEVHNATKTP 60
 |||||
 Db 228 appvagsvflfpkpkdtlmisrtpevtcvvvdvshedpevqfnvydgvvevhnaktkp 287
 |||||

QY 61 REEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIETISKTK 109
 |||||
 Db 288 reeqfnstfrvsvltvvhqdwlngkeyckvsnkglpapietisktk 336
 |||||

RESULT 14
 AAY93734
 ID AAY93734 standard; Protein; 451 AA.
 XX
 AC AAY93734;
 DT 03-OCT-2000 (first entry)
 XX
 DE The heavy chain of immunoglobulin clone 11.2.1.
 XX
 KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
 KW proliferative disorder; cancer; immunodeficient disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200037504-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 23-DEC-1999; 99WO-US30895.
 XX
 PR 23-DEC-1998; 98US-0113647.
 XX
 PA (PFIZ) PFIZER INC.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
 PI Corvalan JR;
 XX
 DR WPI: 2000-442647/38.
 DR N-PSDB; AAA46898.
 XX
 XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful
 PT for treating, e.g. immune disorders -
 XX
 PS Claim 2; Fig 22q; 157pp; English.
 XX
 CC The present sequence represents a heavy chain of an antibody of the
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
 CC variable region, comprising a modified contiguous sequence from a
 CC FRL-PR3 sequence encoded by a human VH3-33 family gene. The
 CC modifications are contained in CDRI, CDR2 and/or framework regions.
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune
 CC disease, diabetes and graft rejection) and proliferative disorders
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
 CC immune system to up-regulate immunodeficient disorders.
 XX
 SQ Sequence 451 AA;

Query Match 100.0%; Score 583; DB 21; Length 451;
 Best Local Similarity 100.0%; Pred. No. 5.7e-51;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNMYVDGVEVHNATKTP 60
 |||||
 Db 236 appvagsvflfpkpkdtlmisrtpevtcvvvdvshedpevqfnvydgvvevhnaktkp 295
 |||||

QY 61 REEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIETISKTK 109
 |||||
 Db 296 reeqfnstfrvsvltvvhqdwlngkeyckvsnkglpapietisktk 344
 |||||

RESULT 15
 AAB72236
 ID AAB72236 standard; Protein; 461 AA.
 XX
 AC AAB72236;
 DT 10-MAY-2001 (first entry)
 XX
 DE Humanised 323/A3 (IgG2cys) antibody heavy chain amino acid sequence.
 XX
 KW Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
 KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
 KW heavy chain.
 XX
 OS Mus sp.
 OS Homo sapiens.
 XX
 PN WO200107082-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 23-JUL-1999; 99WO-EP05271.
 XX
 PR 23-JUL-1999; 99WO-EP05271.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Knick VC, Stimmel JB, Thurmond LM;
 XX
 DR WPI: 2001-182729/18.
 XX
 PT Combination for treating cancer (e.g. breast, gastric or prostate
 PT cancers), or in the manufacture of a medicament for anti-cancer
 PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody
 PT with a chemotherapeutic agent -
 XX
 PS Example 8; Fig 14; 103pp; English.
 XX
 CC This invention relates to a combination of an anti-Ep-CAM (cyclic
 CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is
 CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
 CC phase or the second growth phase (M) of cell enlargement (G2)/DNA
 CC replication. The antibody exhibits cytostatic activity and is useful in
 CC the manufacture of a medicament for use in anti-cancer therapy,
 CC characterised in that a chemotherapeutic agent, which is capable of
 CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is
 CC co-administered to a patient with an anti-Ep-CAM antibody. The
 CC combination is useful for treating cancer, particularly colorectal
 CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
 CC lung cancer. The present sequence represents the heavy chain of
 CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG2cys) which can be
 CC used in the combination of the invention.
 XX
 SQ Sequence 461 AA;

Query Match 100.0%; Score 583; DB 22; Length 461;
 Best Local Similarity 100.0%; Pred. No. 5.8e-51;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNMYVDGVEVHNATKTP 60
 |||||
 Db 246 appvagsvflfpkpkdtlmisrtpevtcvvvdvshedpevqfnvydgvvevhnaktkp 305
 |||||

QY 61 REEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIETISKTK 109
 |||||
 Db 306 reeqfnstfrvsvltvvhqdwlngkeyckvsnkglpapietisktk 354
 |||||

Search completed: June 21, 2002, 08:36:07
Job time: 321 sec

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	535	91.8	701	4	Q96PQ8	Q96pq8 homo sapien
2	450	77.2	337	6	Q95M34	Q95m34 equus caball
3	421	72.2	437	11	Q9RIA4	Q9ria4 mus musculus
4	431	72.2	463	11	Q9RIC4	Q9ric4 mus musculus
5	388	66.6	473	11	Q9DBI4	Q9dbi4 mus musculus
6	388	66.6	473	11	Q9I2O5	Q9i2o5 mus musculus
7	380	65.2	468	11	Q99L31	Q99l31 mus musculus
8	330	65.2	473	11	Q99L25	Q99l25 mus musculus
9	145	24.9	375	4	Q9BSZ1	Q9bsz1 homo sapien
10	145	24.9	597	4	Q9BOB8	Q9bob8 homo sapien
11	145	24.9	597	4	Q9BUL0	Q9bul0 homo sapien
12	145	24.9	597	4	Q96BB9	Q96bb9 homo sapien
13	145	24.9	613	4	Q96EY0	Q96ey0 homo sapien
14	145	24.9	614	4	Q96GA6	Q96ga6 homo sapien
15	145	24.9	618	4	Q96AA6	Q96aa6 homo sapien
16	123.5	21.2	384	4	Q9UP60	Q9up60 homo sapien

```
AC Q95M34;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE IMMUNOGLOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
DE (FRAGMENT).
GN IGHG1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [12]
RA Wagner B.;
RA Wagner B.; Overesch G.; Sheoran A.; Holmes M.; Richards C.;
RA Leibold W.; Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199;105-119(1998).
DR EMBL; AJ300675; CAC44624.1; -.
FT NON_TER 1
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 77.2%; Score 450; DB 6; Length 337;
Best Local Similarity 74.5%; Pred. No. 4.4e-42;
Matches 79; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTKPREE 63
Db 123 LGGPSVFIFPPPKDVLITLTPKVTCTVVDVSKDDPEVQFSWFDVHTAQTQPREQFNS 182

QY 64 QFNSTRVSVLTVVHODWLNKGKCKVSNKGLPAPIETISKTK 109
Db 183 QFNSTRVSVLRIQHDLWSGKFRCKVNNQALPQPIETITTK 228

RESULT 3
Q9RIA4 PRELIMINARY; PRT; 437 AA.
ID Q9RIA4;
AC Q9RIA4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
```

```
Query Match 72.2%; Score 421; DB 11; Length 437;
Best Local Similarity 73.5%; Pred. No. 1.e-38;
Matches 75; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 8 SVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTKPREQFNS 67
Db 229 SVFIFPPKPKDVLITLTPKVTCTVVDVSKDDPEVQFSWFDVHTAQTQPREQFNS 288

QY 68 TFRVSVLTVVHODWLNKGKCKVSNKGLPAPIETISKTK 109
Db 289 TFRSVSELPIMHODWLNKGKFCRVNSAAPPAPIETISKTK 330

RESULT 4
Q99LC4 PRELIMINARY; PRT; 463 AA.
ID Q99LC4;
AC Q99LC4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 72.2%; Score 421; DB 11; Length 463;
Best Local Similarity 73.5%; Pred. No. 1.e-38;
Matches 75; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 8 SVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTKPREQFNS 67
Db 255 SVFIFPPKPKDVLITLTPKVTCTVVDVSKDDPEVQFSWFDVHTAQTQPREQFNS 314

QY 68 TFRVSVLTVVHODWLNKGKCKVSNKGLPAPIETISKTK 109
Db 315 TFRSVSELPIMHODWLNKGKFCRVNSAAPPAPIETISKTK 356

RESULT 5
Q9DBL4 PRELIMINARY; PRT; 473 AA.
ID Q9DBL4;
AC Q9DBL4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE 1810060009RIK PROTEIN.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK007918; BAB25349.1; -.
DR HSSP: P01842; 7FAB.
DR MGD: MGI:96443; Igh-1.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGC1; 3.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IG_like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 66.6%; Score 388; DB 11; Length 473;
Best Local Similarity 62.3%; Pred. No. 5.6e-35;
Matches 71; Conservative 18; Mismatches 19; Indels 6; Gaps 1;

QY 2 PPVA-----GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHN 55
Db 253 PCPAAPDLGGPSVFIFPPKIKDVLMSLSPMTVCVVVDVSEDDPDVQISWFVNVEVHT 312

QY 56 AKTKPREQFNSTFRVSVLTVVHQDLNGKEYCKVSKNGLPAPIEKTISKTK 109
Db 313 AQQTREDYNSTLRVVSALPIQHDWMSGKFKCKVKNRNLALPSPIEKTISKPR 366

RESULT 6
QY91205 ID Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 51.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

```

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Query Match 66.6%; Score 388; DB 11; Length 473;
Best Local Similarity 66.3%; Pred. No. 5.6e-35;
Matches 69; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

QY 6 GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNKTKPREEQF 65
Db 263 GRSVFIFPPKIKDVLMSLTPKTCVVVDVSEDDPDVQISWFVNVEVHTAQQTREDY 322

QY 66 NSTFRVSVLTVVHQDLNGKEYCKVSKNGLPAPIEKTISKTK 109
Db 323 NSTIRVVSALPIQHDWMSGKFKCKVKNKDLPSPIERTISKIK 366

RESULT 7
QY9L31 ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC003878; AAH03878.1; -.
DR HSSP: P01842; 7FAB.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGC1; 3.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IG_like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 65.2%; Score 380; DB 11; Length 468;
Best Local Similarity 65.1%; Pred. No. 4.3e-34;
Matches 69; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 4 VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNKTKPREE 63
Db 256 LGGPSVFIFPPKIKDVLMSLSPMTVCVVVDVSEDDPDVQISWFVNVEVHTAQQTRE 315

QY 64 QNSTFRVSVLTVVHQDLNGKEYCKVSKNGLPAPIEKTISKTK 109
Db 316 DYNSTLRVVSALPIQHDWMSGKFKCKVKNKALPAPIERTISKPK 361

RESULT 8
QY9L25 ID Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC003888; AAH03888.1; -
DR HSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 65.2%; Score 380; DB 11; Length 473;
Best Local Similarity 65.1%; Pred. No. 4.3e-34;
Matches 69; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVVHNNAKTKPREE 63
DB 261 LGGFSVFIFFPKDKVIMLSLSPWTCVVVDSEDDPDVQISWFWNVNVEVLTAAQTTHRE 320
QY 64 QFNSTFRVSVLTVVHQQDLNGLNGKEYCKVSNKGLPAPIETKISKTK 109
DB 321 DYNSTLRVVSALPIQHDWMSGKEFKCKVNNKALPAPIERTISKPK 366

RESULT 9
ID Q9BSZ1 PRELIMINARY; PRT; 375 AA.
AC Q9BSZ1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 41.3 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH, LYMPHOMA;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC004476; AAH04476.1; -
DR HSP; P01857; 1FC1.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 375 AA; 41314 MW; B1A0A0998F473619 CRC64;

Query Match 24.9%; Score 145; DB 4; Length 375;
Best Local Similarity 29.7%; Pred. No. 5.6e-08;
Matches 30; Conservative 25; Mismatches 44; Indels 2; Gaps 2;

QY 9 VFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVVHNNAKTKPREEQFNST 68
DB 146 VFAIPPS-FASIFLTKSTKLTCLVTLDTYD-SVTISWTRQNGEAVKTHNTISESHPNAT 203
QY 65 FRVVSVLTVVHQQDLNGLNGKEYCKVSNKGLPAPIETKISKTK 109
DB 204 FSAVGEASICDDWNSGERFTCVVTHDLPSPKQITSRPK 244

RESULT 10
Q9BQB8 PRELIMINARY; PRT; 597 AA.
ID Q9BQB8;
AC Q9BQB8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RHABDOMYOSARCOMA;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPHOMA;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC006180; AAH06180.1; -
DR EMBL; BC001872; AAH01872.1; -
DR HSP; P01825; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 24.9%; Score 145; DB 4; Length 597;
Best Local Similarity 29.7%; Pred. No. 9.9e-08;
Matches 30; Conservative 25; Mismatches 44; Indels 2; Gaps 2;

QY 9 VFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVVHNNAKTKPREEQFNST 68
DB 368 VFAIPPS-FASIFLTKSTKLTCLVTLDTYD-SVTISWTRQNGEAVKTHNTISESHPNAT 425
QY 69 FRVVSVLTVVHQQDLNGLNGKEYCKVSNKGLPAPIETKISKTK 109
DB 426 FSAVGEASICDDWNSGERFTCVVTHDLPSPKQITSRPK 466

RESULT 11
ID Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 65.3 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH, LYMPHOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC002963; AAH02963.1; -
DR HSP; P01825; 7FAB.
DR InterPro; IPR003599; Ig.

NW hypometrical protein.
SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;

Db 426 FSAVGFASTCEDDWSNGERFCTVYTHDTLPSPIKOTISPPK 166

Search completed: June 21, 2002, 08:59:31
Job time: 1630 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:00:24 ; Search time 48.19 Seconds
(without alignments)
87.579 Million cell updates/sec

Title: US-09-674-857-5
Perfect score: 583
Sequence: 1 APPVAGPSVFLPPKPKDTL.....CKVSNKGLPAPIETISKTK 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	593	100.0	326	1 GC2_HUMAN	P01859 homo sapien
2	535	91.8	330	1 GC1_HUMAN	P01857 homo sapien
3	528	90.6	327	1 GC4_HUMAN	P01861 homo sapien
4	527	90.4	290	1 GC3_HUMAN	P01860 homo sapien
5	456	74.8	329	1 GC2_CAVPO	P01862 cavia porce
6	429	73.6	323	1 GC_RABIT	P01870 oryctolagus
7	428	73.4	333	1 GCB_RAT	P02761 rattus norv
8	421.5	72.3	329	1 GC3_MOUSE	P22436 mus musculu
9	421.5	72.3	398	1 GC3_MOUSE	P03987 mus musculu
10	421	72.2	324	1 GC1_MOUSE	P01868 mus musculu
11	421	72.2	393	1 GC1_MOUSE	P01869 mus musculu
12	405	69.5	329	1 GCC_RAT	P20762 rattus norv
13	389	66.7	326	1 GC1_RAT	P20759 rattus norv
14	389	66.7	330	1 GCAA_MOUSE	P01865 mus musculu
15	389	66.7	399	1 GCAM_MOUSE	P01863 mus musculu
16	388	66.6	335	1 GCAB_MOUSE	P01864 mus musculu
17	388	66.6	336	1 GCB_MOUSE	P01866 mus musculu
18	388	66.6	405	1 GCBM_MOUSE	P01867 mus musculu
19	333	60.5	322	1 GCA_RAT	P20760 rattus norv
20	170.5	29.2	428	1 EPC_HUMAN	P01854 homo sapien
21	154	26.4	429	1 EPC_RAT	P01855 rattus norv
22	153	26.2	421	1 EPC_MOUSE	P06336 mus musculu
23	148	25.4	457	1 MUC_SUNMU	P20768 suncus muri
24	146	25.0	391	1 MUCB_HUMAN	P04220 homo sapien
25	145	24.9	454	1 MUCB_HUMAN	P01871 homo sapien
26	140	24.0	106	1 KAC_HUMAN	P01834 homo sapien
27	139	23.8	454	1 MUC_MESAU	P06337 mesocricetu
28	139	23.8	455	1 MUC_MOUSE	P01872 mus musculu
29	139	23.8	476	1 MUC_MOUSE	P01873 mus musculu
30	134.5	23.1	299	1 ALC_RABIT	P01879 oryctolagus
31	127	21.8	458	1 MUC_RABIT	P03988 oryctolagus
32	127	21.8	479	1 MUCM_RABIT	P04221 oryctolagus
33	124.5	21.4	450	1 MUC_CANFA	P01874 canis famil

ALIGNMENTS

RESULT 1

ID	GC2_HUMAN	STANDARD;	PRT;	326 AA.
AC	P01859;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig gamma-2 chain C region.			
DE	IGHG2.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE OF 2-326 FROM N.A.			
RX	MEDLINE=82197621; PubMed=6804948;			
RA	Ellison J.W., Hood L.E.;			
RT	"Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).			
RL	[2]			
RN				
RP	SEQUENCE OF 88-115 FROM N.A.			
RC	TISSUE=Fetal liver;			
RX	MEDLINE=83001943; PubMed=6811139;			
RA	Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;			
RT	"Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";			
RT	Cell 29:671-679(1982).			
RL	[3]			
RN				
RP	SEQUENCE OF 99-177 AND 310-326 FROM N.A.			
RC	TISSUE=Fetal liver;			
RX	MEDLINE=84235992; PubMed=6329676;			
RA	Krawinkel U., Rabbitts T.H.;			
RT	"Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes.";			
RT	EMBO J. 1:403-407(1982).			
RL	[4]			
RN				
RP	SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).			
RX	MEDLINE=81007873; PubMed=6774012;			
RA	Wang A.-C., Tung E., Fudenberg H.H.;			
RT	"The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.";			
RT	J. Immunol. 125:1048-1054(1980).			
RL	[5]			
RN				
RP	SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).			
RX	MEDLINE=80001357; PubMed=113060;			
RA	Connell G.E., Parr D.M., Hofmann T.;			
RT	"The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";			
RT	Can. J. Biochem. 57:758-767(1979).			
RL	[6]			
RN				
RP	SEQUENCE OF 238-275 (ZIE).			
RX	MEDLINE=80114419; PubMed=118920;			
RA	Hofmann T., Parr D.M.;			
RT	"A note of the amino acid sequence of residues 381-391 of human			

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RT  immunoglobulins gamma chains." ;
RL  Mol. Immunol. 16:923-925(1979).
RN  [7]
RA  REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RP  Hofmann T., Parr D.M.;
RL  Submitted (MAR-1980) to the PIR data bank.
RN  [8]
RA  SEQUENCE OF 1-121 (DOT).
RP  MEDLINE=9525298; PubMed=7737190;
RX  Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT  "Characterization of the two unique human anti-flavin monoclonal
RN  immunoglobulins." ;
RL  Eur. J. Biochem. 228:886-893(1995).
RN  [9]
RA  DISULFIDE BONDS.
RP  MEDLINE=72033500; PubMed=4940472;
RX  Milstein C., Frangione B.;
RT  "Disulphide bridges of the heavy chain of human immunoglobulin G2." ;
RL  Biochem. J. 121:217-225(1971).
RN  [10]
RA  DISULFIDE BONDS.
RP  MEDLINE=69064124; PubMed=5782707;
RX  Frangione B., Milstein C., Pink J.R.L.;
RT  "Structural studies of immunoglobulin G." ;
RL  Nature 221:145-148(1969).
RN  [11]
RA  -----
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CC  -----
DR  EMBL; J00230; AAB59393.1; -.
DR  PIR; A02148; G2HU
DR  HSRP; P01857; 1FC1.
DR  MIM; 147110; -.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003597; Ig_C1.
DR  InterPro; IPR003600; Ig_Like.
DR  Pfam; PF00047; Ig_3.
DR  SMART; SM00410; Ig_Like; 1.
DR  SMART; SM00407; IGL1; 2.
DR  PROSITE; PS00290; IG_MHC; 2.
DR  Immunoglobulin domain; Immunoglobulin C region.
DR  NON_TER 1
FT  DOMAIN 1 98
FT  DOMAIN 99 110
FT  HINGE.
FT  DOMAIN 111 219
FT  DOMAIN 220 326
FT  DISULFID 14 14
FT  INTERCHAIN (WITH A LIGHT CHAIN).
FT  DISULFID 27 83
FT  INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID 102 102
FT  INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID 103 103
FT  INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID 106 106
FT  INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID 109 109
FT  INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID 140 200
FT  DISULFID 246 304
FT  DISULFID 155 155
FT  SITE 156 156
FT  MOD_RES 326 326
FT  VARIANT 60 60
FT  CONFLICT 109 109
FT  SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
SQ
Query Match 100.0%; Score 583; DB 1; Length 326;
Best Local Similarity 100.0%; Pred. No. 3e-52;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTKP 60
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Db 111 APPVAGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVVHNAKTKP 170
QY 61 REEQFNSTRFVSVLTVVHQQDLNGKEYKCKVSNKGLPAPIETISKTK 109
|||||
Db 171 REEQFNSTRFVSVLTVVHQQDLNGKEYKCKVSNKGLPAPIETISKTK 219
RESULT 2
GCL_HUMAN
ID GCL_HUMAN STANDARD; PRT; 330 AA.
AC P01857.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W.; Berson B.J.; Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene." ;
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A.; Rutishauser U.; Gall W.E.; Gottlieb P.D.;
RA Waxdal M.J.; Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RL acid sequence of heavy-chain cyanogen bromide fragments H1-H4." ;
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U.; Cunningham B.A.; Bennett C.; Konigsberg W.H.;
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RL acid sequence of heavy-chain cyanogen bromide fragments H5-H7." ;
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H.; Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a
RL monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The
RL chymotryptic peptides of the H-chain, alignment of the tryptic
RL peptides and discussion of the complete structure." ;
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E.; Jung H.-D.; Palm W.; Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RL structure of crystallized monoclonal immunoglobulin IgG1 KOL, I." ;
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E.; Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RL Intrachain disulfide bonds." ;
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L.; Schwarz J.; Reichel W.; Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RL IgG1 immunoglobulin (myeloma protein NIE). I: Purification and
RL characterization of the protein, the L- and H-chains, the
RL cyanogen bromide cleavage products, and the disulfide bridges." ;
RT

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RL Hoppé-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RA MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -!- MISCELLANEOUS: NIE HAS THE GLM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GLM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GLM(3)
 CC MARKER & THE GLM (NON-1) MARKERS.
 CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
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 DR EMBL; J00228; AAC82527.1; ALT_INIT.
 DR PIR; A02146; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR MIM; 147100; -.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; Ig_like; 1.
 DR SMART; SM00407; Ig_c1; 2.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 1 98
 FT DOMAIN 99 110
 FT DOMAIN 111 223
 FT DOMAIN 224 330
 FT DISULFID 27 83
 FT DISULFID 103 103
 FT DISULFID 109 109
 FT DISULFID 112 112
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 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT STRAND 123 126
 FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 148
 FT STRAND 158 162
 FT TURN 163 164
 FT STRAND 165 166
 FT STRAND 175 178
 FT STRAND 183 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 206

FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 240
 FT TURN 241 242
 FT STRAND 245 256
 FT STRAND 260 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 324
 SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;
 Query Match 91.8%; Score 535; DB 1; Length 330;
 Best Local Similarity 87.7%; Pred. No. 2.4e-47;
 Matches 100; Conservative 5; Mismatches 3; Indels 6; Gaps 1;
 QY 2 PP-----VAGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 55
 || : |||||
 Db 110 PPCPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 169
 QY 56 AKTKPREQFNSTFVSVVLTVVHODWLNKKEYCKVSKNGLPAPLEKTSKTK 109
 |||||
 Db 170 AKTKPREQFNSTFVSVVLTVVHODWLNKKEYCKVSKNGLPAPLEKTSKTK 223
 RESULT 3
 GC4_HUMAN
 ID GC4_HUMAN STANDARD; PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-4 chain C region.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83157104; PubMed=6299662;
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 1:11-18(1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE=70207560; PubMed=4192699;
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 RT constant region of a gamma 4 chain.";
 RL Biochem. J. 117:33-47(1970).
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 DR EMBL; K01316; AAB59394.1; ALT_INIT.
 DR PIR; A02150; G4HU.
 DR HSP; P01842; 7FAB.


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FT VARIANT      227      227      S -> N (IN OMM).
FT VARIANT      227      227      /FTid=VAR_003894.
FT VARIANT      227      227      MISSING (IN ZUC).
FT VARIANT      279      279      /FTid=VAR_003895.
FT VARIANT      279      279      F -> Y (IN OMM).
FT SEQUENCE     290 AA; 32331 MW; E59CB9C95705B2F46 CRC64;

Query Match      90.4%; Score 527; DB 1; Length 290;
Best Local Similarity 91.5%; Pred. NO. 1.3e-46;
Matches 97; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY      4 VAGPSVFLFPKPKDTLMISRPETCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPRE 63
DB      78 LGGPSVFLFPKPKDTLMISRPETCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREQ 137

QY      64 QPNSTFRVSVLTVHQWLNGKEYCKVSNKGLPAPIEKTISKTK 109
DB      138 QPNSTFRVSVLTVHLQNLDCKEYCKVSNKALPAPIEKTISKTK 183

RESULT 5
GC2_CAVPO
ID GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshstein B.K., Hussain Q.Z., Cebrá J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cystine joining heavy and light chains."
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebrá J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments."
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebrá J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies."
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebrá J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies."
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin."

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RL Biochemistry 10:26-31(1971).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; 2FGP.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 16
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match      74.8%; Score 436; DB 1; Length 329;
Best Local Similarity 74.5%; Pred. NO. 2.9e-37;
Matches 82; Conservative 10; Mismatches 16; Indels 2; Gaps 1;

QY      2 PP--VAGPSVFLFPKPKDTLMISRPETCVVVDVSHEDPEVQFNWYDGVGVHNAKTK 59
DB      112 PPENLGSPSVFLFPKPKDTLMISLTPRTCVVVDVSDPEVQFTWFDNKPVGNAETK 171

QY      60 PREQFNSTFRVSVLTVHQWLNGKEYCKVSNKGLPAPIEKTISKTK 109
DB      172 PRVEQNTFRVSVLPIQHQLRGKFKCKVKNKALPAPIEKTISKTK 221

RESULT 6
GC_RABIT
ID GC_RABIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-I haplotype."
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype."
RL Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes."
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.

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RX MEDLINE=70110015; PubMed=5461106;
RA Frucher R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RL immunoglobulin G.";
RL Biochem. J. 116:245-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (In) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC -I- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC MARKERS AND REF.5 THE E15 MARKER.
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CC -----
CC EMBL: M16426; AAA31289.1; -
DR PIR: A02161; GHRB.
DR HSSP: P01857; 1FC1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_c1.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00407; IGc1; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 73.6%; Score 429; DB 1; Length 323;
Best Local Similarity 71.8%; Pred. No. 1.5e-36;
Matches 79; Conservative 11; Mismatches 18; Indels 2; Gaps 1;

QY 2 PP--VAGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTK 59
DB 11 : ||||| ||||| : ||||| ||||| : ||||| ||||| : ||||| ||||| :
107 PPELLGQSVFIFPPKDKTLMISRTPEVTCVVVDVSDQDPEVQFTWYINNEQVETARPP 166

QY 60 PREEQFNSTFRVSVLTIVHVDWLNKGKCKVSNKGLPAPIETKTK 109
DB 11 : ||||| ||||| : ||||| ||||| : ||||| ||||| : ||||| ||||| :
167 LREQQFNSTIRVSTLPITHQDWLRGKFKCKVHNKALPAPIETKISKAR 216

RESULT 7
GCB_RAT
ID GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Bruggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR: PS0018; PS0018.
DR HSSP: P01842; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_c1.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00410; IG-like; 1.
DR SMART: SM00407; IGc1; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 73.4%; Score 428; DB 1; Length 333;
Best Local Similarity 70.8%; Pred. No. 1.9e-36;
Matches 75; Conservative 19; Mismatches 12; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVQFNWYDGVGVHNAKTKPREE 63
DB 121 LGGPSVFIFPPKDKILLISQNAKVTCTVVVDVSEEDPDVQFSWFVNNVEVHTAQTPREE 180

QY 64 QFNSTFRVSVLTIVHVDWLNKGKCKVSNKGLPAPIETKISKTK 109
DB 181 QYNSTFRVSVLPIQHDWMSGKFKCKVNNKALPSPIEKTSKPK 226

RESULT 8
GCB_MOUSE
ID GCB_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
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FT DISULFID 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT DISULFID 244 302 POTENTIAL.
FT TRANSMEM 340 357 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 358 393
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7AICE27 CRC64;

Query Match 72.2%; Score 421; DB 1; Length 393;
Best Local Similarity 73.5%; Pred. No. 1.2e-35;
Matches 75; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 8 SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNKATKPREEQFNS 67
Db 116 SVFIFFPKPKDVLITLTLPKVTCTVVDVSKDPDQVQSFVDFVDEVHTAQTQPREEQFNS 175

QY 68 TFRVSVLTVVHODWLNKGEYKCKVSNKGLPAPIETISKTK 109
Db 176 TFRSVSELPIMHODWLNKGEYKCKVSNKGLPAPIETISKTK 217

RESULT 12
GCC_RAT ID GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2C heavy chain constant
region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
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CC -----
CC EMBL; X07189; CAA30169.1; -.
CC PIR; S00847; S00847.
CC HSSP; P01857; 1FC1.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig_C1.
CC InterPro; IPR003600; Ig_Like.
CC Pfam; PF00047; Ig_3.
CC SMART; SM00410; IG_Like; 1.
CC SMART; SM00407; IG_C1; 2.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
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FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 69.5%; Score 405; DB 1; Length 329;
Best Local Similarity 69.9%; Pred. No. 4.2e-34;
Matches 72; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 7 PSYFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNKATKPREEQFN 66
Db 120 PSYFIFFPKPKDILMITLTLPKVTCTVVDVSEEPDQVQSFVDFVDEVHTAQTQPREEQFN 179

QY 67 STRFVSVLTVVHODWLNKGEYKCKVSNKGLPAPIETISKTK 109
Db 180 GTFRVVSTLTIHQDWMGSKGEYKCKVSNKGLPAPIETISKTK 222

RESULT 13
GCC_RAT ID GCC_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
RL PIR; PS0017; PS0017.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00407; IG_C1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 66.7%; Score 389; DB 1; Length 326;
Best Local Similarity 68.0%; Pred. No. 1.8e-32;
Matches 68; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

QY 8 SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNKATKPREEQFNS 67
Db 118 SVFIFFPKPKDVLITLTLPKVTCTVVDVSDQDPEVHFSVDFVDEVHTAQTQPREEQFNS 177

QY 68 TFRVSVLTVVHODWLNKGEYKCKVSNKGLPAPIETISKTK 107
Db 178 TFRSVSELPILHQDWLNKGEYKCKVSNKGLPAPIETISKTK 217

RESULT 14
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GCMA_MOUSE STANDARD; PRT; 330 AA.
ID GCMA_MOUSE
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-2A chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=81076554; PubMed=6777755;
RA Skotav J.L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RL Balb/c gamma 2a heavy chain messenger RNA."
RL Nucleic Acids Res. 8:3143-3155(1980).
[2]
SEQUENCE FROM N.A.
MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
and evolution of heavy chain genes: further evidence for intervening
sequence-mediated domain transfer."
RL Nucleic Acids Res. 9:1365-1381(1981).
[3]
SEQUENCE FROM N.A.
MEDLINE=81223894; PubMed=6787604;
RA Ollo R., Auffray C., Morchamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
suggests that exons can be exchanged between genes in a multigenic
family."
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
[4]
MYELOMA PROTEIN MOPC 173.
MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
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immunoglobulin:amino-acid sequence of the Fc fragment. Implications
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RL Eur. J. Biochem. 43:423-435(1974).
[5]
DISULFIDE BONDS.
MEDLINE=73056887; PubMed=4565406;
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RL Eur. J. Biochem. 30:452-462(1972).
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EMBL; J00798; CAA24178.1; -.
PIR; A02152; G2MSA.
HSSP; P01842; 7FAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; Ig_like; 1.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
NON_TER 1
DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT

GCMA_MOUSE STANDARD; PRT; 399 AA.
ID GCMA_MOUSE
AC P01865;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=82222190; PubMed=6283537;
RA Yamawaki-kataoka Y., Nakai S., Miyata T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
[2]
ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED-
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
SEGMENT OF MU CHAINS.
[3]
MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
THE A ALLELE.
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EMBL; J00471; AAB59661.1; ALT_INIT.
PIR; A02154; G2MSAM.
HSSP; P01857; 1FCL.
MGD; MGI:96443; Igh-1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; Ig_like; 1.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Transmembrane; Alternative splicing.
NON_TER 1
DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 15 15
FT DISULFID 15 15 INTERCHAIN (WITH A HEAVY CHAIN).
FT

Query Match 66.7%; Score 389; DB 1; Length 330;
Best Local Similarity 66.0%; Pred. No. 1.8e-32;
Matches 70; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; B84361C5445A6864 CRC64;

QY 4 VAGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
Db 118 LGGSPVFIFFPKIKDVLMSLSPVTCVVVDVSEDDPDQVSWFVNNVEVHTAQTQTHRE 177
QY 64 QFNSTFRVSVLTVVHODWLNKGYCKVSNKGLPAPIETKTSKTK 109
Db 178 DYNSTLRVVSALPIQHDWMSGRFKCKVNNKDLPAPIETKTSKPK 223

RESULT 15
GCMA_MOUSE
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DT 21-JUL-1986 (Rel. 01, Created)
DE 01-AUG-1991 (Rel. 19, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
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CC ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
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CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC SEGMENT OF MU CHAINS.
CC [3]
CC MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
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CC THE A ALLELE.
CC
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CC PIR; A02154; G2MSAM.
CC HSSP; P01857; 1FCL.
CC MGD; MGI:96443; Igh-1.
CC InterPro; IPR003006; Ig_MHC.
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CC FT DISULFID 15 15
CC FT DISULFID 15 15 INTERCHAIN (WITH A HEAVY CHAIN).
CC FT
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FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT DISULFID 346 363
FT TRANSMEM 364 399
FT DOMAIN 180 180
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SQ SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;

Query Match 66.7%; Score 389; DB 1; Length 399;
Best Local Similarity 66.0%; Pred. No. 2.2e-32;
Matches 70; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

QY 4 VAGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNWYVDGVEVHNAKTKPREE 63
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Db 118 LGGPSVFIAPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISWFEVNNVEVHTAQOTHRE 177

QY 64 QFNSTFRVSVLTVVHODWLNKGKCKYKSNKGLPAPIEKTISKTK 109
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Db 178 DYNSTLRVVSALPIQHDWMSGKEFKCKYNNKDLPAPIERTISKPK 223
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